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We found 64 dictionaries with English definitions that include the word *gene*:

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➤ **General** (19 matching dictionaries)

1. [gene](#) : Merriam-Webster's Online Dictionary, 10th Edition [[home](#), [info](#)]
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3. [gene](#) : Cambridge International Dictionary of English [[home](#), [info](#)]
4. [gene](#) : The Wordsmyth English Dictionary-Thesaurus [[home](#), [info](#)]
5. [gene](#) : The American Heritage® Dictionary of the English Language [[home](#), [info](#)]
6. [gene](#) : Infoplease Dictionary [[home](#), [info](#)]
7. [-gene](#), [gene](#), [gene-](#) : Dictionary.com [[home](#), [info](#)]
8. [Gene](#), [gene](#) : UltraLingua English Dictionary [[home](#), [info](#)]
9. [gene](#) : Cambridge Dictionary of American English [[home](#), [info](#)]
10. [Gene](#) : Wikipedia, the Free Encyclopedia [[home](#), [info](#)]
11. [gene](#) : Rhymezone [[home](#), [info](#)]
12. [gene](#), [gene](#) : AllWords.com Multi-Lingual Dictionary [[home](#), [info](#)]
13. [gene](#) : All About Homonyms [[home](#), [info](#)]
14. [gene](#) : Columbia Encyclopedia, Six Edition [[home](#), [info](#)]
15. [gene](#) : The New Dictionary of Cultural Literacy [[home](#), [info](#)]
16. [Gene](#) : Encarta® Online Encyclopedia, North American Edition [[home](#), [info](#)]
17. [gene](#) : WordNet 1.7 Vocabulary Helper [[home](#), [info](#)]
18. [gene](#) : LookWAYup Translating Dictionary/Thesaurus [[home](#), [info](#)]
19. [gene](#) : Encyclopedia.com [[home](#), [info](#)]

➤ **Art** (1 matching dictionary)

Quick definitions (*Gene*)

- **noun:** (genetics) a segment of DNA that is involved in producing a polypeptide chain; it can include regions preceding and following the coding DNA as well as introns between the exons; it is considered a unit of heredity (Example: "Genes were formerly called factors")
- **name:** A male given name (common: 1 in 1149 males; popularity rank in the U.S.: #200)
- **name:** A female given name (rare: 1 in 20000 females; popularity rank in the U.S.: #1299)
- **name:** A surname (very rare: popularity rank in the U.S.: #40659)

Encyclopedia article

The word "**gene**" is shared by many

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:26:23 ; Search time 26.6667 Seconds
(without alignments)
118.319 Million cell updates/sec

Title: SEQ1

Perfect score: 56
Sequence: 1 gytftsydin 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL_25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 47 | 83.9 | 448 | 16 | Q8A516 |
| 2 | 47 | 83.9 | 480 | 11 | Q8K024 |
| 3 | 47 | 83.9 | 497 | 4 | Q8WY24 |
| 4 | 45 | 80.4 | 147 | 11 | Q925S3 |
| 5 | 43 | 76.8 | 473 | 11 | Q9D8L4 |
| 6 | 42 | 75.0 | 241 | 11 | Q921A6 |
| 7 | 42 | 75.0 | 481 | 11 | Q91WT1 |
| 8 | 41 | 73.2 | 550 | 5 | O02490 |
| 9 | 40 | 71.4 | 102 | 5 | Q9VF36 |
| 10 | 40 | 71.4 | 109 | 11 | Q9JL75 |
| 11 | 40 | 71.4 | 119 | 5 | Q9GY22 |
| 12 | 40 | 71.4 | 120 | 11 | Q920E8 |
| 13 | 40 | 71.4 | 123 | 11 | Q8VJ11 |
| 14 | 40 | 71.4 | 137 | 11 | Q924R6 |
| 15 | 40 | 71.4 | 139 | 11 | Q924R5 |
| 16 | 40 | 71.4 | 140 | 11 | Q924P8 |

| | | | | | | |
|----|----|------|------|----|--------|--------------------|
| 17 | 40 | 71.4 | 140 | 11 | Q924R2 | Q924r2 mus musculu |
| 18 | 40 | 71.4 | 141 | 11 | Q924Q4 | Q924q4 mus musculu |
| 19 | 40 | 71.4 | 142 | 11 | Q924Q1 | Q924q1 mus musculu |
| 20 | 40 | 71.4 | 142 | 11 | Q924Q2 | Q924q2 mus musculu |
| 21 | 40 | 71.4 | 143 | 11 | Q91VA2 | Q91va2 mus musculu |
| 22 | 40 | 71.4 | 143 | 11 | Q924Q5 | Q924q5 mus musculu |
| 23 | 40 | 71.4 | 143 | 11 | Q91V67 | Q91v67 mus musculu |
| 24 | 40 | 71.4 | 143 | 11 | Q924Q0 | Q924q0 mus musculu |
| 25 | 40 | 71.4 | 143 | 11 | Q924R7 | Q924r7 mus musculu |
| 26 | 40 | 71.4 | 143 | 11 | Q924P6 | Q924p6 mus musculu |
| 27 | 40 | 71.4 | 143 | 11 | Q924R0 | Q924r0 mus musculu |
| 28 | 40 | 71.4 | 143 | 11 | Q924P9 | Q924p9 mus musculu |
| 29 | 40 | 71.4 | 144 | 11 | Q924P5 | Q924p5 mus musculu |
| 30 | 40 | 71.4 | 145 | 11 | Q924Q6 | Q924q6 mus musculu |
| 31 | 40 | 71.4 | 145 | 11 | Q924Q9 | Q924q9 mus musculu |
| 32 | 40 | 71.4 | 145 | 11 | Q924R3 | Q924r3 mus musculu |
| 33 | 40 | 71.4 | 145 | 11 | Q924Q7 | Q924q7 mus musculu |
| 34 | 40 | 71.4 | 145 | 11 | Q924P7 | Q924p7 mus musculu |
| 35 | 40 | 71.4 | 145 | 11 | Q924R1 | Q924r1 mus musculu |
| 36 | 40 | 71.4 | 145 | 11 | Q924R4 | Q924r4 mus musculu |
| 37 | 40 | 71.4 | 146 | 11 | Q924R8 | Q924r8 mus musculu |
| 38 | 40 | 71.4 | 146 | 11 | Q924Q3 | Q924q3 mus musculu |
| 39 | 40 | 71.4 | 146 | 11 | Q924Q8 | Q924q8 mus musculu |
| 40 | 40 | 71.4 | 278 | 11 | Q921K1 | Q921k1 mus musculu |
| 41 | 40 | 71.4 | 482 | 11 | Q8K172 | Q8k172 mus musculu |
| 42 | 40 | 71.4 | 486 | 11 | Q91207 | Q91207 mus musculu |
| 43 | 40 | 71.4 | 488 | 11 | Q8K0F2 | Q8k0f2 mus musculu |
| 44 | 40 | 71.4 | 1061 | 5 | Q9GUL6 | Q9guif caenorhabdi |
| 45 | 39 | 69.6 | 118 | 4 | Q9UL91 | Q9ul91 homo sapien |

ALIGNMENTS

RESULT 1

Q8A516 ID Q8A516 PRELIMINARY; PRT; 448 AA.
AC Q8A516;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative outer membrane protein TolC.
GN BT253.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550558; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
DR EMBL; A8016935; AA077360.1; -;
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; F:transport; IEA.
DR InterPro; IPR003423; OEP.
DR Pfam; PF02321; OEP; 2.
KW Complete proteome.
SQ SEQUENCE 448 AA; 51254 MW; E4DA4539991DFB28 CRC64;

Query Match 83.9%; Score 47; DB 16; Length 448;
Best Local Similarity 80.0%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GYFTSYDIN 10
Db 299 GYTKNYDIN 308

RESULT 2

Q8K0Z4 Q8K0Z4 PRELIMINARY; PRT; 480 AA.
 AC Q8K0Z4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to expressed sequence A1833585.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029188; AAH29188.1; -
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 2.
 DR PROSITE; PS00290; IG_MHC; 2.
 SQ SEQUENCE 480 AA; 51645 MW; 8690A63C669CDBED CRC64;

Query Match 83.9%; Score 47; DB 11; Length 480;
 Best Local Similarity 80.0%; Pred. No. 3.7;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFYSYDIN 10
 |||||:
 Db 45 GYTFISFDIS 54

RESULT 3
 Q8WY24 Q8WY24 PRELIMINARY; PRT; 497 AA.
 AC Q8WY24;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SMC66 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
 RT Identification and characterization of SMC66, a Ig-like gene which is
 RT down-regulated in colorectal cancer.
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF283666; AAL36987.1; -
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;

Query Match 83.9%; Score 47; DB 4; Length 497;
 Best Local Similarity 80.0%; Pred. No. 3.8;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYTFYSYDIN 10
 |||||:
 Db 45 GYTFISFDIS 54

Db 45 GYTFIAYDIN 54
 RESULT 4
 Q925S3 Q925S3 PRELIMINARY; PRT; 147 AA.
 AC Q925S3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MRP3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX PubMed=11819679;
 RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
 Su C.;
 RT Mechanism of exogenous nucleic acids and their precursors improving
 RT the repair of intestinal epithelium after irradiation in mice.;
 RL World J. Gastroenterol. 6:709-717(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Cui D., Zeng G., Yan X., Li X., Su C.;
 RT Cloning of mouse genes related to repairing of intestinal epithelium
 RT of the irradiated mice by treatment with the intestinal RNA of mice of
 RT the same strain.;
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
 DR EMBL; AF240166; AAK43731.1; -
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG-LIKE; 1.
 SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match 80.4%; Score 45; DB 11; Length 147;
 Best Local Similarity 80.0%; Pred. No. 2.4;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYTFYSYDIN 10
 |||||:
 Db 28 GYTFISYDID 37

RESULT 5
 Q9D8L4 Q9D8L4 PRELIMINARY; PRT; 473 AA.
 AC Q9D8L4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 1810060009Rik protein.
 GN IGH-1 OR 1810060009RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wegner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszawski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK007918; BAE25349.1; -;
 DR PIR: S26746; S26746.
 DR HSSP: P01842; 7FAB.
 DR MGD: MGI:96443; Igh-1.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; ig_3.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 1.
 SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 76.8%; Score 43; DB 11; Length 473;
 Best Local Similarity 80.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYFTSYDIN 10
 DB 45 GYFTDYIN 54

RESULT 6
 Q921A6 PRELIMINARY; PRT; 241 AA.
 AC Q921A6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-CEA 79 single chain Fv fragment (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98170165; PubMed=9509435;
 RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
 RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
 RT "Cloning and characterization of cDNAs encoding VH and VL of a
 RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
 RT generation of a single-chain Fv molecule (scfv).";
 RL Mol. Cells 7:816-819(1997).
 DR EMBL: U88067; AAB48044.1; -;
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; ig_2.
 DR SMART: SM00406; IGV; 2.
 DR PROSITE: PS00835; IG_LIKE; 2.
 FT NON_TER 1
 FT NON_TER 241
 SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 75.0%; Score 42; DB 11; Length 241;
 Best Local Similarity 70.0%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYFTSYDIN 10
 DB 26 GYFTDYIN 35

RESULT 7
 Q91WT1 PRELIMINARY; PRT; 481 AA.
 ID Q91WT1
 AC Q91WT1
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL EMBL: BC013490; AAH13490.1; -;
 DR Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; ig_4.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 2.
 KW Hypothetical protein_MHC; 2.
 SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 75.0%; Score 42; DB 11; Length 481;
 Best Local Similarity 80.0%; Pred. No. 29;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDIN 10
 DB 45 GYFTSYIIN 54

RESULT 8
 O02490 PRELIMINARY; PRT; 550 AA.
 ID O02490
 AC O02490;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Fructofuranosidase (EC 3.2.1.26).
 OS Trichomonas foetus (Trichomonas foetus).
 OC Eukaryota; Parabasalida; Trichomonadida; Trichomonadidae;
 OC Tritrichomonadinae; Tritrichomonas.
 OX NCBI_TaxID=5724;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MT85-330.1;
 RA Granger B.L., Hillemeier P.B., Warwood S.J.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
 DR EMBL: U66071; AAB51115.1; -;
 DR EMBL: U66071; AAB51117.1; -;
 DR GO: GO:0004564; F-beta-fructofuranosidase activity; IEA.
 DR GO: GO:0005975; P-carbohydrate metabolism; IEA.
 DR InterPro: IPR001362; Glyco_hydro_32.
 DR Pfam: PF00251; Glyco_hydro_32; 1.
 DR SMART: SM00640; Glyco_32; 1.
 DR PROSITE: PS00609; GLYCOSYL_HYDROL_F32; 1.
 KW Glycoprotein; Glycosidase; Hydrolase.
 SQ SEQUENCE 550 AA; 62598 MW; 4BA2DF706E1B4438 CRC64;

Query Match 73.2%; Score 41; DB 5; Length 550;
 Best Local Similarity 70.0%; Pred. No. 51;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYFTSYDIN 10


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Db 222 GYTFKYNN 231
||||| | |
222 GYTFKYNN 231

RESULT 9
Q9VF36 PRELIMINARY; PRT; 102 AA.
AC Q9VF36;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cg18505 protein.
GN ACY2 OR Cg18505.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Ballou R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista A.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fessler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mankulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003710; AAF55224.1; -
DR HSSP; P41500; 2ACV.
DR FlyBase; FBgn0038363; ACY2.
DR GO; GO:0003998; F-acylphosphatase activity; IEA.
DR InterPro; IPR001792; Acylphosphatase.
DR Pfam; PF00708; Acylphosphatase; 1.
DR PRINTS; PR00112; ACYLPHPTASE.
DR ProDom; PD001884; ACYLPHPTASE; 1.
DR PROSITE; PS00150; ACYLPHOSPHATASE 1; 1.
SQ SEQUENCE 102 AA; 11765 MW; 3CD509E7FF96F8DE CRC64;

Query Match 71.4%; Score 40; DB 5; Length 102;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFYSY 7
Db 17 GYTFYSY 23

RESULT 11
Q9GY22 PRELIMINARY; PRT; 119 AA.
AC Q9GY22;
DT 01-MAR-2001 (TREMBLrel. 15, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -
DR HSSP; P01772; 2FB4.
```

DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 119 119
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FACAB CRC64;

Query Match 71.4%; Score 40; DB 5; Length 119;
 Best Local Similarity 70.0%; Pred. No. 15;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYFTTSYDIN 10
 |||||
 Db 26 GYFTGYNN 35

RESULT 12

Q920E8 PRELIMINARY; PRT; 120 AA.

AC Q920E8
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Pterin-mimicking anti-idiotope heavy chain variable region (Fragment).
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
 RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF307936; AAL09420.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 120 120
 FT NON_TER 120 120
 SQ SEQUENCE 120 AA; 13204 MW; DC4834AB1DE56F3C CRC64;

Query Match 71.4%; Score 40; DB 11; Length 120;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTTSYDIN 10
 |||||
 Db 26 GYFTGYNN 35

RESULT 13

Q8VIJ1 PRELIMINARY; PRT; 123 AA.

AC Q8VIJ1
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-DNA heavy chain (Fragment).
 GN J558.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C3H/HeJ-lpr/lpr;
 RC MEDLINE=96409289; PubMed=6814271;

RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;
 RT "Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
 RL Eur. J. Immunol. 26:2225-2233(1996).
 DR EMBL; U59154; AAB02916.1; -
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 1.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 123 123
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13806 MW; CC0037A806E9911E CRC64;

Query Match 71.4%; Score 40; DB 11; Length 123;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTTSYDIN 10
 |||||
 Db 26 GYFTGYNN 35

RESULT 14

Q924R6 PRELIMINARY; PRT; 137 AA.

AC Q924R6
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067783; BAB63268.1; -
 DR PIR; F28833; F28833.
 DR PIR; PH1105; PH1105.
 DR PIR; PH1108; PH1108.
 DR PIR; PH1114; PH1114.
 DR PIR; PH1118; PH1118.
 DR PIR; PH1119; PH1119.
 DR PIR; PH1125; PH1125.
 DR PIR; PH1126; PH1126.
 DR PIR; PH1128; PH1128.
 DR PIR; PH1129; PH1129.
 DR PIR; PH1131; PH1131.
 DR PIR; PH1134; PH1134.
 DR PIR; PH1137; PH1137.
 DR PIR; PH1139; PH1139.
 DR PIR; PH1142; PH1142.
 DR PIR; PH1144; PH1144.
 DR PIR; PH1147; PH1147.
 DR PIR; PH1149; PH1149.
 DR PIR; PH1150; PH1150.
 DR PIR; PH1151; PH1151.
 DR PIR; PH1152; PH1152.
 DR PIR; PH1153; PH1153.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 137 137
 FT NON_TER 137 137

SQ SEQUENCE 137 AA; 15171 MW; 5C38D966DC6A4124 CRC64;
 Query Match 71.4%; Score 40; DB 11; Length 137;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSY 7
 |||||
 Db 26 GYTFTSY 32

RESULT 15
 Q924RS PRELIMINARY; PRT; 139 AA.
 AC Q924RS;
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE VH186-2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067784; BAB63269.1; -
 DR PIR; PH1137; PH1137;
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 139 139
 SQ SEQUENCE 139 AA; 15221 MW; 8491E2F85614736A CRC64;

Query Match 71.4%; Score 40; DB 11; Length 139;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSY 7
 |||||
 Db 26 GYTFTSY 32

Search completed: April 21, 2004, 17:37:13
 Job time : 28.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:48 ; Search time 5.07246 Seconds
(without alignment)
102.653 Million cell updates/sec

Title: SEQ1
Perfect score: 56
Sequence: 1 gytftsytidin 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 56 | 100.0 | 127 | 1 HV52_MOUSE | P06327 mus musculus |
| 2 | 49 | 87.5 | 120 | 1 HV03_MOUSE | P01747 mus musculus |
| 3 | 49 | 87.5 | 140 | 1 HV02_MOUSE | P01746 mus musculus |
| 4 | 41 | 73.2 | 533 | 1 INV_DEBOC | P24133 debaryomyce |
| 5 | 40 | 71.4 | 114 | 1 HV00_MOUSE | P01741 mus musculus |
| 6 | 40 | 71.4 | 117 | 1 HV04_MOUSE | P01748 mus musculus |
| 7 | 40 | 71.4 | 117 | 1 HV05_MOUSE | P01749 mus musculus |
| 8 | 40 | 71.4 | 117 | 1 HV06_MOUSE | P01750 mus musculus |
| 9 | 40 | 71.4 | 117 | 1 HV09_MOUSE | P01753 mus musculus |
| 10 | 40 | 71.4 | 117 | 1 HV10_MOUSE | P01754 mus musculus |
| 11 | 40 | 71.4 | 117 | 1 HV49_MOUSE | P06328 mus musculus |
| 12 | 40 | 71.4 | 118 | 1 HV51_MOUSE | P06330 mus musculus |
| 13 | 40 | 71.4 | 120 | 1 HV50_MOUSE | P06329 mus musculus |
| 14 | 40 | 71.4 | 137 | 1 HV11_MOUSE | P01755 mus musculus |
| 15 | 40 | 71.4 | 139 | 1 HV07_MOUSE | P01751 mus musculus |
| 16 | 40 | 71.4 | 946 | 1 IHB_DROME | O61643 drosophila |
| 17 | 39 | 69.6 | 117 | 1 HV14_MOUSE | P01758 mus musculus |
| 18 | 39 | 69.6 | 532 | 1 INV1_YEAST | P10594 saccharomyc |
| 19 | 39 | 69.6 | 532 | 1 INV2_YEAST | P00724 saccharomyc |
| 20 | 39 | 69.6 | 532 | 1 INV4_YEAST | P20596 saccharomyc |
| 21 | 38 | 67.9 | 217 | 1 COAT_PSVJ | P22116 peanut stun |
| 22 | 38 | 67.9 | 229 | 1 COAT_TAV | P23627 tomato aspe |
| 23 | 38 | 67.9 | 409 | 1 EF1G_SCHPO | P40921 schizosacch |
| 24 | 37 | 66.1 | 121 | 1 HV01_MOUSE | P01745 mus musculus |
| 25 | 37 | 66.1 | 1383 | 1 NPC1_CABEL | O19127 caenorhabdi |
| 26 | 37 | 66.1 | 1398 | 1 PLS_PYRPU | P72186 pyrococcus |
| 27 | 36 | 64.3 | 117 | 1 HV12_MOUSE | P01756 mus musculus |
| 28 | 36 | 64.3 | 117 | 1 HV13_MOUSE | P01757 mus musculus |
| 29 | 36 | 64.3 | 117 | 1 HV13_HUMAN | P23083 homo sapien |
| 30 | 36 | 64.3 | 136 | 1 HV15_MOUSE | P01759 mus musculus |
| 31 | 36 | 64.3 | 531 | 1 PYRG_SULTO | Q97669 sulfobolus |
| 32 | 36 | 64.3 | 1256 | 1 MRP_STRSU | P32653 streptococc |
| 33 | 35 | 62.5 | 117 | 1 HV15_HUMAN | P01743 homo sapien |

| | | | | | |
|----|----|------|-----|--------------|---------------------|
| 34 | 35 | 62.5 | 117 | 1 HV55_MOUSE | P18526 mus musculus |
| 35 | 35 | 62.5 | 218 | 1 COAT_CMVAS | O66154 cucumber mo |
| 36 | 35 | 62.5 | 242 | 1 YHW_ECOLI | P37638 escherichia |
| 37 | 35 | 62.5 | 465 | 1 EGLC_RHIME | Q823q2 rhizobium m |
| 38 | 35 | 62.5 | 525 | 1 YMJ6_YEAST | Q04489 saccharomyc |
| 39 | 35 | 62.5 | 534 | 1 FM2_ACTNA | P12616 actinomyc |
| 40 | 35 | 62.5 | 550 | 1 INV1_HANAN | P40912 hansecula a |
| 41 | 35 | 62.5 | 591 | 1 LAC1_CRYPA | Q03966 cryphonectr |
| 42 | 35 | 62.5 | 663 | 1 MNE1_YEAST | P24720 saccharomyc |
| 43 | 35 | 62.5 | 988 | 1 BLM_CABEL | O18017 caenorhabdi |
| 44 | 34 | 60.7 | 120 | 1 HV3E_HUMAN | P01765 homo sapien |
| 45 | 34 | 60.7 | 169 | 1 MOAB_BACAA | Q81ki3 bacillus an |

ALIGNMENTS

| | | | | | |
|------------|---|-----------|------|---------|--|
| RESULT 1 | | | | | |
| HV52_MOUSE | | | | | |
| ID | HV52_MOUSE | STANDARD; | PRT; | 117 AA. | |
| AC | P06327; | | | | |
| DT | 01-JAN-1988 (Rel. 06, Created) | | | | |
| DT | 01-JAN-1988 (Rel. 06, Last sequence update) | | | | |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update) | | | | |
| DE | Ig heavy chain V region VH558 Al/A4 precursor. | | | | |
| OS | Mus musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| OX | NCBI_TaxID=10090; | | | | |
| RN | [1]_TaxID=10090; | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=85099340; PubMed=2578321; | | | | |
| RA | Yancopoulos G.D., Alt F.W.; | | | | |
| RT | "Developmentally controlled and tissue-specific expression of unarranged VH gene segments."; | | | | |
| RL | Cell 40:271-281(1985). | | | | |
| CC | ----- | | | | |
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| CC | ----- | | | | |
| DR | EMBL; M13787; AAA38499.1; - | | | | |
| DR | PIR; A02029; HVMSA1. | | | | |
| DR | HSSP; P01810; 2FEU. | | | | |
| DR | InterPro; IPR007110; Ig-like. | | | | |
| DR | InterPro; IPR003596; Ig_v. | | | | |
| DR | Pfam; PF00047; Ig_1. | | | | |
| DR | SMART; SM00406; Igv; 1. | | | | |
| DR | PROSITE; PS00835; IG_LIKE; 1. | | | | |
| KW | Immunoglobulin V region; Signal. | | | | |
| FT | SIGNAL | 1 | 19 | | |
| FT | CHAIN | 20 | 117 | | |
| FT | DOMAIN | 20 | 49 | | |
| FT | DOMAIN | 50 | 54 | | |
| FT | DOMAIN | 55 | 68 | | |
| FT | DOMAIN | 69 | 85 | | |
| FT | DOMAIN | 86 | 117 | | |
| FT | DISULFID | 41 | 115 | | |
| FT | NON_TER | 117 | 117 | | |
| SQ | SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64; | | | | |

| | | | | | |
|-----------------------|-----------------|---------|-------------------|-------|---------------------------------|
| Query Match | | 100.0%; | Score 56; | DB 1; | Length 117; |
| Best Local Similarity | | 100.0%; | Pred. No. 0.0013; | | |
| Matches | | 10; | Conservative | 0; | Mismatches 0; Indels 0; Gaps 0; |
| QY | 1 GYFTSYDIN 10 | | | | |
| | | | | | |
| Db | 45 GYFTSYDIN 54 | | | | |

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RESULT 2
ID HV03 MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
PT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 87.5%; Score 49; DB 1; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFSTSYDIN 10
DB 25 GYTFSTSYGIN 34

RESULT 3
ID HV02 MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RA Sime J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; X17604; CAA35606.1; --
CC PIR; S13528; S13528.
CC InterPro; IPR001362; Glyco_hydro_32.
CC Pfam; PF00251; Glyco_hydro_32; 1.
CC SMART; SM00640; Glyco 32; 1.
CC PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 533 INVERTASE.
FT ACT_SITE 50 50 BY SIMILARITY.

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CC
CC EMBL; J00493; AAA38128.1; --
CC PIR; A94264; HVMSG7.
CC HSP; P01810; 2FBU.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 87.5%; Score 49; DB 1; Length 140;
Best Local Similarity 90.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFSTSYDIN 10
DB 45 GYTFSTSYGIN 54

RESULT 4
ID INV DEBOC STANDARD; PRT; 533 AA.
AC P24133;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Invertase precursor (EC 3.2.1.26) (Beta-fructofuranosidase)
DE (Saccharase).
DE INV.
OS Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=27300;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 2076;
RX MEDLINE=90090692; PubMed=2688929;
RA Klein R.D., Poorman R.A., Favreau M.A., Shea M.H.,
RA Hatzenbuehler N.T., Nulf S.C.;
RT "Cloning and sequence analysis of the gene encoding invertase from
RT the yeast Schwanniomyces occidentalis.";
RL Curr. Genet. 16:145-152(1989).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing beta-D-
CC fructofuranoside residues in beta-D-fructofuranosides.
CC -!- SIMILARITY: Belongs to family 32 of glycosyl hydrolases.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X17604; CAA35606.1; --
CC PIR; S13528; S13528.
CC InterPro; IPR001362; Glyco_hydro_32.
CC Pfam; PF00251; Glyco_hydro_32; 1.
CC SMART; SM00640; Glyco 32; 1.
CC PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 533 INVERTASE.
FT ACT_SITE 50 50 BY SIMILARITY.

```

```

FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 533 AA; 60839 MW; C7CE833F30778088 CRC64;

Query Match 73.2%; Score 41; DB 1; Length 533;
Best Local Similarity 70.0%; Pred. No. 4.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYTFSSYDIN 10
DB 158 GYTFKYENN 167

RESULT 5
HV00 MOUSE STANDARD; PRT; 114 AA.
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region (Anti-arsenate antibody).
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=79195438; PubMed=109536;
RA Capra J.D.; Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idiotype."
RL J. Immunol. 123:279-284 (1979).
CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02022; GIMSAA.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-Like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 106 IG-LIKE.
FT NON TER 114 114
SQ SEQUENCE 114 AA; 12555 MW; 99DDF0B6A69F4BE CRC64;

Query Match 71.4%; Score 40; DB 1; Length 114;
Best Local Similarity 66.7%; Pred. No. 1.2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSSYDI 9
DB 26 GYTFSSYEL 34

RESULT 6
HV04 MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M.; Paskind M.; Reth M.; Imanishi-Kari T.; Rajewsky K.;
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637 (1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
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CC EMBL; J00536; AAA38605.1; -.
 CC FIR; A02031; HVMS3.
 CC HSP; P01810; 2FBJ.
 CC MGD; MGI:96486; Igh-VJ558.
 CC InterPro; IPR007110; IG-like.
 CC InterPro; IPR003596; IG_v.
 CC Pfam; PF00047; IG_1.
 CC SMART; SM00406; IGV_1.
 CC PROSITE; PS50835; IG_LIKE; 1.
 CC Immunoglobulin V region; Signal.
 KW SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117
 SQ SEQUENCE 117 AA; 13016 MW; 427C861CS3975EDC CRC64;

Query Match 71.4%; Score 40; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;
 QY 1 GYFTSY 7
 Db 45 GYFTSY 51

RESULT 8
 HV06 MOUSE
 ID HV06 MOUSE STANDARD; PRT; 117 AA.
 AC P01750;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG heavy chain V region 102 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6;
 RX MEDLINE=81234548; PubMed=6789376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of antibodies; somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 CC PIR; D90809; HVMS61.
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.

FT NON TER 117
 SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;
 Query Match 71.4%; Score 40; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;
 QY 1 GYFTSY 7
 Db 45 GYFTSY 51

RESULT 9
 HV09 MOUSE
 ID HV09 MOUSE STANDARD; PRT; 117 AA.
 AC P01753; P11271;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG heavy chain V region 186-1 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6;
 RX MEDLINE=81234548; PubMed=6789376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of antibodies; somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 CC PIR; D90809; HVMS61.
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117
 SQ SEQUENCE 117 AA; 12890 MW; 16191A08CB17F5A CRC64;

Query Match 71.4%; Score 40; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;
 QY 1 GYFTSY 7
 Db 45 GYFTSY 51

RESULT 10
 HV10 MOUSE
 ID HV10 MOUSE STANDARD; PRT; 117 AA.
 AC P01754; P11270;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE IG heavy chain V region 145 precursor.
 OS Mus musculus (Mouse).

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 CC -----
 CC EMBL; J00539; AAA38172.1; -
 CC PIR; A02038; G2MS43.
 CC HSP; P01810; 2FBJ.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003596; Ig_V.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00406; IGV; 1.
 CC PROSITE; PS50835; IG_LIKE; 1.
 CC Immunoglobulin V region; Signal.
 CC SIGNAL 1 13
 CC CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
 CC FT DOMAIN 20 49 FRAMEWORK-1.
 CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 CC FT DOMAIN 55 68 FRAMEWORK-2.
 CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 CC FT DOMAIN 86 117 FRAMEWORK-3.
 CC FT DOMAIN 118 122 D SEGMENT.
 CC FT DOMAIN 123 137 JH2 SEGMENT.
 CC FT DISULFID 41 115 BY SIMILARITY.
 CC FT NON TER 137 137
 CC SQ SEQUENCE 137 AA; 15200 MW; ADD5861BF44B9EC9 CRC64;
 CC
 CC Query Match 71.4%; Score 40; DB 1; Length 137;
 CC Best Local Similarity 100.0%; Pred. No. 1.5;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Qy 1 GYTFSTY 7
 CC Db 45 GYTFSTY 51
 CC
 CC RESULT 15
 CC HV07_MOUSE STANDARD; PRT; 139 AA.
 CC AC P01751; P01752;
 CC DT 21-JUL-1986 (Rel. 01, Created)
 CC DT 21-JUL-1986 (Rel. 01, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Ig heavy chain V region BI-8/186-2 precursor.
 CC OS Mus musculus (Mouse);
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC OX NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=C57BL/6;
 CC RX MEDLINE=81234548; PubMed=6788376;
 CC RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 CC RA Baltimore D.;
 CC RT "Heavy chain variable region contribution to the NPB family of
 CC RT antibodies: somatic mutation evident in a gamma 2a variable region."
 CC RL Cell 24:625-637(1981).
 CC CC -1- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
 CC CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 CC CC (NPB ANTIBODIES).
 CC CC
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 CC -----
 CC EMBL; J00529; AAA38170.1; -
 CC PIR; A02037; MHMS15.
 CC HSP; P01810; 2FBJ.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003596; Ig_V.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00406; IGV; 1.
 CC PROSITE; PS50835; IG_LIKE; 1.
 CC Immunoglobulin V region.
 CC SIGNAL 1 98
 CC CHAIN 99 105 D SEGMENT.
 CC FT DOMAIN 99 105 D SEGMENT.
 CC FT DOMAIN 106 120 J SEGMENT.
 CC FT DISULFID 22 96 BY SIMILARITY.
 CC FT NON TER 120 120
 CC SQ SEQUENCE 120 AA; 13311 MW; 914453B426F09834 CRC64;
 CC
 CC Query Match 71.4%; Score 40; DB 1; Length 120;
 CC Best Local Similarity 100.0%; Pred. No. 1.3;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Qy 1 GYTFSTY 7
 CC Db 26 GYTFSTY 32
 CC
 CC RESULT 14
 CC HV11_MOUSE STANDARD; PRT; 137 AA.
 CC AC P017E5;
 CC DT 21-JUL-1986 (Rel. 01, Created)
 CC DT 21-JUL-1986 (Rel. 01, Last sequence update)
 CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
 CC DE Ig heavy chain V region S43 precursor.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC OX NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC MEDLINE=81234548; PubMed=6788376;
 CC RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 CC RA Baltimore D.;
 CC RT "Heavy chain variable region contribution to the NPB family of
 CC RT antibodies: somatic mutation evident in a gamma 2a variable region."
 CC RL Cell 24:625-637(1981).
 CC CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
 CC CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 CC CC (NPB ANTIBODIES).
 CC CC

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DR PIR; A90809; MEMS18.
DR PDB; 1AGU; 27-MAY-98.
DR PDB; 1AGW; 15-JUL-98.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 139
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 124
FT DOMAIN 125 139
FT DISULFID 41 115
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 71.4%; Score 40; DB 1; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSTY 7
Db 45 GYTFSTY 51

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Search completed: April 21, 2004, 17:33:56
Job time : 6.07246 secs


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Db      18 GYTFSTYDIN 27

RESULT 3
HVMSA1
IG heavy chain precursor V region (A1/A4) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 22-Jun-1999
C/Accession: A02029
R/Yancopoulos, G.D.; Alt, F.W.
Cell 40, 271-281, 1985
A/Title: Developmentally controlled and tissue-specific expression of unrearranged V-H gene
A/Reference number: A90860; MUID:85099340; PMID:2578321
A/Accession: A02029
A/Molecule type: DNA
A/Residues: 1-117 <V>N>
A/Cross-references: GB:M13787; NID:G196006; PIDN:AAA38499.1; PID:G466291
A/Note: the sequence was determined from the germline gene
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (A1/A4) #status predicted <MAT>
F:20-49/Region: framework 1
F:34-117/Domain: immunoglobulin homology <IMM>
F:50-54/Region: complementarity-determining 1
F:55-68/Region: framework 2
F:69-85/Region: complementarity-determining 2
F:86-117/Region: framework 3
F:41-115/Disulfide bonds: #status predicted

Query Match      100.0%; Score 56; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTYDIN 10
      |||||
Db      45 GYTFSTYDIN 54

RESULT 4
S34014
IG heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C/Accession: S34014; S30535
R/Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A/Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A/Reference number: S34001; MUID:93209281; PMID:7681398
A/Accession: S34014
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-127 <VAR>
A/Cross-references: EMBL:Z18321
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 56; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTYDIN 10
      |||||
Db      26 GYTFSTYDIN 35

RESULT 5
S31600
IG heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31600
```

```
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31600
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-136 <CUI>
A/Cross-references: EMBL:Z14165; NID:G30994; PIDN:CAA78534.1; PID:G30995
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 56; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTYDIN 10
      |||||
Db      45 GYTFSTYDIN 54

RESULT 6
PH0988
IG heavy chain V region (clone 178-c3) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PH0988
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B cell
A/Reference number: PH0971; MUID:92381444; PMID:1512540
A/Accession: PH0988
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-111 <TIL>
A/Experimental source: B cell, strain [NZB x NZW]F1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      94.6%; Score 53; DB 2; Length 111;
Best Local Similarity 90.0%; Pred. No. 0.022;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTYDIN 10
      |||||
Db      26 GYTFSTYDIN 35

RESULT 7
S31596
IG heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31596
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31596
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-132 <CUI>
A/Cross-references: EMBL:Z14166; NID:G30996; PIDN:CAA78535.1; PID:G30997
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      91.1%; Score 51; DB 2; Length 132;
Best Local Similarity 90.0%; Pred. No. 0.06;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GYTFTSYDIN 10
 |||||
 Db 45 GYTFTSYDID 54

RESULT 8

B28572
 IG heavy chain V regions (CR-Id 7, CR-Id 14) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jul-2000
 C:Accession: B28572
 R:Siekevitz, M.; Huang, S.Y.; Gefter, M.L.
 Eur. J. Immunol. 13, 123-132, 1983
 A>Title: The genetic basis of antibody production: a single heavy chain variable region
 A:Reference number: A91262; MUID:83157801; PMID:6403356
 A:Accession: B28572
 A:Molecule type: DNA
 A:Residues: 1-76 <SIE>
 A:Cross-references: GB:K02154; GB:M17032; NID:9196176; PIDN:AAA38613.1; PID:g196177
 A>Note: this sequence was determined from the germline gene
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 76;
 Best Local Similarity 90.0%; Pred. No. 0.078; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 11 GYTFTSYGIN 20

RESULT 9

B24754
 IG heavy chain V region (SE1.3) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 28-Sep-1987 #sequence_revision 06-Nov-1992 #text_change 16-Aug-1996
 C:Accession: B24754
 R:Haba, S.; Rosen, E.M.; Meek, K.; Nisonoff, A.
 J. Exp. Med. 164, 291-302, 1986
 A:Reference number: A24754; MUID:86253060; PMID:3088196
 A:Accession: B24754
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-98 <HAB>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 98;
 Best Local Similarity 90.0%; Pred. No. 0.1; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 9 GYTFTSYGIN 18

RESULT 10

A28572
 IG heavy chain V region (II CR-Id 11) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
 C:Accession: A28572
 R:Siekevitz, M.; Huang, S.Y.; Gefter, M.L.
 Eur. J. Immunol. 13, 123-132, 1983
 A>Title: The genetic basis of antibody production: a single heavy chain variable region
 A:Reference number: A91262; MUID:83157801; PMID:6403356
 A:Accession: A28572
 A:Molecule type: DNA
 A:Residues: 1-98 <SIE>
 A>Note: this sequence was determined from the germline gene
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 49; DB 2; Length 98;
 Best Local Similarity 90.0%; Pred. No. 0.1; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 26 GYTFTSYGIN 35

RESULT 11

PH1490
 IG heavy chain V region (clone XR6-1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: PH1490
 R:Giusti, A.M.; Manser, T.
 J. Exp. Med. 177, 797-809, 1993
 A>Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.
 A:Reference number: PH1482; MUID:93171820; PMID:8436910
 A:Accession: PH1490
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-102 <GIU>
 A:Experimental source: hybridoma cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 102;
 Best Local Similarity 90.0%; Pred. No. 0.11; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 7 GYTFTSYGIN 16

RESULT 12

PH1491
 IG heavy chain V region (clone XR26-3) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: PH1491
 R:Giusti, A.M.; Manser, T.
 J. Exp. Med. 177, 797-809, 1993
 A>Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.
 A:Reference number: PH1482; MUID:93171820; PMID:8436910
 A:Accession: PH1491
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-102 <GIU>
 A:Experimental source: hybridoma cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 102;
 Best Local Similarity 90.0%; Pred. No. 0.11; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 7 GYTFTSYGIN 16

RESULT 13

S42176
 IG gamma chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
 C:Accession: S42176

R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A;Reference number: S42176; MUID:94009207; PMID:7651608
A;Accession: S42176
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-102 <MOJ>
A;Cross-references: EMBL:225441; NID:9407810; PID:CAAS0928.1; PID:9407811
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;15-96/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 49; DB 2; Length 102;
Best Local Similarity 80.0%; Pred. No. 0.11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
DB 26 GYTFDYDMN 35

RESULT 14
PHI522
IG heavy chain V region (clone PR14-3-3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PHI522
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
d for somatic mutation.
A;Reference number: PHI482; MUID:93171820; PMID:8436910
A;Accession: PHI522
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-114 <GIU>
A;Experimental source: hybridoma cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 49; DB 2; Length 114;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
DB 29 GYTFTSYGIN 38

RESULT 15
PHI523
IG heavy chain V region (clone PR18-1-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PHI523
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
d for somatic mutation.
A;Reference number: PHI482; MUID:93171820; PMID:8436910
A;Accession: PHI523
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-114 <GIU>
A;Experimental source: hybridoma cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 49; DB 2; Length 114;
Best Local Similarity 90.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYTFTSYDIN 10
DB 29 GYTFTSYGIN 38

Search completed: April 21, 2004, 17:38:27
Job time : 10.1304 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:33:24 ; Search time 148.696 Seconds
(without alignments)
65.641 Million cell updates/sec

Title: SEQ1
Perfect score: 56
Sequence: 1 gyftsydin 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/prodata/2/paa/PCUTUS_COMB.pep.*
2: /cgn2_6/prodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/prodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/prodata/2/paa/US080_COMB.pep.*
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27: /cgn2_6/prodata/2/paa/US101_COMB.pep.*
28: /cgn2_6/prodata/2/paa/US102_COMB.pep.*
29: /cgn2_6/prodata/2/paa/US103_COMB.pep.*
30: /cgn2_6/prodata/2/paa/US104_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
|------------|-------|-------------|--------|----|-------------|

| | | | | | | |
|----|----|-------|----|----|----------------------|-------------------|
| 1 | 56 | 100.0 | 10 | 1 | PCT-US03-38234-125 | Sequence 125, App |
| 2 | 56 | 100.0 | 10 | 32 | US-10-726-332-125 | Sequence 125, App |
| 3 | 56 | 100.0 | 92 | 1 | PCT-US01-00663-34182 | Sequence 34182, A |
| 4 | 56 | 100.0 | 92 | 23 | US-09-864-761-47202 | Sequence 47202, A |
| 5 | 56 | 100.0 | 92 | 27 | US-10-182-997-24903 | Sequence 24903, A |
| 6 | 56 | 100.0 | 92 | 28 | US-10-203-135-33269 | Sequence 33269, A |
| 7 | 56 | 100.0 | 92 | 28 | US-10-203-136-34115 | Sequence 34115, A |
| 8 | 56 | 100.0 | 92 | 28 | US-10-203-137-34182 | Sequence 34182, A |
| 9 | 56 | 100.0 | 96 | 1 | PCT-US03-22011-3 | Sequence 3, Appli |
| 10 | 56 | 100.0 | 96 | 27 | US-10-194-975-3 | Sequence 43, Appl |
| 11 | 56 | 100.0 | 98 | 1 | PCT-US03-38450-43 | Sequence 289, App |
| 12 | 56 | 100.0 | 98 | 1 | PCT-US03-00398-289 | Sequence 290, App |
| 13 | 56 | 100.0 | 98 | 1 | PCT-US03-00398-290 | Sequence 285, App |
| 14 | 56 | 100.0 | 98 | 1 | PCT-US03-00398-295 | Sequence 296, App |
| 15 | 56 | 100.0 | 98 | 1 | PCT-US03-00398-296 | Sequence 342, App |
| 16 | 56 | 100.0 | 98 | 1 | PCT-US03-00398-342 | Sequence 344, App |
| 17 | 56 | 100.0 | 98 | 1 | PCT-US03-00398-344 | Sequence 348, App |
| 18 | 56 | 100.0 | 98 | 1 | PCT-US03-00398-348 | Sequence 350, App |
| 19 | 56 | 100.0 | 98 | 1 | PCT-US03-00398-350 | Sequence 361, App |
| 20 | 56 | 100.0 | 98 | 1 | PCT-US03-00398-361 | Sequence 362, App |
| 21 | 56 | 100.0 | 98 | 1 | PCT-US03-00398-362 | Sequence 373, App |
| 22 | 56 | 100.0 | 98 | 1 | PCT-US03-00398-373 | Sequence 374, App |
| 23 | 56 | 100.0 | 98 | 1 | PCT-US03-00398-374 | Sequence 3, Appli |
| 24 | 56 | 100.0 | 98 | 1 | PCT-US03-06598-3 | Sequence 31, Appl |
| 25 | 56 | 100.0 | 98 | 20 | US-09-674-752-31 | Sequence 45, Appl |
| 26 | 56 | 100.0 | 98 | 22 | US-09-751-181-45 | Sequence 27332, A |
| 27 | 56 | 100.0 | 98 | 22 | US-09-791-537-27332 | Sequence 77776, A |
| 28 | 56 | 100.0 | 98 | 22 | US-09-791-537-77778 | Sequence 45, Appl |
| 29 | 56 | 100.0 | 98 | 26 | US-10-029-926B-45 | Sequence 45, Appl |
| 30 | 56 | 100.0 | 98 | 26 | US-10-029-988B-45 | Sequence 45, Appl |
| 31 | 56 | 100.0 | 98 | 26 | US-10-032-037B-45 | Sequence 45, Appl |
| 32 | 56 | 100.0 | 98 | 26 | US-10-032-423A-45 | Sequence 289, App |
| 33 | 56 | 100.0 | 98 | 26 | US-10-041-860-289 | Sequence 290, App |
| 34 | 56 | 100.0 | 98 | 26 | US-10-041-860-290 | Sequence 235, App |
| 35 | 56 | 100.0 | 98 | 26 | US-10-041-860-295 | Sequence 236, App |
| 36 | 56 | 100.0 | 98 | 26 | US-10-041-860-296 | Sequence 342, App |
| 37 | 56 | 100.0 | 98 | 26 | US-10-041-860-342 | Sequence 344, App |
| 38 | 56 | 100.0 | 98 | 26 | US-10-041-860-344 | Sequence 348, App |
| 39 | 56 | 100.0 | 98 | 26 | US-10-041-860-348 | Sequence 350, App |
| 40 | 56 | 100.0 | 98 | 26 | US-10-041-860-350 | Sequence 361, App |
| 41 | 56 | 100.0 | 98 | 26 | US-10-041-860-361 | Sequence 362, App |
| 42 | 56 | 100.0 | 98 | 26 | US-10-041-860-362 | Sequence 373, App |
| 43 | 56 | 100.0 | 98 | 26 | US-10-041-860-373 | Sequence 374, App |
| 44 | 56 | 100.0 | 98 | 26 | US-10-041-860-374 | Sequence 45, Appl |
| 45 | 56 | 100.0 | 98 | 27 | US-10-189-258A-45 | |

ALIGNMENTS

RESULT 1
PCT-US03-38234-125
; Sequence 125, Application PC/TUS0338234
; GENERAL INFORMATION:
; APPLICANT: Abgenix, Inc.
; APPLICANT: Lexicon Genetics Incorporated
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 AND USES THEREOF
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: PCT/US03/38234
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125

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; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38234-125

Query Match      100.0%; Score 56; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
DB      1 GYTFTSYDIN 10

RESULT 2
US-10-726-332-125
; Sequence 125, Application US/10726332
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-125

Query Match      100.0%; Score 56; DB 32; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
DB      1 GYTFTSYDIN 10

RESULT 3
PCT-US01-00663-34182
; Sequence 34182, Application PC/TUS0100663
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: PCT/US01/00663
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/532,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 34182
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39
; OTHER INFORMATION: EST_HUMAN HIT: AW405627.1, EVALUE 8.00e-48
PCT-US01-00663-34182

Query Match      100.0%; Score 56; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
DB      17 GYTFTSYDIN 26

RESULT 4
US-09-864-761-47202
; Sequence 47202, Application US/09864761
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/532,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408

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; CURRENT APPLICATION NUMBER: US/10/203,136
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38578
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 34115
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: AW405627.1, EVALUE 8.00e-48
US-10-203-136-34115

```

```

Query Match          100.0%; Score 56; DB 28; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GYFTSYDIN 10
        |||||
DB      17 GYFTSYDIN 26

```

```

RESULT 8
US-10-203-137-34182
; Sequence 34182, Application US/10203137
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: US/10/203,137
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 34182
; LENGTH: 92

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: AW405627.1, EVALUE 8.00e-48
US-10-203-137-34182

```

```

Query Match          100.0%; Score 56; DB 28; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GYFTSYDIN 10
        |||||
DB      17 GYFTSYDIN 26

```

```

RESULT 9
PCT-US02-22011-3
; Sequence 3, Application PC/TUS0222011
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.02
; CURRENT APPLICATION NUMBER: PCT/US02/22011
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-22011-3

```

```

Query Match          100.0%; Score 56; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GYFTSYDIN 10
        |||||
DB      24 GYFTSYDIN 33

```

```

RESULT 10
US-10-194-975-3
; Sequence 3, Application US/10194975
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-3

```

```

Query Match          100.0%; Score 56; DB 27; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GYFTSYDIN 10

```

```

Db      24  GYTFTSYDIN 33
|||||
RESULT 11
PCT-US02-38450-43
; Sequence 43, Application PC/TUS0238450
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: PCT/US02/38450
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
PCT-US02-38450-43

Query Match      100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GYTFTSYDIN 10
|||||
Db      26  GYTFTSYDIN 35
|||||

RESULT 12
PCT-US03-00398-289
; Sequence 289, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gadi
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 289
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-00398-289

Query Match      100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GYTFTSYDIN 10
|||||
Db      26  GYTFTSYDIN 35
|||||

RESULT 13
PCT-US03-00398-290
; Sequence 290, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gadi
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 290
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-00398-290

Query Match      100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GYTFTSYDIN 10
|||||
Db      26  GYTFTSYDIN 35
|||||

RESULT 14
PCT-US03-00398-295
; Sequence 295, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gadi
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-00398-295

Query Match      100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GYTFTSYDIN 10
|||||
Db      26  GYTFTSYDIN 35
|||||

RESULT 15
PCT-US03-00398-296
; Sequence 296, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gadi
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-00398-296

Query Match      100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GYTFTSYDIN 10
|||||
Db      26  GYTFTSYDIN 35
|||||

```

```
; FILE REFERENCE: AGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-00398-296

Query Match      100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
Db      26 GYTFSTSYDIN 35

Search completed: April 21, 2004, 17:57:21
Job time : 148.696 secs
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:34:09 ; Search time 7.10145 Seconds
(without alignments)
39.310 Million cell updates/sec

Title: SEQ1
Perfect score: 56
Sequence: 1 gytftsytidin 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198209 seqs, 2791599 residues

Total number of hits satisfying chosen parameters: 198209

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New:
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 56 | 100.0 | 10 | 1 | PCT-US03-38234A-125 |
| 2 | 52 | 92.9 | 118 | 5 | US-09-926-323A-2 |
| 3 | 51 | 91.1 | 127 | 6 | US-10-793-479-4122 |
| 4 | 48 | 85.7 | 10 | 1 | PCT-US03-36870-31 |
| 5 | 48 | 85.7 | 113 | 1 | PCT-US03-36870-3 |
| 6 | 48 | 85.7 | 113 | 1 | PCT-US03-36870-5 |
| 7 | 48 | 85.7 | 113 | 1 | PCT-US03-36870-7 |
| 8 | 48 | 85.7 | 113 | 1 | PCT-US03-36870-8 |
| 9 | 48 | 85.7 | 113 | 1 | PCT-US03-36870-9 |
| 10 | 48 | 85.7 | 113 | 1 | PCT-US03-36870-10 |
| 11 | 48 | 85.7 | 113 | 1 | PCT-US03-36870-11 |
| 12 | 47 | 83.9 | 116 | 6 | US-10-800-197-120 |
| 13 | 47 | 83.9 | 226 | 6 | US-10-813-977-17 |
| 14 | 47 | 83.9 | 245 | 6 | US-10-800-197-7 |
| 15 | 46 | 82.1 | 115 | 6 | US-10-488-673-4 |
| 16 | 46 | 82.1 | 479 | 1 | PCT-US03-34610-12 |
| 17 | 45 | 80.4 | 149 | 6 | US-10-693-629-56 |
| 18 | 44 | 78.6 | 109 | 6 | US-10-800-197-147 |
| 19 | 44 | 78.6 | 118 | 6 | US-10-789-090-9 |
| 20 | 44 | 78.6 | 118 | 6 | US-10-803-653-165 |
| 21 | 44 | 78.6 | 118 | 6 | US-10-803-622-165 |
| 22 | 44 | 78.6 | 120 | 6 | US-10-793-479-4111 |
| 23 | 44 | 78.6 | 121 | 6 | US-10-793-479-4115 |
| 24 | 43 | 76.8 | 10 | 1 | PCT-US04-05247-6 |
| 25 | 43 | 76.8 | 10 | 6 | US-10-018-245A-1 |
| 26 | 43 | 76.8 | 92 | 6 | US-10-681-421-84 |

| | | | | | | |
|----|----|------|-----|---|--------------------|-------------------|
| 27 | 43 | 76.8 | 112 | 6 | US-10-681-421-20 | Sequence 20, Appl |
| 28 | 43 | 76.8 | 121 | 6 | US-10-627-556-406 | Sequence 406, App |
| 29 | 43 | 76.8 | 121 | 6 | US-10-627-556-410 | Sequence 410, App |
| 30 | 43 | 76.8 | 121 | 6 | US-10-681-421-7 | Sequence 7, Appli |
| 31 | 43 | 76.8 | 121 | 6 | US-10-681-421-31 | Sequence 31, Appl |
| 32 | 43 | 76.8 | 121 | 6 | US-10-681-421-52 | Sequence 52, Appl |
| 33 | 43 | 76.8 | 121 | 6 | US-10-681-421-111 | Sequence 111, App |
| 34 | 43 | 76.8 | 122 | 6 | US-10-627-556-242 | Sequence 242, App |
| 35 | 43 | 76.8 | 122 | 6 | US-10-793-479-7801 | Sequence 7801, Ap |
| 36 | 43 | 76.8 | 122 | 6 | US-10-818-765-2 | Sequence 2, Appli |
| 37 | 43 | 76.8 | 123 | 6 | US-10-681-421-109 | Sequence 109, App |
| 38 | 43 | 76.8 | 130 | 1 | PCT-US03-32349-15 | Sequence 15, Appl |
| 39 | 43 | 76.8 | 130 | 1 | PCT-US03-32349-17 | Sequence 17, Appl |
| 40 | 43 | 76.8 | 137 | 1 | PCT-US04-05247-2 | Sequence 2, Appli |
| 41 | 43 | 76.8 | 137 | 6 | US-10-469-125-7 | Sequence 7, Appli |
| 42 | 43 | 76.8 | 140 | 5 | US-09-911-703A-6 | Sequence 6, Appli |
| 43 | 43 | 76.8 | 140 | 5 | US-09-905-928A-6 | Sequence 6, Appli |
| 44 | 43 | 76.8 | 140 | 5 | US-09-911-692B-6 | Sequence 6, Appli |
| 45 | 43 | 76.8 | 140 | 5 | US-09-905-927A-6 | Sequence 6, Appli |

ALIGNMENTS

RESULT 1
PCT-US03-38234A-125
; Sequence 125, Application PC/TUS0338234A
; GENERAL INFORMATION:
; APPLICANT: AGENIX, INC.
; APPLICANT: LEXICON GENETICS INCORPORATED
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 AND USES THEREOF
; FILE REFERENCE: ARGENIX 072VPC
; CURRENT APPLICATION NUMBER: PCT/US03/38234A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US03/38234
; PRIOR FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38234A-125

Query Match 100.0%; Score 56; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-09-926-323A-2
; Sequence 2, Application US/09926323A
; GENERAL INFORMATION:
; APPLICANT: Schmitt, Manfred
; APPLICANT: Noack, Frank
; APPLICANT: Magdolen, Viktor
; APPLICANT: Graeff, Henner
; APPLICANT: Luther, Thomas
; APPLICANT: Albrecht, Sybille
; APPLICANT: Muller, Martin
; APPLICANT: Wilhelm, Olaf

```

; APPLICANT: Harbeck, Nadia
; TITLE OF INVENTION: Diagnostic and Therapeutic Use of Antibodies Against The
; TITLE OF INVENTION: Urokinase Receptor
; FILE REFERENCE: 2923-508
; CURRENT APPLICATION NUMBER: US/09/926,323A
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: PCT/EP00/03347
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phage sequence
US-09-926-323A-2

Query Match      92.9%; Score 52; DB 5; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.038;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYTFSTSYDIN 10
Db      26 GYSFTSYDIN 35

RESULT 3
US-10-793-479-4122
; Sequence 4122, Application US/10793479
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/10/793,479
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US/09/513,999
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4122
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19...-1
; OTHER INFORMATION: score 9.7
; OTHER INFORMATION: seq ILFLVAATSAHS/QV
US-10-793-479-4122

Query Match      91.1%; Score 51; DB 6; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GYTFSTSYDIN 10
Db      45 GYTFVSYDIN 54

RESULT 4
PCT-US03-36870-31
; Sequence 31, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; APPLICANT: Ruben J. Boado
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapiro & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US03/36870
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 31
PCT-US03-36870-31

Query Match      85.7%; Score 48; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.018;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYFTSYDIN 10
Db      1 GYFTNYDIH 10

RESULT 5
PCT-US03-36870-3
; Sequence 3, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; APPLICANT: Ruben J. Boado
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapiro & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US03/36870
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411

```

```
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3
PCT-US03-36870-3

Query Match      85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
DB      26 GYTFNVDIH 35

RESULT 6
PCT-US03-36870-5
; Sequence 5, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapero & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7
PCT-US03-36870-7

Query Match      85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
DB      26 GYTFNVDIH 35

RESULT 8
PCT-US03-36870-8
; Sequence 8, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapero & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5
PCT-US03-36870-5

Query Match      85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
DB      26 GYTFNVDIH 35

RESULT 7
PCT-US03-36870-7
```

```
; Sequence 7, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapero & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7
PCT-US03-36870-7

Query Match      85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
DB      26 GYTFNVDIH 35

RESULT 8
PCT-US03-36870-8
; Sequence 8, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapero & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7
PCT-US03-36870-7
```

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 0180.0038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 319-5411
TELEFAX: (310) 319-5401
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8
PCT-US03-36870-8
Query Match 85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYFTSYDIN 10
Db 26 GYFTNYDIH 35
RESULT 9
PCT-US03-36870-9
Sequence 9, Application PC/TUS0336870
GENERAL INFORMATION:
APPLICANT: William M. Pardridge
TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
Via The Human Insulin Receptor
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shapiro & Dupont LLP
STREET: 233 Wilshire Boulevard, Suite 700
CITY: Santa Monica
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 2000
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US03/36870
FILING DATE: 18-Nov-2003
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 0180.0038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 319-5411
TELEFAX: (310) 319-5401
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9
PCT-US03-36870-9
Query Match 85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTSYDIN 10
Db 26 GYFTNYDIH 35
RESULT 10
PCT-US03-36870-10
Sequence 10, Application PC/TUS0336870
GENERAL INFORMATION:
APPLICANT: William M. Pardridge
TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
Via The Human Insulin Receptor
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shapiro & Dupont LLP
STREET: 233 Wilshire Boulevard, Suite 700
CITY: Santa Monica
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 2000
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US03/36870
FILING DATE: 18-Nov-2003
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 0180.0038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 319-5411
TELEFAX: (310) 319-5401
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10
PCT-US03-36870-10
Query Match 85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYFTSYDIN 10
Db 26 GYFTNYDIH 35
RESULT 11
PCT-US03-36870-11
Sequence 11, Application PC/TUS0336870
GENERAL INFORMATION:
APPLICANT: William M. Pardridge
TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
Via The Human Insulin Receptor
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shapiro & Dupont LLP
STREET: 233 Wilshire Boulevard, Suite 700
CITY: Santa Monica
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:


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/
/ MEDIUM TYPE: Floppy Disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: Windows 2000
/ SOFTWARE: MS Word
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US03/36870
/ FILING DATE: 18-Nov-2003
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Oldenkamp, David J.
/ REGISTRATION NUMBER: 29,421
/ REFERENCE/DOCKET NUMBER: 0180.0038
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (310) 319-5411
/ TELEFAX: (310) 319-5401
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 113 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 11
PCT-US03-36870-11

Query Match      85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
Db      26 GYTFNYDIH 35

RESULT 12
US-10-800-197-120
/ Sequence 120, Application US/10800197
/ GENERAL INFORMATION:
/ APPLICANT: Morton, Philip A et al.
/ TITLE OF INVENTION: ANTIBODIES TO IGF-I RECEPTOR FOR THE TREATMENT OF CANCERS
/ FILE REFERENCE: 01343/1
/ CURRENT APPLICATION NUMBER: US/10/800,197
/ CURRENT FILING DATE: 2004-03-12
/ PRIOR APPLICATION NUMBER: 60/455,094
/ PRIOR FILING DATE: 2003-03-14
/ NUMBER OF SEQ ID NOS: 157
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 120
/ LENGTH: 116
/ TYPE: PRT
/ ORGANISM: artificial
/ FEATURE:
/ OTHER INFORMATION: phage display generated VH or VL region
US-10-800-197-120

Query Match      83.9%; Score 47; DB 6; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.26;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 GYTFSTSYDIN 10
Db      26 GYTFNYDIH 35

RESULT 13
US-10-813-977-17
/ Sequence 17, Application US/10813977
/ GENERAL INFORMATION:
/ APPLICANT: Dyanan, William
/ APPLICANT: Takeda, Yoshihiko
/ APPLICANT: Li, Shuyi
/ TITLE OF INVENTION: Compositions and Methods for Modulating DNA Repair
/ FILE REFERENCE: 791301-1010

/
/ MEDIUM TYPE: Floppy Disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: Windows 2000
/ SOFTWARE: MS Word
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US03/36870
/ FILING DATE: 18-Nov-2003
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Oldenkamp, David J.
/ REGISTRATION NUMBER: 29,421
/ REFERENCE/DOCKET NUMBER: 0180.0038
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (310) 319-5411
/ TELEFAX: (310) 319-5401
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 113 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 11
PCT-US03-36870-11

Query Match      85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
Db      26 GYTFNYDIH 35

RESULT 12
US-10-800-197-120
/ Sequence 120, Application US/10800197
/ GENERAL INFORMATION:
/ APPLICANT: Morton, Philip A et al.
/ TITLE OF INVENTION: ANTIBODIES TO IGF-I RECEPTOR FOR THE TREATMENT OF CANCERS
/ FILE REFERENCE: 01343/1
/ CURRENT APPLICATION NUMBER: US/10/800,197
/ CURRENT FILING DATE: 2004-03-12
/ PRIOR APPLICATION NUMBER: 60/455,094
/ PRIOR FILING DATE: 2003-03-14
/ NUMBER OF SEQ ID NOS: 157
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 120
/ LENGTH: 116
/ TYPE: PRT
/ ORGANISM: artificial
/ FEATURE:
/ OTHER INFORMATION: phage display generated VH or VL region
US-10-800-197-120

Query Match      83.9%; Score 47; DB 6; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.26;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 GYTFSTSYDIN 10
Db      26 GYTFNYDIH 35

RESULT 13
US-10-813-977-17
/ Sequence 17, Application US/10813977
/ GENERAL INFORMATION:
/ APPLICANT: Dyanan, William
/ APPLICANT: Takeda, Yoshihiko
/ APPLICANT: Li, Shuyi
/ TITLE OF INVENTION: Compositions and Methods for Modulating DNA Repair
/ FILE REFERENCE: 791301-1010

/
/ MEDIUM TYPE: Floppy Disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: Windows 2000
/ SOFTWARE: MS Word
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US03/36870
/ FILING DATE: 18-Nov-2003
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Oldenkamp, David J.
/ REGISTRATION NUMBER: 29,421
/ REFERENCE/DOCKET NUMBER: 0180.0038
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (310) 319-5411
/ TELEFAX: (310) 319-5401
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 113 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 11
PCT-US03-36870-11

Query Match      85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
Db      26 GYTFNYDIH 35

RESULT 12
US-10-800-197-120
/ Sequence 120, Application US/10800197
/ GENERAL INFORMATION:
/ APPLICANT: Morton, Philip A et al.
/ TITLE OF INVENTION: ANTIBODIES TO IGF-I RECEPTOR FOR THE TREATMENT OF CANCERS
/ FILE REFERENCE: 01343/1
/ CURRENT APPLICATION NUMBER: US/10/800,197
/ CURRENT FILING DATE: 2004-03-12
/ PRIOR APPLICATION NUMBER: 60/455,094
/ PRIOR FILING DATE: 2003-03-14
/ NUMBER OF SEQ ID NOS: 157
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 120
/ LENGTH: 116
/ TYPE: PRT
/ ORGANISM: artificial
/ FEATURE:
/ OTHER INFORMATION: phage display generated antibody
US-10-800-197-7

Query Match      83.9%; Score 47; DB 6; Length 245;
Best Local Similarity 80.0%; Pred. No. 0.52;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 GYTFSTSYDIN 10
Db      26 GYTFNYDIH 35

RESULT 15
US-10-488-673-4
/ Sequence 4, Application US/10488673
/ GENERAL INFORMATION:
/ APPLICANT: KEIO UNIVERSITY
/ TITLE OF INVENTION: PEMPHIGUS MONOCLONAL ANTIBODIES
/ FILE REFERENCE: P10000238
/ CURRENT APPLICATION NUMBER: US/10/488,673
/ CURRENT FILING DATE: 2004-03-03
/ PRIOR APPLICATION NUMBER: JP P2001-267653
/ PRIOR FILING DATE: 2001-09-04
/ NUMBER OF SEQ ID NOS: 55
/ SOFTWARE: Patent in Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 115
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-488-673-4

Query Match      82.1%; Score 46; DB 6; Length 115;
Best Local Similarity 90.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;
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Qy 1 GYFTSYDIN 10
| | | | |
Db 26 GYFTSYWIN 35

Search completed: April 21, 2004, 17:58:24
Job time : 8.10145 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:18 ; Search time 40 Seconds
(without alignments)
70.637 Million cell updates/sec

Title: SEQ1

Perfect score: 56

Sequence: 1 gyftsydin 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 56 | 100.0 | 92 | 4 | AAM20077 Peptide # |
| 2 | 56 | 100.0 | 92 | 4 | AAM33913 Peptide # |
| 3 | 56 | 100.0 | 92 | 4 | ABG55467 Human liv |
| 4 | 56 | 100.0 | 92 | 5 | ABG43604 Human pep |
| 5 | 56 | 100.0 | 98 | 3 | AAY50958 Human FVI |
| 6 | 56 | 100.0 | 98 | 5 | ABG78170 Human Fv |
| 7 | 56 | 100.0 | 98 | 5 | ABG31861 Human ant |
| 8 | 56 | 100.0 | 98 | 6 | ABO27070 Human ger |
| 9 | 56 | 100.0 | 116 | 2 | AAR79241 Heavy cha |
| 10 | 56 | 100.0 | 117 | 2 | AAR66302 Human imm |
| 11 | 56 | 100.0 | 119 | 6 | ABJ18572 Ganglios |
| 12 | 56 | 100.0 | 119 | 6 | ABJ18570 Ganglios |
| 13 | 56 | 100.0 | 120 | 4 | AAB62747 Human HIV |
| 14 | 56 | 100.0 | 122 | 6 | ABR55829 Heavy cha |
| 15 | 56 | 100.0 | 139 | 6 | ABG74245 Mouse ant |
| 16 | 56 | 100.0 | 146 | 3 | AAB53510 Human col |
| 17 | 56 | 100.0 | 149 | 6 | ABO44846 Human epi |
| 18 | 56 | 100.0 | 199 | 2 | AAY34302 IGM antib |
| 19 | 56 | 100.0 | 203 | 2 | AAY34301 IGM antib |
| 20 | 56 | 100.0 | 555 | 4 | AAB19871 Activatin |
| 21 | 56 | 100.0 | 565 | 4 | AAB19873 Activatin |
| 22 | 56 | 100.0 | 577 | 4 | AAB19872 Activatin |
| 23 | 56 | 100.0 | 704 | 4 | ABJ19888 MLV envel |
| 24 | 54 | 96.4 | 120 | 6 | ABR55815 Heavy cha |
| 25 | 53 | 94.6 | 120 | 6 | AAO29544 Human 7.1 |

| | | | | | |
|----|----|------|-----|---|--------------------|
| 26 | 53 | 94.6 | 120 | 6 | ABG71906 Human ant |
| 27 | 53 | 94.6 | 243 | 7 | ABM78999 Monoclona |
| 28 | 53 | 94.6 | 243 | 7 | ABM78998 Monoclona |
| 29 | 52 | 92.9 | 118 | 3 | ABE11391 Murine II |
| 30 | 52 | 92.9 | 123 | 4 | AAU02552 Anti-adip |
| 31 | 51 | 91.1 | 119 | 5 | ABO07175 Mouse 09 |
| 32 | 51 | 91.1 | 127 | 3 | AAG00041 Human sec |
| 33 | 51 | 91.1 | 134 | 3 | AAY64688 Human 5, |
| 34 | 51 | 91.1 | 850 | 4 | ABG04634 Novel hum |
| 35 | 50 | 89.3 | 122 | 3 | AAY50959 Human FVI |
| 36 | 50 | 89.3 | 122 | 3 | AAY50966 Human FVI |
| 37 | 50 | 89.3 | 476 | 2 | AAW88464 Monoclona |
| 38 | 49 | 87.5 | 127 | 4 | AAU02622 Anti-adip |
| 39 | 49 | 87.5 | 248 | 5 | ABP44997 Human Bly |
| 40 | 49 | 87.5 | 561 | 2 | AAY17415 Mouse imm |
| 41 | 48 | 85.7 | 10 | 3 | AAY78322 Anti-zeta |
| 42 | 48 | 85.7 | 115 | 2 | AAR52051 Heavy cha |
| 43 | 48 | 85.7 | 123 | 3 | AAY78325 Anti-zeta |
| 44 | 48 | 85.7 | 268 | 2 | AAK44226 ChimERIC |
| 45 | 48 | 85.7 | 532 | 3 | AAY78328 Bispecifi |

ALIGNMENTS

RESULT 1
AAM20077
ID AAM20077 standard; protein; 92 AA.
XX
AC AAM20077;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #511 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX
KW cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000670.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX Gene expression in human cervical epithelial cells.
XX
PS Claim 27; SEQ ID NO 24903; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP; see AAI10068-AA128459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form

```
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 92 AA;

Query Match      100.0%; Score 56; DB 4; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
Db 17 GYTFTSYDIN 26

RESULT 2
ID AAM33913 standard; protein; 92 AA.
XX
AC AAM33913;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #7950 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW Genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 34182; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AA31315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 92 AA;

Query Match      100.0%; Score 56; DB 4; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
Db 17 GYTFTSYDIN 26

RESULT 3
```

```
ABG55467
ID ABG55467 standard; peptide; 92 AA.
XX
AC ABG55467;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID NO 34115.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 27; SEQ ID NO 34115; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 92 AA;

Query Match      100.0%; Score 56; DB 4; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
Db 17 GYTFTSYDIN 26

RESULT 4
ID ABG43604 standard; peptide; 92 AA.
XX
AC ABG43604;
XX
DT 19-AUG-2002 (first entry)
XX
```

Human peptide encoded by genome-derived single exon probe SEQ ID 33269.

Human; single exon probe; asthma; lung cancer; COPD; IID;
 Chronic obstructive pulmonary disease; interstitial lung disease;
 familial idiopathic pulmonary fibrosis; neurofibromatosis;
 tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;
 pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 primary ciliary dyskinesia; pulmonary hypertension;
 hyaline membrane disease.

OS Homo sapiens.

XX WO200186003-A2.

XX 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US000665.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234587P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
 WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to
 measure gene expression in human lung samples.

XX Claim 27; SEQ ID NO 33269; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon
 nucleic acid probes for measuring gene expression in a sample derived
 from human lung comprising single exon nucleic acid probes having one of
 12614 nucleic acid sequences mentioned in the specification, or their
 complements or the 12387 open reading frames derived from the 12614
 probes. Also included are a microarray comprising the novel set of probes
 ; the novel set of probes which hybridise at high stringency to a nucleic
 acid expressed in the human lung; measuring gene expression in a sample
 derived from human lung, comprising (a) contacting the array with a
 collection of detectably labeled nucleic acids derived from human lung
 mRNA, and (b) measuring the label detectably bound to each probe of the
 array; identifying exons in a eukaryotic genome, comprising (a)
 algorithmically predicting at least one exon from genomic sequences of
 the eukaryote; and (b) detecting specific hybridisation of detectably
 labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 in the above mentioned microarray; assigning exons to a single gene,
 comprising (a) identifying exons from genomic sequence by the method
 above and (b) measuring the expression of each of the exons in several
 tissues and/or cell types using hybridisation to a single exon
 microarrays having a probe with the exon, where a common pattern of
 expression of the exons in the tissues and/or cell types indicates that
 the exons should be assigned to a single gene; a peptide comprising one
 of 12011 sequences, mentioned in the specification, or encoded by the
 probes/open reading frames (ORF). The probes are used for gene expression
 analysis, and for identifying exons in a gene, particularly using human
 lung derived mRNA and for the study of lung diseases such as asthma, lung
 cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 Pudlak syndrome, sarcoidosis, pulmonary haemorrhoidosis, pulmonary
 histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 dyskinesia, pulmonary hypertension and hyaline membrane disease. The

CC present sequence is a peptide/protein encoded by a single exon probe of
 the invention. Note: The sequence data for this patent did not form part
 of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 92 AA;

Query Match 100.0%; Score 56; DB 5; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYTFTSYDIN 10
 |||||
 DB 17 GYTFTSYDIN 26

RESULT 5
 AAY50958
 ID AAY50958 standard; protein; 98 AA.
 AC AAY50958;
 XX 23-MAR-2000 (first entry)
 DE Human FVIII antibody A3-C1 scFv heavy chain protein DP-15.
 XX Human; heavy chain; antibody; factor VIII; hemostatic; hemophilia A;
 KW scFv; A3-C1.
 OS Homo sapiens.
 XX WO9958680-A2.
 PN 18-NOV-1999.
 PD 07-MAY-1999; 99WO-NL000285.
 XX 08-MAY-1998; 98EP-00201543.
 XX (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.
 PA Voorberg JJ, Van Den Brink EN, Turenhout EM;
 PI WPI; 2000-053102/04.
 DR New polynucleotide, polypeptide and antibody useful for diagnosing the
 PT presence of neutralizing antibodies against factor VIII and for treatment
 of hemophilia A patients with these antibodies.

XX Example 8; Fig 9A; 61pp; English.

XX This invention describes a novel polynucleotide (I) (and complements and
 hybridizable polynucleotides) comprising a contiguous nucleotide sequence
 coding for a human antibody with factor VIII specificity which has
 hemostatic activity. (I) is useful as a primer or probe for detecting the
 presence of inhibitory antibodies directed against factor VIII. The
 polypeptides of the invention and the antibodies generated from them are
 useful in compositions for neutralizing factor VIII inhibiting antibodies
 in hemophilia A patients. This sequence represents the human factor VIII
 antibody A3-C1 specific scFv protein DP-15 which is used in the method of
 the invention

XX Sequence 98 AA;

Query Match 100.0%; Score 56; DB 3; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYTFTSYDIN 10
 |||||
 DB 26 GYTFTSYDIN 35

```

RESULT 6
ABG78170
ID ABG78170 standard; protein; 98 AA.
XX
AC ABG78170;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human Fv molecule hypervariable region related peptide #45.
XX
KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
OS Homo sapiens.
XX
PN WO200259264-A2.
XX
PD 01-AUG-2002.
XX
PF 31-DEC-2001; 2001WO-US049440.
XX
PR 29-DEC-2000; 2000US-00751181.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
PI Plaksin D, Peretz T;
XX
DR WPI; 2002-619166/66.
XX
PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favor of other
PT cells.
XX
PS Claim 13; Page 168-169; 232pp; English.
XX
CC The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention
XX
SQ Sequence 98 AA;
Query Match 100.0%; Score 56; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. NO. 0.064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYTFSTSYDIN 10
DB 26 GYTFSTSYDIN 35
RESULT 7
ABG91861
ID ABG91861 standard; protein; 98 AA.
XX
AC ABG91861;
XX
DT 04-DEC-2002 (first entry)
XX

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DE Human antibody fragment #45.
XX
KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US049442.
XX
PR 29-DEC-2000; 2000US-00751181.
XX
PR 29-DEC-2000; 2000US-0258948P.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR WPI; 2002-674776/72.
XX
PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
PS Disclosure; Page 246; Opp; English.
XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention
XX
SQ Sequence 98 AA;
Query Match 100.0%; Score 56; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. NO. 0.064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYTFSTSYDIN 10
DB 26 GYTFSTSYDIN 35
RESULT 8
ABO27070
ID ABO27070 standard; protein; 98 AA.
XX
AC ABO27070;
XX
DT 10-SEP-2003 (first entry)
XX

```

XX DE Human germline heavy chain variable region gene segment #3.
 XX KW Human; heavy chain variable region; VH; humanised antibody;
 KW chimeric antibody; complementarity determining region; CDR;
 KW canonical CDR structure type.
 XX OS Homo sapiens.
 XX US2003039649-A1.
 XX 27-FEB-2003.
 XX 12-JUL-2002; 2002US-00194975.
 XX 12-JUL-2001; 2001US-0305111P.
 XX (FOOT/) FOOTE J.
 XX Foote J;
 XX WPI; 2003-492151/46.
 XX Making humanized antibody for converting antibody, by making chimeric
 PT antibodies containing complementarity determining region from non-human
 PT antibody and appropriate framework sequences of human antibodies.
 XX Example 1; Fig 1; 3lpp; English.
 XX The invention describes a method of making a humanised antibody,
 CC comprising making chimeric antibodies containing a complementarity
 CC determining region (CDR) from a non-human antibody and appropriate
 CC framework sequences (I) of human antibodies. (I) is selected by using
 CC canonical CDR structure types of non-human antibody in comparison to
 CC germline canonical CDR structure types of human antibodies as the basis
 CC for selection, for humanisation. The method is useful for making a
 CC humanised antibody or a converted antibody. The method is applicable for
 CC converting a subject antibody sequence of any subject species to a less
 CC immunogenic form suitable for use in an object species. The method is
 CC reliable for identifying suitable human framework sequences to support
 CC non-human CDR regions and to provide humanised antibodies that retain
 CC high antigen binding with low immunogenicity in humans, without the need
 CC for direct comparison of framework sequences, without the need for
 CC determining critically important amino acid residues in the framework,
 CC and without the need for multiple iteration and construction to obtain
 CC humanised antibodies with suitable therapeutic properties. The antibody
 CC has high affinity and low immunogenicity without need for comparing
 CC framework sequences between non-human and human antibodies. This sequence
 CC represents a human heavy chain variable region gene segment used in the
 CC creation of humanised antibodies
 XX SQ Sequence 98 AA;
 Query Match 100.0%; Score 56; DB 6; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYFTTSYDIN 10
 |||||
 Db 26 GYFTTSYDIN 35
 RESULT 9
 ID AAR79241
 ID AAR79241 standard; protein; 116 AA.
 XX AC AAR79241;
 XX 25-MAR-2003 (revised)
 DT 21-DEC-1995 (first entry)
 XX Heavy chain variable region for monoclonal antibody 4A10.
 DE DE

KW Monoclonal antibody; heavy metal; mercury; variable region; heavy chain.
 XX Synthetic.
 OS WO9520607-A1.
 PN 03-AUG-1995.
 PD 27-JAN-1995; 95WO-US001199.
 PF 27-JAN-1994; 94US-00187407.
 PR (BION-) BIONEERASKA INC.
 PA Lopez O, Wylie DE, Wagner F;
 XX WPI; 1995-275415/36.
 DR N-PSDB; AAQ97498.
 XX New polypeptide(s) which bind heavy metals, esp. mercury - derived from
 PT monoclonal antibodies, used for detecting, removing, adding or
 PT neutralising heavy metals.
 XX Claim 13; Page 54; 106pp; English.
 PS Hybridoma antibodies have been produced with the spleen cells of BALB/c
 XX mouse that had received multiple injections of mercuric ions reacted with
 CC glutathione to produce a mercuric ion coordinate covalent compound which
 CC was covalently bound to keyhole limpet hemocyanin (KLH). Eight hybridomas
 CC (1F10, 4A10, 1C11, 5G4, 23F8, 2D5, 5B6 and 3E8) were producing MAbs that
 CC against glutathione without mercuric ions. RNA was isolated from
 CC hybridoma cells with guanidine isothiocyanate. First strand cDNA
 CC synthesis was catalysed by MuLV reverse transcriptase. The primers used
 CC for cDNA synthesis were complementary to the 5' end of the CH1 domain of
 CC the heavy chain expressed by the hybridoma of interest, or to the 5' and
 CC the C kappa domain. Some of the primers used for cDNA synthesis are
 CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
 CC variable region of a particular antibody polypeptide was also used for
 CC PCR amplification of that variable region, in conjunction with an
 CC appropriate V-region primer. In addition, the VH primer AAQ97518 was used
 CC to amplify the mAb 2D5 and 5B6 heavy chains. The sequences of the PCR
 CC and the deduced AA sequences were determined. These are given in AAQ97498-Q97510
 CC against nucleotides were determined. The sequences of the PCR
 CC descriptions of the SEQ ID nos given on pp 44-45 and in the claims are
 CC different from the descriptions in the sequence listings. The
 CC descriptions in the sequence listings are used here. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX SQ Sequence 116 AA;
 Query Match 100.0%; Score 56; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.076;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYFTTSYDIN 10
 |||||
 Db 26 GYFTTSYDIN 35
 RESULT 10
 ID AAR66302
 ID AAR66302 standard; protein; 117 AA.
 XX AC AAR66302;
 XX 25-MAR-2003 (revised)
 DT 02-AUG-1995 (first entry)
 XX Human immunoglobulin variable heavy chain #8.
 DE DE
 XX Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 KW cosmid; placenta; vector; pJB81; E.coli; mammalian.
 KW

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XX OS Homo sapiens.
XX PN WO9426895-A1.
XX PD 24-NOV-1994.
XX PF 10-MAY-1993; 93WO-JP000603.
XX PR 10-MAY-1993; 93WO-JP000603.
XX PA (NIBS) JAPAN TOBACCO INC.
XX PI Honjo T, Matsuda F;
XX PT DNA fragment comprising human immunoglobulin Vh genes - for the
XX PS production of human immunoglobulin in mammalian hosts.
XX PS Claim 17; Page 41-42; 130pp; Japanese.
XX CC Protein sequences (AAR66295-51) are novel human immunoglobulin heavy
XX CC chain sequences encoded by novel isolated genes. The genes (AAQ78939-
XX CC 79002) were isolated and cloned from a series of cosmid constructs: Y202;
XX CC Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131, by PCR amplification using
XX CC primers AAQ78917-38. The genes are subdivided into 5 families of Vh
XX CC genes. The fragments cover a region of 800 kb. The DNA fragments were
XX CC isolated from high molecular weight DNA from human placenta. The DNA was
XX CC partially digested with Taqi restriction enzyme. The fragments were
XX CC separated by gel electrophoresis and 35-45 kb fractions were collected.
XX CC The fragments were ligated with ClaI-digested cosmid vector pJ891. The
XX CC ligation products were in vitro packed and infected into E.coli 490A. The
XX CC fragments were then subcloned by colony hybridisation. The Vh genes and
XX CC the DNA fragments encoding them are useful in producing human
XX CC immunoglobulin in mammalian hosts. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 117 AA;
    Query Match 100.0%; Score 56; DB 2; Length 117;
    Best Local Similarity 100.0%; Pred. No. 0.076;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
Db 45 GYTFTSYDIN 54

RESULT 11
ABJ18572
AC ABJ18572 standard; protein; 119 AA.
XX AC ABJ18572;
XX DT 18-FEB-2003 (first entry)
XX DE Ganglioside-associated recombinant antibody related VhLE10 protein #2.
XX KW Cytostatic; chimeric antibody; monoclonal antibody; ECACC 94113026;
XX KW N-glycosylated ganglioside; anti-idiotypic monoclonal 1E10; metastatic;
XX KW breast cancer; melanoma; tumour; lung; digestive; urogenital tract;
XX KW sarcoma; neuroectodermal.
XX OS Unidentified.
XX PN WO200281496-A2.
XX PD 17-OCT-2002.
XX PF 08-APR-2002; 2002WO-CU000003.
XX PR 06-APR-2001; 2001CU-00000084.
XX PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX PA (DRIO/) MATEO DE ACOSTA DEL RIO C M.
XX PA (VALL/) LOMBARDEO VALLADARES J.
XX PA (NAVA/) ROQUE NAVARRO L T.
XX PA (REQU/) LOPEZ REQUENA A.
XX PI Mateo De Acosta Del Rio CM, Lombardero Valladares J;
XX PI Roque Navarro LT, Lopez Requena A;

RESULT 12
ABJ18570
ID ABJ18570 standard; protein; 119 AA.
XX AC ABJ18570;
XX DT 18-FEB-2003 (first entry)
XX DE Ganglioside-associated recombinant antibody related Vh 1E10 protein.
XX KW Cytostatic; chimeric antibody; monoclonal antibody; ECACC 94113026;
XX KW N-glycosylated ganglioside; anti-idiotypic monoclonal 1E10; metastatic;
XX KW breast cancer; melanoma; tumour; lung; digestive; urogenital tract;
XX KW sarcoma; neuroectodermal.
XX OS Unidentified.
XX PN WO200281496-A2.
XX PD 17-OCT-2002.
XX PF 08-APR-2002; 2002WO-CU000003.
XX PR 06-APR-2001; 2001CU-00000084.
XX PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX PA (DRIO/) MATEO DE ACOSTA DEL RIO C M.
XX PA (VALL/) LOMBARDEO VALLADARES J.
XX PA (NAVA/) ROQUE NAVARRO L T.
XX PA (REQU/) LOPEZ REQUENA A.
XX PI Mateo De Acosta Del Rio CM, Lombardero Valladares J;
XX PI Roque Navarro LT, Lopez Requena A;

PR 06-APR-2001; 2001CU-00000084.
XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX PA (DRIO/) MATEO DE ACOSTA DEL RIO C M.
XX PA (VALL/) LOMBARDEO VALLADARES J.
XX PA (NAVA/) ROQUE NAVARRO L T.
XX PA (REQU/) LOPEZ REQUENA A.
XX PI Mateo De Acosta Del Rio CM, Lombardero Valladares J;
XX PI Roque Navarro LT, Lopez Requena A;

New chimeric antibodies, useful for treatment, prevention and diagnosis
of tumors that express gangliosides, are derived from monoclonal
antibodies P3 or 1E10.

Example 6; Fig 8; 31pp; Spanish.

The invention relates to a chimeric antibody, derived from a monoclonal
antibody, which recognises N-glycosylated gangliosides and is produced by
hybridoma ECACC 94113026. The chimeric antibody, and similar antibodies
derived from the anti-idiotypic monoclonal 1E10 (recognising P3) are used
for treatment, localisation and in vivo identification of breast cancer
and melanoma, their metastases and relapses, tumours of lung, digestive
and urogenital tracts, and sarcoma and tumours of neuroectodermal origin.
This sequence represents a protein relating to the chimeric antibody of
the invention

XX SQ Sequence 119 AA;
    Query Match 100.0%; Score 56; DB 6; Length 119;
    Best Local Similarity 100.0%; Pred. No. 0.078;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
Db 26 GYTFTSYDIN 35

```



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XX DR WPI; 2003-046857/04.
XX DR N-PSDB; ABL14040.
XX PT New chimeric antibodies, useful for treatment, prevention and diagnosis
XX PT of tumors that express gangliosides, are derived from monoclonal
XX PT antibodies P3 or 1B10.
XX PS Example 6; Fig 6; 31pp; Spanish.
XX CC The invention relates to a chimeric antibody, derived from a monoclonal
XX CC antibody, which recognises N-glycosylated gangliosides and is produced by
XX CC hybridoma ECACC 94113026. The chimeric antibody, and similar antibodies
XX CC derived from the anti-idiotypic monoclonal 1B10 (recognising P3) are used
XX CC for treatment, localisation and in vivo identification of breast cancer
XX CC and melanoma, their metastases and relapses, tumours of lung, digestive
XX CC and urogenital tracts, and sarcoma and tumours of neuroectodermal origin.
XX CC This sequence represents a protein relating to the chimeric antibody of
XX CC the invention
XX SQ Sequence 119 AA;
Query Match 100.0%; Score 56; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYTFTSYDIN 10
DB 26 GYTFTSYDIN 35
RESULT 13
AAB62747
ID AAB62747 standard; protein; 120 AA.
XX AC
XX AC AAB62747;
XX DT 03-APR-2001 (first entry)
XX DE Human HIV-1 monoclonal antibody SEQ ID NO: 46.
XX KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX KW envelope glycoprotein; gp120; diagnosis.
XX OS Homo sapiens.
XX PN WO200100678-A1.
XX PD 04-JAN-2001.
XX PF 23-JUN-2000; 2000WO-US017327.
XX PR 30-JUN-1999; 99US-0141701P.
XX PS (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Watkins BA, Reitz MS;
XX PI WPI; 2001-112438/12.
XX DR N-PSDB; AAF29048.
XX XX Novel human monoclonal antibody immunoreactive with human
XX PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
XX PT in biological sample and providing passive immunotherapy to HIV-1
XX PT infected mammal.
XX PS Claim 1; Page 51-52; 81pp; English.
XX CC The present invention provides the protein and coding sequences for the
XX CC variable regions of human monoclonal antibodies which are immunoreactive
XX CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX CC These can be used in diagnosis and therapy of HIV-1 infection

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SQ Sequence 120 AA;
Query Match 100.0%; Score 56; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYTFTSYDIN 10
DB 27 GYTFTSYDIN 36
RESULT 14
AAR55829
ID AAR55829 standard; protein; 122 AA.
XX AC AAR55829;
XX DT 02-SEP-2003 (first entry)
XX DE Heavy chain variable region of anti-Ang-2 antibody IP-2C11 HC.
XX KW Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic;
XX KW synaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
XX KW angiogenesis; antibody.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT Region 26..36
XX FT /note= "complementarity determining region (CDR) 1"
XX FT Region 50..66
XX FT /note= "complementarity determining region (CDR) 2"
XX FT Region 96..112
XX FT /note= "complementarity determining region (CDR) 3"
XX PN WO2003030833-A2.
XX PD 17-APR-2003.
XX PF 11-OCT-2002; 2002WO-US032613.
XX PR 11-OCT-2001; 2001US-0328604P.
XX PR 10-OCT-2002; 2002US-00269805.
XX PS (AMGE-) AMGEN INC.
XX PI Olinier JD;
XX PI WPI; 2003-504963/47.
XX PS Claim 1; Page 93; 161pp; English.
XX CC The invention relates to a specific binding agent, which comprises at
XX CC least one peptide selected from any of 62 peptides (AAR55769-830) or its
XX CC fragment. The binding agents are antibodies that recognize and bind to
XX CC angiopoietin-2 (Ang-2). The specific binding agent, particularly the
XX CC antibody, is useful for inhibiting undesired angiogenesis, treating
XX CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
XX CC 2 activity, modulating vascular permeability or plasma leakage, or
XX CC treating a disease (e.g. ocular neovascular disease, obesity,
XX CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
XX CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
XX CC disease, bone-related disease, or psoriasis) in a mammal. The present
XX CC sequence represents a heavy chain variable region of an anti-Ang-2
XX CC antibody
XX SQ Sequence 122 AA;
Query Match 100.0%; Score 56; DB 6; Length 122;

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Best Local Similarity 100.0%; Pred. No. 0.079;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: April 21, 2004, 17:33:09

Job time : 42 secs

QY 1 GYTFTSYDIN 10

Db 26 GYTFTSYDIN 35

RESULT 15

ABG74245

ID ABG74245 standard; protein; 139 AA.

XX AC

XX ABG74245;

DT 22-APR-2003 (first entry)

DE Mouse antibody 4D4 heavy chain variable region.

XX T-cell receptor; cytostatic; dermatological; neuroprotective;

XX immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;

XX 3E11; prostate-specific membrane antigen; zeta signalling chain;

XX CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;

XX small cell lung cancer; heavy chain variable region; mouse.

OS Mus sp.

XX US2002132983-A1.

XX 19-SEP-2002.

XX 10-DEC-2001; 2001US-00006773.

XX 30-NOV-2000; 2000US-0250087P.

XX 30-NOV-2000; 2000US-0250089P.

XX (JUNG/) JUNGHANS R P.

XX Junghans RP;

XX WPI; 2003-208946/20.

XX N-PSDB; ABX16571.

XX New chimeric molecule useful in treating patients with disorders, such as

XX melanoma, neuroendocrine disorders, prostate and small cell lung cancer

XX comprises GD3 and/or PSMA binding domains of antibody.

PS Disclosure; Page 14-15; 35pp; English.

XX The invention relates to a chimaeric molecule comprising the GD3

XX (ganglioside antigen) binding domain of antibody MB3.6, with any of 3

XX variable gene sequences, or the PSMA (prostate-specific membrane antigen)

XX binding domain of antibody 3D8, 4D4 and 3E11, with variable gene

XX sequences, the zeta signalling chain of the T cell receptor and an

XX intervening CD8alpha hinge in which cysteine residues have been mutated.

XX The chimaeric molecules expressed in T cells or NK cells or other

XX effector cells are useful in treating patients with cancers expressing

XX the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),

XX and/or together with each other or with heterologous constructs to engage

XX additional stimulatory and functional properties of the effector cells to

XX enhance the antitumour therapeutic efficacy (claimed). They are

XX particularly useful in disorders including melanoma, neuroendocrine

XX tumours and prostate and small cell lung cancer. The present sequence

XX represents the mouse antibody 4D4 heavy chain variable region

SQ Sequence 139 AA;

Query Match 100.0%; Score 56; DB 6; Length 139;

Best Local Similarity 100.0%; Pred. No. 0.09;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10

Db 45 GYTFTSYDIN 54

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2004, 17:37:29 ; Search time 30.1449 Seconds

(without alignments)
91.715 Million cell updates/sec

Title: SEQ1

Perfect score: 56

Sequence: 1 gytfstsydin 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 56 | 100.0 | 92 | 9 | US-09-864-761-47202 |
| 2 | 56 | 100.0 | 96 | 14 | US-10-194-975-3 |
| 3 | 56 | 100.0 | 98 | 12 | US-10-453-698-43 |
| 4 | 56 | 100.0 | 98 | 12 | US-10-029-926B-45 |
| 5 | 56 | 100.0 | 98 | 14 | US-10-041-860-289 |
| 6 | 56 | 100.0 | 98 | 14 | US-10-041-860-290 |
| 7 | 56 | 100.0 | 98 | 14 | US-10-041-860-295 |
| 8 | 56 | 100.0 | 98 | 14 | US-10-041-860-296 |
| 9 | 56 | 100.0 | 98 | 14 | US-10-041-860-342 |
| 10 | 56 | 100.0 | 98 | 14 | US-10-041-860-344 |
| 11 | 56 | 100.0 | 98 | 14 | US-10-041-860-348 |
| 12 | 56 | 100.0 | 98 | 14 | US-10-041-860-350 |
| 13 | 56 | 100.0 | 98 | 14 | US-10-041-860-361 |
| 14 | 56 | 100.0 | 98 | 14 | US-10-041-860-362 |
| 15 | 56 | 100.0 | 98 | 14 | US-10-041-860-373 |

ALIGNMENTS

RESULT 1

US-09-864-761-47202
; Sequence 47202, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Weisheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aescmca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

Sequence 374, App
Sequence 43, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 1, Appli
Sequence 61, Appl
Sequence 38, Appl
Sequence 48, Appl
Sequence 200, App
Sequence 203, App
Sequence 237, App
Sequence 238, App
Sequence 240, App
Sequence 343, App
Sequence 372, App
Sequence 19, Appl
Sequence 21, Appl
Sequence 199, App
Sequence 201, App
Sequence 236, App
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Sequence 242, App
Sequence 360, App
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Sequence 67, Appl
Sequence 13, Appl

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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47202
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62
; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39
; OTHER INFORMATION: EST_HUMAN HIT: AW405627.1, EVALUE 8.00e-48
US-09-864-761-47202
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Query Match 100.0%; Score 56; DB 9; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GYTFTSYDIN 10
| | | | |
DB 17 GYTFTSYDIN 26
```

RESULT 2

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US-10-194-975-3
; Sequence 3, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-3
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Query Match 100.0%; Score 56; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GYTFTSYDIN 10
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DB 24 GYTFTSYDIN 33
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RESULT 3

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US-10-453-698-43
; Sequence 43, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
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; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-453-698-43

Query Match 100.0%; Score 56; DB 12; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GYTFTSYDIN 10
| | | | |
DB 26 GYTFTSYDIN 35
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RESULT 4

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US-10-029-926B-45
; Sequence 45, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-45
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Query Match 100.0%; Score 56; DB 12; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GYTFTSYDIN 10
| | | | |
DB 26 GYTFTSYDIN 35
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RESULT 5

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US-10-041-860-289
; Sequence 289, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiaochi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyan
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX 051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 289
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
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US-10-041-860-299

Query Match 100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
| | | | | | | |
DB 26 GYTFTSYDIN 35

RESULT 6

US-10-041-860-299
; Sequence 290, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 290
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-290

Query Match 100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
| | | | | | | |
DB 26 GYTFTSYDIN 35

RESULT 7

US-10-041-860-295
; Sequence 295, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-295

Query Match 100.0%; Score 56; DB 14; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
| | | | | | | |
DB 26 GYTFTSYDIN 35

RESULT 8

US-10-041-860-296
; Sequence 296, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-296

Query Match 100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
| | | | | | | |
DB 26 GYTFTSYDIN 35

RESULT 9

US-10-041-860-342
; Sequence 342, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 342
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-342

Query Match 100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 26 GYTFTSYDIN 35

RESULT 10
 US-10-041-860-344
 ; Sequence 344, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 344
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-344

Query Match 100.0%; Score 56; DB 14; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 26 GYTFTSYDIN 35

RESULT 11
 US-10-041-860-348
 ; Sequence 348, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 348
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-348

Query Match 100.0%; Score 56; DB 14; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 26 GYTFTSYDIN 35

RESULT 12
 US-10-041-860-350
 ; Sequence 350, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 350
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; NAME/KEY: VARIANT
 ; LOCATION: 55
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 55
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 US-10-041-860-350

Query Match 100.0%; Score 56; DB 14; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 26 GYTFTSYDIN 35

RESULT 13
 US-10-041-860-361
 ; Sequence 361, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 361
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-361

Query Match 100.0%; Score 56; DB 14; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.03;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTSYDIN 10
Db 26 GYTFTSYDIN 35

RESULT 14

US-10-041-860-362
; Sequence 362, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 362
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 57
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 57
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-362

Query Match 100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTSYDIN 10
Db 26 GYTFTSYDIN 35

RESULT 15

US-10-041-860-373
; Sequence 373, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 98
; TYPE: PRT

; ORGANISM: homo sapiens
US-10-041-860-373

Query Match 100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTSYDIN 10
Db 26 GYTFTSYDIN 35

Search completed: April 21, 2004, 18:02:05
Job time : 31.1449 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:48 ; Search time 7.6087 seconds
(without alignments)

102.653 Million cell updates/sec

Title: SEQ2

Perfect score: 82

Sequence: 1 inpsngntdyackfq 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 71 | 86.6 | 117 | 1 | P23083 homo sapien |
| 2 | 62 | 75.6 | 117 | 1 | P01743 homo sapien |
| 3 | 62 | 75.6 | 117 | 1 | P01743 homo sapien |
| 4 | 57 | 69.5 | 117 | 1 | P01756 mus musculus |
| 5 | 57 | 69.5 | 117 | 1 | P01757 mus musculus |
| 6 | 57 | 69.5 | 118 | 1 | P06330 mus musculus |
| 7 | 51 | 62.2 | 117 | 1 | P01753 mus musculus |
| 8 | 51 | 62.2 | 117 | 1 | P01754 mus musculus |
| 9 | 51 | 62.2 | 117 | 1 | P06328 mus musculus |
| 10 | 51 | 62.2 | 139 | 1 | P01751 mus musculus |
| 11 | 50 | 61.0 | 120 | 1 | P06329 mus musculus |
| 12 | 50 | 61.0 | 138 | 1 | P03980 mus musculus |
| 13 | 49 | 59.8 | 117 | 1 | P01748 mus musculus |
| 14 | 45 | 54.9 | 120 | 1 | P01747 mus musculus |
| 15 | 45 | 54.9 | 137 | 1 | P01755 mus musculus |
| 16 | 42 | 51.2 | 117 | 1 | P01750 mus musculus |
| 17 | 42 | 51.2 | 136 | 1 | P01759 mus musculus |
| 18 | 41 | 50.0 | 140 | 1 | P01746 mus musculus |
| 19 | 40 | 48.8 | 117 | 1 | P01758 mus musculus |
| 20 | 40 | 48.8 | 117 | 1 | P01742 homo sapien |
| 21 | 40 | 48.8 | 518 | 1 | P58994 buchnera ap |
| 22 | 40 | 48.8 | 1068 | 1 | P12221 marchantia |
| 23 | 40 | 48.8 | 3329 | 1 | P97929 mus musculus |
| 24 | 39 | 47.6 | 114 | 1 | P01741 mus musculus |
| 25 | 39 | 47.6 | 117 | 1 | P06327 mus musculus |
| 26 | 39 | 47.6 | 202 | 1 | P96309 arabidopsis |
| 27 | 39 | 47.6 | 323 | 1 | Q7VQC1 candidatus |
| 28 | 39 | 47.6 | 374 | 1 | Q03286 saccharomyc |
| 29 | 39 | 47.6 | 398 | 1 | P22760 homo sapien |
| 30 | 39 | 47.6 | 504 | 1 | Q58205 methanococ |
| 31 | 39 | 47.6 | 546 | 1 | P36938 escherichia |
| 32 | 39 | 47.6 | 566 | 1 | Q05332 clostridium |
| 33 | 39 | 47.6 | 887 | 1 | P46935 mus musculus |

```

34 39 47.6 887 1 NED4 RAT
35 39 47.6 1000 1 NED4 HUMAN
36 38.5 47.0 295 1 YB45 PYREFU
37 38.5 47.0 1257 1 CAMEL HUMAN
38 38 46.3 279 1 YB49 STRP3
39 38 46.3 279 1 YE93 STRPY
40 38 46.3 352 1 STSY CATRO
41 38 46.3 2164 1 HGAI PORGI
42 38 46.3 2628 1 HGA2 PORGI
43 37 45.1 124 1 TOXK WILSA
44 37 45.1 128 1 LYCI_PIG
45 37 45.1 140 1 ATPE_YERPE
Q62940 rattus norv
P46934 homo sapien
Q8ulr0 pyrococcus
P32004 homo sapien
Q8k8t3 streptococc
Q99Yy0 streptococc
P18417 catharanthu
P59915 porphyromon
Q51845 porphyromon
Q00948 williopeis
P12067 sus scrofa
P58647 yersinia pe

```

ALIGNMENTS

RESULT 1

HVIG_HUMAN

ID HVIG_HUMAN STANDARD; PRT; 117 AA.

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AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMOB J. 7:1047-1051(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

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```

EMBL; X07448; -; NOT_ANNOTATED_CDS.

PIR; S00476; HVHU35.

HSSP; P01772; 2PB4.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Signal.

SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.

FT DOMAIN 20 >117 IG-LIKE.

FT NON_TER 117

SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match

Best Local Similarity 86.6%; Score 71; DB 1; Length 117;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYACKFK 15

Db 70 INPNSGGTNYACKFK 84


```

RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RL immunoglobulin epsilon chain expressed in a myeloma cell line.";
RN Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RP Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSSP; P01789; 1MCP.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; P:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT DOMAIN 20 131 IG-LIKE
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
FT SEQUENCE 147 AA; 16491 MW; 949F9F72A5366C20 CRC64;

Query Match 75.6%; Score 62; DB 1; Length 147;
Best Local Similarity 73.3%; Pred. No. 0.0014;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15
Db |||||:|:|:|:|:|
70 INPNSGNTDYAOKFQ 84

RESULT 4
ID HV12 MOUSE STANDARD; PRT; 117 AA.
AC P01756; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Oct. 42, Last annotation update)
DE Ig heavy chain V region MOPC 1043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OK NCBI_TaxID=10090;
RN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RP MEDLINE=83075344; PubMed=6816276;
RX Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RL heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02039; MEMS4E.
CC HSSP; P01789; 1MCP.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.

```

```
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 69.5%; Score 57; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 0.0078;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNNGGTSYNQKFK 65

RESULT 5
ID HV13 MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE

Query Match 69.5%; Score 57; DB 1; Length 118;
Best Local Similarity 66.7%; Pred. No. 0.0079;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNNGGTSYNQKFK 65

RESULT 7
ID HV09 MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M.; Paskind M.; Reth M.; Imanishi-Kari T.; Rajewsky K.;
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR; D90809; HVM561.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117

Query Match 69.5%; Score 57; DB 1; Length 118;
Best Local Similarity 66.7%; Pred. No. 0.0079;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNNGGTSYNQKFK 65

RESULT 7
ID HV09 MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M.; Paskind M.; Reth M.; Imanishi-Kari T.; Rajewsky K.;
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR; D90809; HVM561.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117

Query Match 69.5%; Score 57; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 0.0078;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNNGGTSYNQKFK 65

RESULT 6
ID HV51 MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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SQ SEQUENCE 117 AA; 12890 MW; 16191A08CB17F5A CRC64;
Query Match 62.2%; Score 51; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 0.083;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKQK 15
DB 70 IDPNSGGTKYNEKFK 84

RESULT 8
HV10 MOUSE
ID HV10 MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE IG heavy chain V region 145 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
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CC -----
CC EMBL; J00533; AAA38602.1; -.
CC PIR; C90809; HVMS45.
CC HSSP; P01810; 2FBJ.
CC MGD; MGI:96486; Igh-VJ558.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC NON_TER 117 117
CC SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 62.2%; Score 51; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 0.083;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKQK 15
DB 70 IDPNSGGTKYNEKFK 84
```

```
RESULT 9
HV49 MOUSE
ID HV49 MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=8509340; PubMed=2578321;
RA Vancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
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CC -----
CC EMBL; M13788; AAA38506.1; -.
CC PIR; A02035; MHWSB4.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; IG_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DISULFID 41 115 BY SIMILARITY.
CC NON_TER 117 117
CC SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 62.2%; Score 51; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 0.083;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKQK 15
DB 70 IDPNSGGTKYNEKFK 84

RESULT 10
HV07 MOUSE
ID HV07 MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RC MEDLINE=81234548; PubMed=6788376;
EX
```

```
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MENA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
CC EMBL: J00529; AAA38170.1; -.
CC PIR: A90809; MHMS18.
CC PDB: 1A6U; 27-MAY-98.
CC PDB: 1A6W; 15-JUL-98.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00047; Ig_1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal; 3D-structure.
CC SIGNAL 1
CC CHAIN 19 IG HEAVY CHAIN V REGION B1-8/186-2.
CC DOMAIN 20 139 FRAMEWORK-1.
CC DOMAIN 21 49 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 22 54 FRAMEWORK-2.
CC DOMAIN 23 58 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 24 85 FRAMEWORK-3.
CC DOMAIN 25 117 D SEGMENT.
CC DOMAIN 26 124 JH2 SEGMENT.
CC DOMAIN 27 139 BY SIMILARITY.
CC DISULFID 41 115
CC NON TER 139 139
CC SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 62.2%; Score 51; DB 1; Length 139;
Best Local Similarity 60.0%; Pred. No. 0.1;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFQ 15
Db 70 IDPNSGGTKYNEKFK 84

RESULT 11
HV50 MOUSE
ID HV50 MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=84182519; PubMed=6201362;
EX Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.

Query Match 61.0%; Score 50; DB 1; Length 138;
Best Local Similarity 53.3%; Pred. No. 0.15;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFQ 15
Db 70 INPNSGNTDYAQKFQ 84

RESULT 12
HV48 MOUSE
ID HV48 MOUSE STANDARD; PRT; 138 AA.
AC P0380;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=84248078; PubMed=6429663;
EX Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMST7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
DR SIGNAL 1 20
DR CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
DR DOMAIN 21 49 FRAMEWORK-1.
DR DOMAIN 22 54 COMPLEMENTARITY-DETERMINING-1.
DR DOMAIN 23 58 FRAMEWORK-2.
DR DOMAIN 24 85 COMPLEMENTARITY-DETERMINING-2.
DR DOMAIN 25 117 FRAMEWORK-3.
DR DOMAIN 26 127 COMPLEMENTARITY-DETERMINING-3.
DR DOMAIN 27 138 FRAMEWORK-4.
DR DISULFID 41 115 BY SIMILARITY.
DR NON TER 138 138
DR SEQUENCE 138 AA; 15576 MW; 748157B4C6907B8E CRC64;

Query Match 61.0%; Score 50; DB 1; Length 138;
Best Local Similarity 53.3%; Pred. No. 0.15;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFQ 15
Db 70 INPNSGNTDYAQKFQ 84

RESULT 13
HV04 MOUSE
ID HV04 MOUSE STANDARD; PRT; 117 AA.
AC P01748;
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 61.0%; Score 50; DB 1; Length 120;
Best Local Similarity 53.3%; Pred. No. 0.13;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFQ 15
Db 51 INPNSGGTYNEKFK 65

RESULT 12
HV48 MOUSE
ID HV48 MOUSE STANDARD; PRT; 138 AA.
AC P0380;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=84248078; PubMed=6429663;
EX Gilliam A.C., Shen A., Richards J.E., Blattner P.R., Mushinski J.F.,
Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMST7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 22 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 23 58 FRAMEWORK-2.
FT DOMAIN 24 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 25 117 FRAMEWORK-3.
FT DOMAIN 26 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 27 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157B4C6907B8E CRC64;

Query Match 61.0%; Score 50; DB 1; Length 138;
Best Local Similarity 53.3%; Pred. No. 0.15;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFQ 15
Db 70 INPNSGGTYNEKFK 84

RESULT 13
HV04 MOUSE
ID HV04 MOUSE STANDARD; PRT; 117 AA.
AC P01748;
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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS; THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC
DR PIR; A02030; HYMS23.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 59.8%; Score 49; DB 1; Length 117;
Best Local Similarity 53.3%; Pred. No. 0.18;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKQFK 15
DB 70 INPGNGYTKYNEKFK 84

RESULT 14
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS; FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -!- SIMILARITY; Contains 1 immunoglobulin-like domain.
DR HSP; P01789; 1MCP.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 54.9%; Score 45; DB 1; Length 120;
Best Local Similarity 53.3%; Pred. No. 0.91;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKQFK 15
DB 50 INPGNGYTKYNEKFK 64

RESULT 15
HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 543 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS; THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
-----
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DR EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; G2MS43.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT DOMAIN 20 137 IG HEAVY CHAIN V REGION 543.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

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Query Match 54.9%; Score 45; DB 1; Length 137;
 Best Local Similarity 53.3%; Pred. No. 1.1;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFPQ 15
 | : | | | | | : | : |
 Db 70 IDPNSGGTTYNEHFR 84

Search completed: April 21, 2004, 17:33:57
 Job time : 8.6087 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:28:28 ; Search time 12.029 Seconds
(without alignments)
42.918 Million cell updates/sec

Title: SEQ1

Perfect score: 56

Sequence: 1 gyftsydin 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|-------|--------|--------------------|----|--------------------|
| 1 | 56 | 100.0 | 116 | 2 | US-08-888-366-2 | | Sequence 2, Appl |
| 2 | 56 | 100.0 | 117 | 3 | US-08-545-809A-96 | | Sequence 96, Appl |
| 3 | 49 | 87.5 | 200 | 6 | 5189147-8 | | Patent No. 5189147 |
| 4 | 49 | 87.5 | 561 | 3 | US-09-192-545-2 | | Sequence 2, Appl |
| 5 | 48 | 85.7 | 115 | 1 | US-07-942-245-22 | | Sequence 22, Appl |
| 6 | 47 | 83.9 | 119 | 1 | US-08-478-039-65 | | Sequence 65, Appl |
| 7 | 47 | 83.9 | 119 | 1 | US-08-476-349A-65 | | Sequence 65, Appl |
| 8 | 45 | 80.4 | 20 | 4 | US-09-556-605-6 | | Sequence 6, Appl |
| 9 | 45 | 80.4 | 119 | 4 | US-09-556-605-1 | | Sequence 1, Appl |
| 10 | 45 | 80.4 | 120 | 2 | US-08-602-725-27 | | Sequence 27, Appl |
| 11 | 45 | 80.4 | 128 | 1 | US-08-478-039-73 | | Sequence 73, Appl |
| 12 | 45 | 80.4 | 128 | 1 | US-08-478-039-102 | | Sequence 102, Appl |
| 13 | 45 | 80.4 | 128 | 1 | US-08-476-349A-73 | | Sequence 73, Appl |
| 14 | 45 | 80.4 | 128 | 1 | US-08-476-349A-102 | | Sequence 102, Appl |
| 15 | 44 | 78.6 | 98 | 3 | US-08-881-037-64 | | Sequence 64, Appl |
| 16 | 44 | 78.6 | 113 | 3 | US-08-881-037-18 | | Sequence 18, Appl |
| 17 | 44 | 78.6 | 117 | 3 | US-08-545-809A-105 | | Sequence 105, Appl |
| 18 | 44 | 78.6 | 121 | 3 | US-08-881-037-65 | | Sequence 65, Appl |
| 19 | 43 | 76.8 | 92 | 3 | US-08-783-853A-84 | | Sequence 84, Appl |
| 20 | 43 | 76.8 | 92 | 4 | US-09-344-050-84 | | Sequence 84, Appl |
| 21 | 43 | 76.8 | 108 | 4 | US-09-893-896-1 | | Sequence 1, Appl |
| 22 | 43 | 76.8 | 108 | 4 | US-09-893-896-3 | | Sequence 3, Appl |
| 23 | 43 | 76.8 | 112 | 3 | US-08-783-853A-20 | | Sequence 20, Appl |
| 24 | 43 | 76.8 | 112 | 3 | US-08-545-809A-113 | | Sequence 113, Appl |
| 25 | 43 | 76.8 | 112 | 4 | US-09-344-050-20 | | Sequence 20, Appl |
| 26 | 43 | 76.8 | 118 | 1 | US-08-425-336-124 | | Sequence 124, Appl |
| 27 | 43 | 76.8 | 118 | 1 | US-08-425-336-126 | | Sequence 126, Appl |

28 43 76.8 118 1 US-08-488-113B-124 Sequence 124, App
29 43 76.8 118 1 US-08-488-113B-126 Sequence 126, App
30 43 76.8 118 1 US-08-477-484B-124 Sequence 124, App
31 43 76.8 118 1 US-08-477-484B-126 Sequence 126, App
32 43 76.8 118 1 US-08-107-669D-28 Sequence 28, Appl
33 43 76.8 118 1 US-08-107-669D-29 Sequence 29, Appl
34 43 76.8 118 1 US-08-107-669D-66 Sequence 66, Appl
35 43 76.8 118 1 US-08-107-669D-67 Sequence 67, Appl
36 43 76.8 118 1 US-08-472-788A-28 Sequence 28, Appl
37 43 76.8 118 1 US-08-472-788A-29 Sequence 29, Appl
38 43 76.8 118 1 US-08-472-788A-88 Sequence 88, Appl
39 43 76.8 118 1 US-08-472-788A-89 Sequence 89, Appl
40 43 76.8 118 2 US-08-477-531B-28 Sequence 28, Appl
41 43 76.8 118 2 US-08-477-531B-29 Sequence 29, Appl
42 43 76.8 118 2 US-08-477-531B-66 Sequence 66, Appl
43 43 76.8 118 2 US-08-477-531B-67 Sequence 67, Appl
44 43 76.8 118 2 US-08-646-360-124 Sequence 124, App
45 43 76.8 118 2 US-08-646-360-126 Sequence 126, App

ALIGNMENTS

RESULT 1
US-08-888-366-2
; Sequence 2, Application US/08889366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchand & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-888-366-2
Query Match      100.0%; Score 56; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.02; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
Db      26 GYTFTSYDIN 35

RESULT 2
US-08-545-809A-96
; Sequence 96, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-96

Query Match      100.0%; Score 56; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.02; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
Db      45 GYTFTSYDIN 54

RESULT 3
5189147-8
; Patent No. 5189147
; APPLICANT: SAITO, HARUO; KRAZ, DAVID M.; ELSER, HERMAN N.;
; TONEGAWA, SUSUMU
; TITLE OF INVENTION: METEROIDIMERIC T LYMPHOCYTE RECEPTOR
; ANTI-BODY
; NUMBER OF SEQUENCES: 21

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/271,216
; FILING DATE: 14-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 666,988
; FILING DATE: 31-OCT-1984
; APPLICATION NUMBER: 620,122
; FILING DATE: 13-JUN-1984
; SEQ ID NO: 8
; LENGTH: 200
5189147-8

Query Match      87.5%; Score 49; DB 6; Length 200;
Best Local Similarity 90.0%; Pred. No. 0.52;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
Db      26 GYTFTSYGIN 35

RESULT 4
US-09-192-545-2
; Sequence 2, Application US/09192545
; Patent No. 6118044
; GENERAL INFORMATION:
; APPLICANT: Karasuyama, Hajime
; APPLICANT: Yonekawa, Hiromichi
; APPLICANT: Taya, Choji
; APPLICANT: Matsuoka, Kunie
; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
; FILE REFERENCE: 799P79570
; CURRENT APPLICATION NUMBER: US/09/192,545
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: JP HEI 9-313989
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Designed heavy
US-09-192-545-2

Query Match      87.5%; Score 49; DB 3; Length 561;
Best Local Similarity 90.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
Db      45 GYTFTSYGIN 54

RESULT 5
US-07-942-245-22
; Sequence 22, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States

```


ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
FILING DATE: 09-SEP-1992
APPLICATION NUMBER: US/07/942,245
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-22

Query Match 85.7%; Score 48; DB 1; Length 115;
Best Local Similarity 80.0%; Pred. No. 0.43;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
||| ||| :
DB 26 GYTFTSYGVN 35

RESULT 6
US-08-478-039-65
; Sequence 65, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE: Monkey
ORGANISM: Monkey
POSITION IN GENOME: clone 1-14
CHROMOSOME/SEGMENT: clone 1-14
US-08-478-039-65

Query Match 83.9%; Score 47; DB 1; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
||| ||| :
DB 26 GYTFTSYVIN 35

RESULT 7
US-08-476-349A-65
; Sequence 65, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids

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; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: clone 1-14
US-08-476-349A-55

Query Match      83.9%; Score 47; DB 1; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
DB      26 GYTFSTSYIN 35

RESULT 8
US-09-556-605-6
; Sequence 6, Application US/09556605
; Patent No. 6417324
; GENERAL INFORMATION:
; APPLICANT: Saliberg, Matti
; APPLICANT: Lazdina, Una
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
; TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
; FILE REFERENCE: TRIPEP.020A
; CURRENT APPLICATION NUMBER: US/09/556,605
; CURRENT FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
US-09-556-605-6

Query Match      80.4%; Score 45; DB 4; Length 20;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
DB      5 GYTFSTSYDID 14

RESULT 9
US-09-556-605-1
; Sequence 1, Application US/09556605
; Patent No. 6417324
; GENERAL INFORMATION:
; APPLICANT: Saliberg, Matti
; APPLICANT: Lazdina, Una
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
; TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
; FILE REFERENCE: TRIPEP.020A
; CURRENT APPLICATION NUMBER: US/09/556,605
; CURRENT FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
US-09-556-605-1

Query Match      80.4%; Score 45; DB 4; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
DB      26 GYTFSTSYAMN 35

Query Match      80.4%; Score 45; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
DB      26 GYTFSTSYAMN 35

Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
DB      25 GYTFSTSYDID 34

RESULT 10
US-08-602-725-27
; Sequence 27, Application US/08602725
; Patent No. 5965710
; GENERAL INFORMATION:
; APPLICANT: BODMER, WALTER F
; APPLICANT: DURBIN, HELGA
; APPLICANT: SNARY, DAVID
; APPLICANT: STEWART, LORNA MD
; APPLICANT: YOUNG, SUSAN
; APPLICANT: BATES, PAUL A
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,725
; FILING DATE: 02-FEB-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA: PCT/GB94/01816
; APPLICATION NUMBER: 19-AUG-1994
; FILING DATE: 19-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9317423
; FILING DATE: 21-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36663
; REFERENCE/DOCKET NUMBER: 1090-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Human RF-TS3 heavy chain
US-08-602-725-27

Query Match      80.4%; Score 45; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
DB      26 GYTFSTSYAMN 35
```

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RESULT 11
US-08-478-039-73
; Sequence 73, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-40
; US-08-478-039-73

Query Match 80.4%; Score 45; DB 1; Length 128;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTFSYDIN 10
|:|:|:|:|:|
Db 26 GFTFSSYDMN 35

RESULT 12
US-08-478-039-102
; Sequence 102, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:

```

```

; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40
; US-08-478-039-102

Query Match 80.4%; Score 45; DB 1; Length 128;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTFSYDIN 10
|:|:|:|:|:|
Db 26 GFTFSSYDMN 35

RESULT 13
US-08-476-349A-73
; Sequence 73, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476.349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-476-349A-73
Query Match 80.4%; Score 45; DB 1; Length 128;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYTFSSYDIN 10
Db 26 GTFSSYDYN 35
RESULT 14
US-08-476-349A-102
Sequence 102. Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476.349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: #40
US-08-476-349A-102
Query Match 80.4%; Score 45; DB 1; Length 128;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYTFSSYDIN 10
Db 26 GTFSSYDYN 35
RESULT 15
US-08-881-037-64
Sequence 64. Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037

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; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Koneki, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-881-037-64

Query Match      78.6%; Score 44; DB 3; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYFTTSYDIN 10
        |||||
Db      26 GYFTTSYGIS 35

Search completed: April 21, 2004, 17:40:03
Job time : 13.029 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:27:33 ; Search time 13.6957 Seconds
(without alignments)
105.353 Million cell updates/sec

Title: SEQ2
Perfect score: 82
Sequence: 1 inpsngtdyaqkf 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 72 | 87.8 | 98 | 2 S26918 | Ig heavy chain V r |
| 2 | 72 | 87.8 | 132 | 2 S31596 | Ig heavy chain V r |
| 3 | 72 | 87.8 | 136 | 2 S31600 | Ig heavy chain V r |
| 4 | 71 | 86.6 | 98 | 2 S26910 | Ig heavy chain V r |
| 5 | 71 | 86.6 | 98 | 2 S26938 | Ig heavy chain V r |
| 6 | 71 | 86.6 | 98 | 2 S26912 | Ig heavy chain pre |
| 7 | 71 | 86.6 | 117 | 1 HVHJ35 | Ig heavy chain V r |
| 8 | 71 | 86.6 | 117 | 2 S31680 | Ig heavy chain V r |
| 9 | 71 | 86.6 | 117 | 2 S31851 | Ig heavy chain V r |
| 10 | 71 | 86.6 | 118 | 2 S36265 | Ig heavy chain V r |
| 11 | 71 | 86.6 | 129 | 2 S46393 | anti-Sm antibody V |
| 12 | 71 | 86.6 | 135 | 2 S49530 | Ig heavy chain V-1 |
| 13 | 69 | 84.1 | 104 | 2 S59899 | Ig heavy chain V-1 |
| 14 | 68 | 82.9 | 123 | 2 D33548 | Ig heavy chain V r |
| 15 | 65 | 79.3 | 171 | 2 S33623 | Ig heavy chain V r |
| 16 | 63 | 76.8 | 110 | 2 PH1668 | Ig heavy chain V r |
| 17 | 63 | 76.8 | 110 | 2 PH1669 | Ig heavy chain V r |
| 18 | 63 | 76.8 | 127 | 2 S34014 | Ig heavy chain V r |
| 19 | 62 | 75.6 | 98 | 2 S26920 | Ig heavy chain V r |
| 20 | 62 | 75.6 | 117 | 1 HVHJ35 | Ig heavy chain pre |
| 21 | 62 | 75.6 | 143 | 1 E3HJND | Ig heavy chain pre |
| 22 | 61 | 74.4 | 110 | 2 PH1670 | Ig heavy chain V r |
| 23 | 61 | 74.4 | 113 | 2 S55535 | Ig heavy chain V r |
| 24 | 61 | 74.4 | 116 | 2 S22553 | Ig heavy chain V r |
| 25 | 60 | 73.2 | 288 | 2 S29690 | Ig heavy chain VDJ |
| 26 | 59 | 72.0 | 86 | 2 S29544 | Ig heavy chain V r |
| 27 | 59 | 72.0 | 98 | 2 S26921 | Ig heavy chain V r |
| 28 | 58 | 70.7 | 71 | 2 PH1167 | Ig heavy chain V r |
| 29 | 58 | 70.7 | 104 | 2 PH1665 | Ig heavy chain V r |

| | | | | | |
|----|----|------|-----|----------|--------------------|
| 30 | 58 | 70.7 | 114 | 2 PH1667 | Ig heavy chain V r |
| 31 | 58 | 70.7 | 118 | 2 PH1666 | Ig heavy chain V r |
| 32 | 57 | 69.5 | 117 | 1 MHMS4E | Ig heavy chain V r |
| 33 | 57 | 69.5 | 117 | 1 MHMSJ5 | Ig heavy chain V r |
| 34 | 57 | 69.5 | 118 | 1 MHMS38 | Ig heavy chain V r |
| 35 | 57 | 69.5 | 128 | 2 I37267 | Ig heavy chain V r |
| 36 | 57 | 69.5 | 140 | 2 T01407 | Ig heavy chain (my |
| 37 | 57 | 69.5 | 142 | 2 A32483 | Ig heavy chain V r |
| 38 | 55 | 67.1 | 98 | 2 PH1156 | Ig heavy chain V r |
| 39 | 55 | 67.1 | 102 | 2 S26471 | Ig heavy chain V r |
| 40 | 55 | 67.1 | 106 | 2 PH1005 | Ig heavy chain V r |
| 41 | 55 | 67.1 | 117 | 2 S18553 | Ig heavy chain V r |
| 42 | 54 | 65.9 | 96 | 2 S17230 | Ig heavy chain V r |
| 43 | 54 | 65.9 | 96 | 2 S17618 | Ig heavy chain V r |
| 44 | 54 | 65.9 | 96 | 2 S17620 | Ig heavy chain V r |
| 45 | 54 | 65.9 | 96 | 2 S17614 | Ig heavy chain V r |

ALIGNMENTS

RESULT 1

S26918
Ig heavy chain V region (DP-15) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26918
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26918
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12317; NID:G32857; PIDN:CAA78187.1; PID:G32858
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 72; DB 2; Length 98;
Best Local Similarity 86.7%; Pred. No. 4.5e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15
Db 51 MNPNSGNTGYAOKFQ 65

RESULT 2

S31596
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31596
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31596
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <CU1>
A:Cross-references: EMBL:Z14166; NID:G30996; PIDN:CAA78535.1; PID:G30997
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 72; DB 2; Length 132;
Best Local Similarity 86.7%; Pred. No. 6.2e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15

Db 70 MNPSGNTGYAOKFQ 84
:|||||||

RESULT 3

IG heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600
R:Cuissinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31600
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CU>
A:Cross-references: EMBL:Z14165; NID:G30994; PIDN:CAA78534.1; PID:G30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 72; DB 2; Length 136;
Best Local Similarity 86.7%; Pred. No. 6.4e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15
:|||||||

Db 70 MNPSGNTGYAOKFQ 84
:|||||||

RESULT 4

IG heavy chain V region (DP-1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S26910
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26910
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12303; NID:G32847; PIDN:CAA78173.1; PID:G32848
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 98;
Best Local Similarity 86.7%; Pred. No. 6.7e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15
:|||||||

Db 51 INPNSGNTGYAOKFQ 65
:|||||||

RESULT 5

IG heavy chain V region (DP-75) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26938
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26938
A>Status: preliminary
A:Molecule type: DNA
A:Gene: GDB:IGHV@
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology

A:Residues: 1-98 <TOM>

A:Cross-references: EMBL:Z14071; NID:G32969; PIDN:CAA78451.1; PID:G32970
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 98;
Best Local Similarity 86.7%; Pred. No. 6.7e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15
:|||||||

Db 51 INPNSGNTGYAOKFQ 65
:|||||||

RESULT 6

IG heavy chain V region (DP-8) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26912
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26912
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12310; NID:G32979; PIDN:CAA78180.1; PID:G32980
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 98;
Best Local Similarity 86.7%; Pred. No. 6.7e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15
:|||||||

Db 51 INPNSGNTGYAOKFQ 65
:|||||||

RESULT 7

IG heavy chain precursor V region (V35) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C:Accession: S00476; S34013
R:Matsuda, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fukuhara
EMBO J. 7, 1047-1051, 1988
A:Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain loc
A:Reference number: S00476; MUID:88296408; PMID:2841108
A:Accession: S00476
A:Molecule type: DNA
A:Residues: 1-117 <MATS>
A:Cross-references: EMBL:X07448; NID:G33104; PIDN:CAB56703.1; PID:G6002173
A:Note: the authors translated the codon AGT for residue 89 as Met
R:Marlette, X.; Teapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal J

A:Reference number: S34001; MUID:93209281; PMID:7681398

A:Accession: S34013

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 20-116 <MAR>

C:Genetics:

A:Gene: GDB:IGHV@

A:Cross-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-117/Product: Ig heavy chain V region (V35) #status predicted <MAT>
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 1; Length 117;
 Best Local Similarity 86.7%; Pred. No. 8.1e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 |||||:|||||
 Db 70 INPNSGGTNYAQKFQ 84

RESULT 8
 S31680
 Ig heavy chain V region - human
 C;Species: Homo sapiens (man)
 C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C;Accession: S31680
 R;Cuissinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
 submitted to the EMBL Data Library, June 1992
 A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A;Reference number: S31585
 A;Accession: S31680
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-117 <CUI>
 A;Cross-references: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796
 C;Genetics:
 A;Introns: 16/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 117;
 Best Local Similarity 86.7%; Pred. No. 8.1e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 |||||:|||||
 Db 70 INPNSGGTNYAQKFQ 84

RESULT 9
 S18551
 Ig heavy chain V region precursor (VI-2) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
 C;Accession: S18551; S23625
 R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
 EMO J. 10, 3641-3645, 1991
 A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
 A;Reference number: S18551; MUID:92037524; PMID:1935893
 A;Accession: S18551
 A;Molecule type: DNA
 A;Residues: 1-117 <SHI>
 A;Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832
 R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defos, M.; Kozin, F.; Carson, D.A.;
 J. Exp. Med. 175, 831-842, 1992
 A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from b
 A;Reference number: S23623; MUID:92156804; PMID:1740665
 A;Accession: S23625
 A;Molecule type: DNA
 A;Residues: 1-117 <OLE>
 A;Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
 C;Genetics:
 A;Introns: 16/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 117;
 Best Local Similarity 86.7%; Pred. No. 8.1e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 |||||:|||||
 Db 70 INPNSGGTNYAQKFQ 84

RESULT 10
 S36265
 Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
 C;Accession: S36265
 R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMBO J. 12, 725-734, 1993
 A;Title: Human anti-self antibodies with high specificity from phage display libraries.
 A;Reference number: S36256; MUID:93178448; PMID:7679990
 A;Accession: S36265
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-118 <GRI>
 A;Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g939900
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 118;
 Best Local Similarity 86.7%; Pred. No. 8.1e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 |||||:|||||
 Db 51 INPNSGGTNYAQKFQ 65

RESULT 11
 S46393
 Ig heavy chain V region - human
 C;Species: Homo sapiens (man)
 C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
 C;Accession: S46393
 R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
 J. Mol. Biol. 239, 68-78, 1994
 A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
 A;Reference number: S46390; MUID:94254092; PMID:8196048
 A;Accession: S46393
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-129 <FIG>
 A;Cross-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1335146
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 129;
 Best Local Similarity 86.7%; Pred. No. 8.9e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 |||||:|||||
 Db 51 INPNSGGTNYAQKFQ 65

RESULT 12
 S49530
 anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
 C;Species: Homo sapiens (man)
 C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
 C;Accession: S49530
 R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.


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submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <NAH>
A:Cross-references: EMBL:Z46348; NID:G560839; PIDN:CAA8467.1; PID:G560840
A:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      86.6%; Score 71; DB 2; Length 135;
Best Local Similarity 86.7%; Pred. No. 9.4e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
   ||||| :|||
Db  70 INPNSGGTNYAQKFQ 84
   ||||| :|||

RESULT 13
S69899
IG heavy chain V region (clone R7S7H), rheumatoid factor - human
C:Species: Homo sapiens (man)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69899
R:Rander, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J.
Eur. J. Immunol. 23, 1220-1225, 1993
A:Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune response
A:Reference number: S69896; MUID:93272805; PMID:8500520
A:Accession: S69899
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-104 <RAN>
A:Cross-references: EMBL:Z34893; NID:G509803; PIDN:CAA84376.1; PID:G509804
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      84.1%; Score 69; DB 2; Length 104;
Best Local Similarity 86.7%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
   ||||| :|||
Db  51 INPNSGGTNYAQKFQ 65
   ||||| :|||

RESULT 14
D33548
IG heavy chain V-1 region (WI12) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D33548
R:Kippes, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression
A:Reference number: A33548; MUID:89345575; PMID:2503826
A:Accession: D33548
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-123 <KIP>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      82.9%; Score 68; DB 2; Length 123;
Best Local Similarity 80.0%; Pred. No. 0.00027;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
   ||||| :|||
Db  51 INPNSGGTNYAQKFQ 65
   ||||| :|||

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RESULT 2
Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
   Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 1
FT NON_TER 119
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13B64F5345FA16E CRC64;

Query Match 76.8%; Score 63; DB 4; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.009;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
   ||||| :|||
Db 51 INPNSWTNYAQKFQ 65
   ||||| :|||

RESULT 3
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
   Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035022; AAD56258.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 1
FT NON_TER 124
FT NON_TER 124

```

```

SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 75.6%; Score 62; DB 4; Length 124;
Best Local Similarity 73.3%; Pred. No. 0.014;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
   ||||| :|||
Db 51 INPSCGSYSYAKFKQ 65
   ||||| :|||

RESULT 4
Q8WY24 PRELIMINARY; PRT; 497 AA.
ID Q8WY24;
AC Q8WY24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SNC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RA "Identification and characterization of SNC66, a Ig-like gene which is
   RT down-regulated in colorectal cancer.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283666; AAL36987.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;

Query Match 75.6%; Score 62; DB 4; Length 497;
Best Local Similarity 66.7%; Pred. No. 0.066;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
   ||||| :|||
Db 70 MNPQTGNTTEFAKFQ 84
   ||||| :|||

RESULT 5
Q96GA6 PRELIMINARY; PRT; 614 AA.
ID Q96GA6;
AC Q96GA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RA Tissue=B-cell;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
DR PIR; S15590; S15590.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000005; HTHarac.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.

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DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
DR PROSITE; PS00041; HTH ARAC FAMILY 1; 1.  
DR PROSITE; PS50835; IG LIKE; 5.  
DR PROSITE; PS00290; IG_WHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;  
  
Query Match 72.0%; Score 59; DB 4; Length 614;  
Best Local Similarity 73.3%; Pred. No. 0.27;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 INPNSGNTDYAQKFQ 15  
| : : : : :  
Db 70 ITPFNGNTYAKRFQ 84  
| : : : : :  
  
RESULT 6  
Q921K1 Q921K1 PRELIMINARY; PRT; 278 AA.  
AC Q921K1  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Srausberg R.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC012207; AAH12207.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; ig; 2.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;  
  
Query Match 70.7%; Score 58; DB 11; Length 278;  
Best Local Similarity 66.7%; Pred. No. 0.16;  
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 INPNSGNTDYAQKFQ 15  
| : : : : :  
Db 70 INPNSGNTDYAKRFQ 84  
| : : : : :  
  
RESULT 7  
Q9QXE9 Q9QXE9 PRELIMINARY; PRT; 117 AA.  
AC Q9QXE9  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Immunoglobulin heavy chain V-D-J region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Clemens A., Radenaekers A., Specht C., Koelsch E.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ225174; CAB65237.1; -.  
DR PIR; F33932; F33932.  
DR HSRF; P01810; 2FSJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig_v.  
  
DR Pfam; PF00047; ig; 1.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
FT NON TER 1  
FT NON TER 117  
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;  
  
Query Match 69.5%; Score 57; DB 11; Length 117;  
Best Local Similarity 66.7%; Pred. No. 0.088; 3; Indels 0; Gaps 0;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 INPNSGNTDYAQKFQ 15  
| : : : : :  
Db 51 INPNSGNTSYNQKFK 65  
| : : : : :  
  
RESULT 8  
Q9QXF0 Q9QXF0 PRELIMINARY; PRT; 117 AA.  
ID Q9QXF0  
AC Q9QXF0  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Immunoglobulin heavy chain V-D-J region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Clemens A., Radenaekers A., Specht C., Koelsch E.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ225171; CAB65236.1; -.  
DR HSRP; P01789; 1MCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
FT NON TER 1  
FT NON TER 117  
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;  
  
Query Match 69.5%; Score 57; DB 11; Length 117;  
Best Local Similarity 66.7%; Pred. No. 0.088; 3; Indels 0; Gaps 0;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 INPNSGNTDYAQKFQ 15  
| : : : : :  
Db 51 INPNSGNTSYNQKFK 65  
| : : : : :  
  
RESULT 9  
Q9JL77 Q9JL77 PRELIMINARY; PRT; 110 AA.  
ID Q9JL77  
AC Q9JL77  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Anti-mycosin immunoglobulin heavy chain variable region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=DKA/2;  
RX MEDLINE=20448942; PubMed=10992488;  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";  
RT
```


RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB067796; BAB63281.1; --
 DR PIR; F28833; F28833.
 DR PIR; PH1105; PH1105.
 DR PIR; PH1108; PH1108.
 DR PIR; PH1114; PH1114.
 DR PIR; PH1118; PH1118.
 DR PIR; PH1119; PH1119.
 DR PIR; PH1125; PH1125.
 DR PIR; PH1126; PH1126.
 DR PIR; PH1128; PH1128.
 DR PIR; PH1129; PH1129.
 DR PIR; PH1131; PH1131.
 DR PIR; PH1134; PH1134.
 DR PIR; PH1137; PH1137.
 DR PIR; PH1139; PH1139.
 DR PIR; PH1142; PH1142.
 DR PIR; PH1144; PH1144.
 DR PIR; PH1147; PH1147.
 DR PIR; PH1149; PH1149.
 DR PIR; PH1150; PH1150.
 DR PIR; PH1151; PH1151.
 DR PIR; PH1152; PH1152.
 DR PIR; PH1153; PH1153.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 141
 SQ SEQUENCE 141 AA; 15561 MW; DDD80482D66B76A0 CRC64;

Query Match 62.2%; Score 51; DB 11; Length 141;

Best Local Similarity 60.0%; Pred. No. 1.1;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15

Db :|||||:|:

51 IDPNSGGTKYNEKFK 65

Search completed: April 21, 2004, 17:37:14
 Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:18 ; Search time 60 seconds
(without alignments)
70.637 Million cell updates/sec

Title: SEQ2
Perfect score: 82
Sequence: 1 inpsngtdyackfq 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_29Jan04:*
- 1: Geneseq1980s:*
 - 2: Geneseq1990s:*
 - 3: Geneseq2000s:*
 - 4: Geneseq2001s:*
 - 5: Geneseq2002s:*
 - 6: Geneseq2003as:*
 - 7: Geneseq2003bs:*
 - 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|---------------------|
| 1 | 77 | 93.9 | 248 | 5 | ABP45370 | Abp45370 Human Bly |
| 2 | 75 | 91.5 | 241 | 5 | ABP45937 | Abp45937 Human Bly |
| 3 | 75 | 91.5 | 249 | 5 | ABP45880 | Abp45880 Human Bly |
| 4 | 72 | 87.8 | 92 | 4 | AAM20077 | Aam20077 Peptide # |
| 5 | 72 | 87.8 | 92 | 4 | AAM33913 | Aam33913 Peptide # |
| 6 | 72 | 87.8 | 92 | 4 | ABG55467 | ABG55467 Human liv |
| 7 | 72 | 87.8 | 92 | 5 | ABG43604 | ABG43604 Human pep |
| 8 | 72 | 87.8 | 98 | 3 | AAV50958 | AAV50958 Human FVI |
| 9 | 72 | 87.8 | 98 | 5 | ABG78170 | ABG78170 Human Fv |
| 10 | 72 | 87.8 | 98 | 5 | ABG91861 | ABG91861 Human ant |
| 11 | 72 | 87.8 | 98 | 6 | ABO27070 | ABO27070 Human ger |
| 12 | 72 | 87.8 | 117 | 2 | AAR66302 | Aar66302 Human imm |
| 13 | 72 | 87.8 | 121 | 4 | AAU02576 | Aau02576 Anti-adip |
| 14 | 72 | 87.8 | 122 | 6 | ABR55829 | ABR55829 Heavy cha |
| 15 | 72 | 87.8 | 149 | 6 | ABO04846 | ABO04846 Human epi |
| 16 | 72 | 87.8 | 199 | 2 | AAV34302 | AAV34302 IGM anti b |
| 17 | 72 | 87.8 | 203 | 2 | AAV34301 | AAV34301 IGM anti b |
| 18 | 72 | 87.8 | 241 | 5 | ABP46020 | ABP46020 Human Bly |
| 19 | 72 | 87.8 | 247 | 5 | ABP44916 | ABP44916 Human Bly |
| 20 | 72 | 87.8 | 247 | 5 | ABP44937 | ABP44937 Human Bly |
| 21 | 72 | 87.8 | 249 | 5 | ABP44908 | ABP44908 Human Bly |
| 22 | 71 | 86.6 | 17 | 2 | AAW95253 | AAW95253 Anti-prog |
| 23 | 71 | 86.6 | 17 | 5 | Aae28548 | Aae28548 scFv anti |
| 24 | 71 | 86.6 | 17 | 5 | Aae28547 | Aae28547 scFv anti |
| 25 | 71 | 86.6 | 98 | 5 | ABG78159 | ABG78159 Human Fv |

| | | | | | | |
|----|----|------|-----|---|----------|--------------------|
| 26 | 71 | 86.6 | 98 | 5 | ABG78160 | ABG78160 Human Fv |
| 27 | 71 | 86.6 | 98 | 5 | ABG78158 | ABG78158 Human Fv |
| 28 | 71 | 86.6 | 98 | 5 | ABG78161 | ABG78161 Human Fv |
| 29 | 71 | 86.6 | 98 | 5 | ABG78156 | ABG78156 Human Fv |
| 30 | 71 | 86.6 | 98 | 5 | ABG91849 | ABG91849 Human ant |
| 31 | 71 | 86.6 | 98 | 5 | ABG91851 | ABG91851 Human ant |
| 32 | 71 | 86.6 | 98 | 5 | ABG91847 | ABG91847 Human ant |
| 33 | 71 | 86.6 | 98 | 5 | ABG91852 | ABG91852 Human ant |
| 34 | 71 | 86.6 | 98 | 5 | ABG91850 | ABG91850 Human ant |
| 35 | 71 | 86.6 | 98 | 6 | ABJ18698 | ABJ18698 Antibody |
| 36 | 71 | 86.6 | 98 | 6 | ABO27068 | ABO27068 Human ger |
| 37 | 71 | 86.6 | 111 | 5 | ABO07180 | ABO07180 CS2iE12 h |
| 38 | 71 | 86.6 | 116 | 5 | ABBS7555 | ABBS7555 HLA-DR-sp |
| 39 | 71 | 86.6 | 117 | 2 | AAR66296 | Aar66296 Human imm |
| 40 | 71 | 86.6 | 118 | 6 | ADA89115 | Ada89115 MS-Pro-2- |
| 41 | 71 | 86.6 | 120 | 2 | AAW27551 | AAW27551 Human Ab |
| 42 | 71 | 86.6 | 120 | 6 | ABJ18719 | ABJ18719 Antibody |
| 43 | 71 | 86.6 | 120 | 6 | ABJ18673 | ABJ18673 Antibody |
| 44 | 71 | 86.6 | 123 | 2 | AAW79228 | AAW79228 Heavy cha |
| 45 | 71 | 86.6 | 126 | 6 | ADA89123 | ADA89123 MS-Pro-54 |

ALIGNMENTS

RESULT 1
ABP45370
ID ABP45370 standard; protein; 248 AA.
XX
AC ABP45370;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BlyS binding scFv SEQ ID 1381.
XX
KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
(HUNA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPI; 2002-114799/15.
XX
DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2051-2052; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX

CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 248 AA;
Query Match 93.9%; Score 77; DB 5; Length 248;
Best Local Similarity 93.3%; Pred. No. 6.7e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 INPNSGNTDYAQKFQ 15
Db 51 INPNSGNTNYAQKFQ 65
RESULT 2
ABP45937
ID ABP45937 standard; protein; 241 AA.
XX
AC ABP45937;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1948.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2725-2726; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC

CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 241 AA;
Query Match 91.5%; Score 75; DB 5; Length 241;
Best Local Similarity 93.3%; Pred. No. 0.00014;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 INPNSGNTDYAQKFQ 15
Db 51 INPNSGNTGYAQKFQ 65
RESULT 3
ABP45880
ID ABP45880 standard; protein; 249 AA.
XX
AC ABP45880;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1891.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2658-2659; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC

CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
XX
SQ Sequence 249 AA;
Query Match 91.5%; Score 75; DB 5; Length 249;
Best Local Similarity 93.3%; Pred. NO. 0.00015;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 INPNSGNTDYAOKFQ 15
DB 51 INPNSGNTHYAOKFQ 65
RESULT 4
AAM20077
ID AAM20077 standard; protein; 92 AA.
AC AAM20077;
XX
XX
DT 12-OCT-2001 (first entry)
DE Peptide #6511 encoded by probe for measuring cervical gene expression.
XX Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer.
XX Homo sapiens.
OS
XX
XX WO200157278-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US0000670.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human cervical epithelial cells.
XX
XX Claim 27; SEQ ID NO 24903; 487bp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
XX (SENPs: see A110068-AA128459). The present sequence is a peptide encoded
XX by one such probe. The SENPs are derived from human HeLa cells. The SENPs
XX can be used to produce a single exon microarray, which can be used for
XX measuring human gene expression in a sample derived from human cervical
XX epithelial cells. By measuring gene expression, the probes are therefore
XX useful in grading and/or staging of diseases of the cervix, notably
XX cervical cancer. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 92 AA;
Query Match 87.8%; Score 72; DB 4; Length 92;
Best Local Similarity 86.7%; Pred. NO. 0.00016;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 INPNSGNTDYAOKFQ 15
DB 42 MNPNSGNTGYAOKFQ 56
RESULT 5
AAM33913
ID AAM33913 standard; protein; 92 AA.
XX
XX AC AAM33913;
XX
XX 17-OCT-2001 (first entry)
DE Peptide #7950 encoded by probe for measuring placental gene expression.
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX Homo sapiens.
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US0000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488997/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 34182; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENPs:
XX see A113135-AA157546). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for producing a microarray for
XX predicting, measuring and displaying gene expression in samples derived
XX from human placenta. The probes are useful for antenatal diagnosis of
XX human genetic disorders
XX
XX SQ Sequence 92 AA;
Query Match 87.8%; Score 72; DB 4; Length 92;
Best Local Similarity 86.7%; Pred. NO. 0.00016;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 INPNSGNTDYAOKFQ 15
DB 42 MNPNSGNTGYAOKFQ 56
RESULT 6
ABG55467
ID ABG55467 standard; peptide; 92 AA.
XX

AC AEG55467;
 XX 25-FEB-2003 (first entry)
 XX Human liver peptide, SEQ ID No 34115.
 XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 XX hypercholesterolaemia; coronary heart disease.
 XX Homo sapiens.
 XX WO200157273-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000664.
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488898/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human adult liver.
 XX Claim 27; SEQ ID NO 34115; 658pp; English.
 XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
 XX measuring human gene expression in a sample derived from human adult
 XX liver, comprising one of 13109 defined nucleotide sequences given in the
 XX specification (or complements/ fragments). The probe hybridises at high
 XX stringency to a nucleic acid molecule expressed in the human adult liver.
 XX (I) may be used for predicting, measuring and displaying gene expression
 XX in samples derived from human adult liver. The genes identified may be
 XX involved in genetic liver diseases such as cirrhosis.
 XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 XX associated with coronary heart disease. ABG47348-ABG5930 represent human
 XX liver single exon encoded peptides of the invention. Note: The sequence
 XX information for this patent does not appear in the printed specification
 XX but was obtained in electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 92 AA;
 XX
 XX Query Match 87.8%; Score 72; DB 4; Length 92;
 XX Best Local Similarity 86.7%; Pred. No. 0.00016;
 XX Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 1 INPNSGNTDYAQKFQ 15
 XX Db 42 MNPNSGNTGYAQKFQ 56
 XX
 XX RESULT 7
 XX ABG43604
 XX ID ABG43604 standard; peptide; 92 AA.
 XX AC ABG43604;
 XX 19-AUG-2002 (first entry)
 XX Human peptide encoded by genome-derived single exon probe SEQ ID 33269.
 XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
 XX

KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX Homo sapiens.
 XX WO200186003-A2.
 XX 15-NOV-2001.
 XX 30-JAN-2001; 2001WO-US000665.
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 XX measure gene expression in human lung samples.
 XX Claim 27; SEQ ID NO 33269; 634pp; English.
 XX The invention relates to a spatially-addressable set of single exon
 XX nucleic acid probes for measuring gene expression in a sample derived
 XX from human lung comprising single exon nucleic acid probes having one of
 XX 12614 nucleic acid sequences mentioned in the specification, or their
 XX complements or the 12614 open reading frames derived from the 12614
 XX probes. Also included are a microarray comprising the novel set of probes
 XX; the novel set of probes which hybridise at high stringency to a nucleic
 XX acid expressed in the human lung; measuring gene expression in a sample
 XX derived from human lung, comprising (a) contacting the array with a
 XX collection of detectably labeled nucleic acids derived from human lung
 XX mRNA, and (b) measuring the label detectably bound to each probe of the
 XX array; identifying exons in a eukaryotic genome, comprising (a)
 XX algorithmically predicting at least one exon from genomic sequences of
 XX the eukaryote; and (b) detecting specific hybridisation of detectably
 XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 XX having a fragment identical to the predicted exon, the probe is included
 XX in the above mentioned microarray; assigning exons to a single gene,
 XX comprising (a) identifying exons from genomic sequence by the method
 XX above and (b) measuring the expression of each of the exons in several
 XX microarrays having a probe with the exon, where a common pattern of
 XX expression of the exons in the tissues and/or cell types indicates that
 XX the exons should be assigned to a single gene; a peptide comprising one
 XX of 12011 sequences, mentioned in the specification, or encoded by the
 XX probes/open reading frames (ORF). The probes are used for gene expression
 XX analysis, and for identifying exons in a gene, particularly using human
 XX lung derived mRNA and for the study of lung diseases such as asthma, lung
 XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 XX tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 XX Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 XX present sequence is a peptide/protein encoded by a single exon probe of
 XX the invention. Note: The sequence data for this patent did not form part
 XX of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

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XX SQ Sequence 92 AA;
XX Query Match 87.8%; Score 72; DB 5; Length 92;
XX Best Local Similarity 86.7%; Pred. No. 0.00016;
XX Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 INPNSGNTDYAQKFQ 15
DB 42 MNPNSGNTGYAQKFQ 56

RESULT 8
AAY50558
ID AAY50558 standard; protein; 98 AA.
XX AC AAY50558;
XX DT 23-MAR-2000 (first entry)
XX DE Human FVIII antibody A3-C1 scFv heavy chain protein DP-15.
XX KW Human; heavy chain; antibody; factor VIII; hemostatic; hemophilia A;
XX KW scFv; A3-C1.
XX OS Homo sapiens.
XX PN WO955680-A2.
XX PD 18-NOV-1999.
XX PF 07-MAY-1999; 99WO-NL000285.
XX PR 08-MAY-1998; 98EP-00201543.
XX PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
XX PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;
XX DR WPI; 2000-053102/04.
XX PT New polynucleotide, polypeptide and antibody useful for diagnosing the
XX presence of neutralizing antibodies against factor VIII and for treatment
XX of hemophilia A patients with these antibodies.
XX Example 8; Fig 9A; 61pp; English.
XX This invention describes a novel polynucleotide (I) (and complements and
XX hybridizable polynucleotides) comprising a contiguous nucleotide sequence
XX coding for a human antibody with factor VIII specificity which has
XX hemostatic activity. (I) is useful a primer or probe for detecting the
XX presence of inhibitory antibodies directed against factor VIII. The
XX polypeptides of the invention and the antibodies generated from them are
XX useful in compositions for neutralizing factor VIII inhibiting antibodies
XX in hemophilia A patients. This sequence represents the human factor VIII
XX antibody A3-C1 specific scFv protein DP-15 which is used in the method of
XX the invention
XX SQ Sequence 98 AA;

Query Match 87.8%; Score 72; DB 3; Length 98;
Best Local Similarity 86.7%; Pred. No. 0.00017;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 INPNSGNTDYAQKFQ 15
DB 51 MNPNSGNTGYAQKFQ 65

RESULT 9
ABG78170
ID ABG78170 standard; protein; 98 AA.

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XX ABG78170;
XX 15-NOV-2002 (first entry)
XX Human Fv molecule hypervariable region related peptide #45.
XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
XX disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
XX lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX OS Homo sapiens.
XX PN WO200259264-A2.
XX PD 01-AUG-2002.
XX PF 31-DEC-2001; 2001WO-US049440.
XX PR 29-DEC-2000; 2000US-00751181.
XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
XX PI Plaksin D, Peretz T;
XX DR WPI; 2002-619166/66.
XX PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
XX or fragment, or construct of fragment with enhanced binding
XX characteristics so as to selectively bind target cell in favor of other
XX cells.
XX Claim 13; Page 168-169; 232pp; English.
XX The invention relates to a peptide or polypeptide comprising an Fv
XX molecule, a construct or fragments or a construct of a fragment with
XX enhanced binding characteristics which selectively and/or specifically
XX binds to a target cell in favour of other cells, where binding is
XX primarily determined by a first hypervariable region and Fv is a single
XX chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
XX association with or attached, coupled, combined, linked or fused to a
XX pharmaceutical agent, is useful in the manufacture of a medicament, where
XX the medicament has activity against a diseased cell, preferably a cancer
XX cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
XX myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
XX acute myeloid leukaemia cell). The peptide is also useful for preparing a
XX composition for use in inhibiting the growth of a diseased or cancer
XX cell. This sequence represents a human Fv molecule hypervariable region
XX related peptide of the invention
XX SQ Sequence 98 AA;

Query Match 87.8%; Score 72; DB 5; Length 98;
Best Local Similarity 86.7%; Pred. No. 0.00017;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 INPNSGNTDYAQKFQ 15
DB 51 MNPNSGNTGYAQKFQ 65

RESULT 10
ABG91861
ID ABG91861 standard; protein; 98 AA.
XX AC ABG91861;
XX DT 04-DEC-2002 (first entry)
XX DE Human antibody fragment #45.
XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;

```

KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW reticentosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Homo sapiens.
 XX
 XX WO200253700-A2.
 XX
 XX 11-JUL-2002.
 XX
 XX 31-DEC-2001; 2001WO-US049442.
 XX
 XX 29-DEC-2000; 2000US-00751181.
 XX
 XX 29-DEC-2000; 2000US-0258948P.
 XX
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 XX Szanthon B, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.
 XX
 XX Novel isolated epitope present on cancer cells and important in
 XX physiological phenomena such as cell rolling, metastasis and
 XX inflammation, for treating autoimmune, inflammatory or cardiovascular
 XX diseases, and cancer.
 XX
 XX Disclosure; Page 246; Opp; English.
 XX
 XX The invention relates to an isolated epitope present on cancer cells and
 XX important in physiological phenomena such as cell rolling, metastasis and
 XX inflammation, where the epitope is capable of being bound by an antibody,
 XX its antigen-binding fragment or its complex comprising at least one
 XX antibody or its binding fragment having a first hypervariable region. The
 XX epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 XX disease, thrombosis, reticentosis, metastasis, growth and/or replication of
 XX tumour or leukaemia cells, increase in number of tumour or leukaemia
 XX cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 XX platelet and/or cell-platelet adhesion or aggregation, for increasing
 XX mortality of tumour or leukaemia cells, for increasing the susceptibility
 XX of diseased cells to damage by anti-disease, anti-cancer or anti-
 XX leukaemia agents, or for decreasing the number of tumour or leukaemia
 XX cells in a patient, or in the manufacture of a medicament for the above
 XX mentioned purposes. The epitopes are useful for diagnosing and treating
 XX diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 XX diseases, cardiovascular diseases such as myocardial infarction,
 XX retinopathic diseases and other diseases mediated by abnormal platelet
 XX function and diseases caused by sulphated tyrosine-dependent protein-
 XX protein interactions. This sequence represents a human antibody fragment
 XX of the invention
 XX
 XX Sequence 98 AA;
 XX
 XX Query Match 87.8%; Score 72; DB 5; Length 98;
 XX Best Local Similarity 86.7%; Pred. No. 0.00017;
 XX Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 1 INPNSGNTDYAQKFQ 15
 XX :|||||
 XX Db 51 MNPNSGNTGYAQKFQ 65
 XX
 XX RESULT 11
 XX ABO27070
 XX ID ABO27070 standard; protein; 98 AA.
 XX
 XX AC ABO27070;
 XX
 XX DT 10-SEP-2003 (first entry)
 XX
 XX DE Human germline heavy chain variable region gene segment #3.
 XX
 XX

KW Human; heavy chain variable region; VH; humanised antibody;
 KW chimeric antibody; complementarity determining region; CDR;
 KW canonical CDR structure type.
 XX
 OS Homo sapiens.
 XX
 XX US2003039649-A1.
 XX
 XX 27-FEB-2003.
 XX
 XX 12-JUL-2002; 2002US-00194975.
 XX
 XX 12-JUL-2001; 2001US-0305111P.
 XX
 XX (FOOT/) FOOTE J.
 XX
 XX Foote J;
 XX
 XX WPI; 2003-492151/46.
 XX
 XX Making humanized antibody for converting antibody, by making chimeric
 XX antibodies containing complementarity determining region from non-human
 XX antibody and appropriate framework sequences of human antibodies.
 XX
 XX Example 1; Fig 1; 3ipp; English.
 XX
 XX The invention describes a method of making a humanised antibody,
 XX comprising making chimeric antibodies containing a complementarity
 XX determining region (CDR) from a non-human antibody and appropriate
 XX framework sequences (I) of human antibodies. (I) is selected by using
 XX canonical CDR structure types of non-human antibody in comparison to
 XX germline canonical CDR structure types of human antibodies as the basis
 XX for selection, for humanisation. The method is useful for making a
 XX humanised antibody or a converted antibody. The method is applicable for
 XX converting a subject antibody sequence of any subject species to a less
 XX immunogenic form suitable for use in an object species. The method is
 XX reliable for identifying suitable human framework sequences to support
 XX non-human CDR regions and to provide humanised antibodies that retain
 XX high antigen binding with low immunogenicity in humans, without the need
 XX for direct comparison of framework sequences, without the need for
 XX determining critically important amino acid residues in the framework,
 XX and without the need for multiple iteration and construction to obtain
 XX humanised antibodies with suitable therapeutic properties. The antibody
 XX has high affinity and low immunogenicity without need for comparing
 XX framework sequences between non-human and human antibodies. This sequence
 XX represents a human heavy chain variable region gene segment used in the
 XX creation of humanised antibodies
 XX
 XX Sequence 98 AA;
 XX
 XX Query Match 87.8%; Score 72; DB 6; Length 98;
 XX Best Local Similarity 86.7%; Pred. No. 0.00017;
 XX Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 1 INPNSGNTDYAQKFQ 15
 XX :|||||
 XX Db 51 MNPNSGNTGYAQKFQ 65
 XX
 XX RESULT 12
 XX AAR66302
 XX ID AAR66302 standard; protein; 117 AA.
 XX
 XX AC AAR66302;
 XX
 XX DT 25-MAR-2003 (revised)
 XX DT 02-AUG-1995 (first entry)
 XX
 XX DE Human immunoglobulin variable heavy chain #8.
 XX
 XX XX Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 XX cosmid; placenta; vector; pJB81; E.Coli; mammalian.
 XX

OS Homo sapiens.
XX WO9426895-A1.
PN 24-NOV-1994.
XX 10-MAY-1993; 93WO-JP000603.
XX 10-MAY-1993; 93WO-JP000603.
XX (NIBS) JAPAN TOBACCO INC.
XX Honjo T, Matsuda F;
XX WPI; 1995-006791/01.
XX N-PSDB; AAQ78946.
XX DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts.
XX Claim 17; Page 41-42; 130pp; Japanese.
XX Protein sequences (AA06295-51) are novel human immunoglobulin heavy
CC chain sequences encoded by novel isolated genes. The genes (AAQ78939-
CC 79002) were isolated and cloned from a series of cosmid constructs: Y202;
CC Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131, by PCR amplification using
CC primers AAQ78917-38. The genes are subdivided into 5 families of Vh
CC genes. The fragments cover a region of 800 kb. The DNA fragments were
CC isolated from high molecular weight DNA from human placenta. The DNA was
CC partially digested with TaqI restriction enzyme. The fragments were
CC separated by gel electrophoresis and 35-45 kb fractions were collected.
CC The fragments were ligated with ClaI-digested cosmid vector pUB81. The
CC ligation products were in vitro packed and infected into E.coli 490A. The
CC fragments were then subcloned by colony hybridisation. The Vh genes and
CC the DNA fragments encoding them are useful in producing human
CC immunoglobulin in mammalian hosts. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX Sequence 117 AA;
SQ
Query Match 87.8%; Score 72; DB 2; Length 117;
Best Local Similarity 86.7%; Pred. No. 0.00021;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 INPNSGNTDYAQKFQ 15
DB 70 MNPNSGNTGYAQKFQ 84
RESULT 13
AAU02576
ID AAU02576 standard; protein; 121 AA.
XX AAU02576;
AC
XX 29-AUG-2001 (first entry)
DT
XX Anti-adipocyte monoclonal antibody heavy chain, FAT 64.
DE
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
KW
XX Homo sapiens.
OS
XX WO200127279-A1.
PN
XX 19-APR-2001.
PD
XX 11-OCT-2000; 2000WO-GB003900.
XX
XX 12-OCT-1999; 99US-0158812P.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA

XX Edwards BM, Main SH, Vaughan TJ;
PI WPI; 2001-282031/29.
XX N-ESDB; AAS03476.
DR
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX Claim 1; Page 140; 182pp; English.
PS
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX Sequence 121 AA;
SQ
Query Match 87.8%; Score 72; DB 4; Length 121;
Best Local Similarity 86.7%; Pred. No. 0.00021;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 INPNSGNTDYAQKFQ 15
DB 51 MNPNSGNTGYAQKFQ 65
RESULT 14
ABR55829
ID ABR55829 standard; protein; 122 AA.
XX ABR55829;
AC
XX 02-SEP-2003 (first entry)
DT
XX Heavy chain variable region of anti-Ang-2 antibody IP-2C11 HC.
DE
XX Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
KW Gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
KW angiogenesis; antibody.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 26..36
FT Region /note= "complementarity determining region (CDR) 1"
FT Region 50..66 /note= "complementarity determining region (CDR) 2"
FT Region 96..112 /note= "complementarity determining region (CDR) 3"
XX WO2003030833-A2.
PN
XX 17-APR-2003.
PD
XX 11-OCT-2002; 2002WO-US032613.
XX
XX 11-OCT-2001; 2001US-0328604P.
XX
XX 10-OCT-2002; 2002US-00269805.
PR

XX (AMGE-) AMGEN INC.
XX Oliner JD;
XX WPI; 2003-504963/47.
XX
XX New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful
XX for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
XX hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
XX
XX Claim 1; Page 93; 161pp; English.
XX
XX The invention relates to a specific binding agent, which comprises at
XX least one peptide selected from any of 62 peptides (AB855769-830) or its
XX fragment. The binding agents are antibodies that recognize and bind to
XX Angiopoietin-2 (Ang-2). The specific binding agent, particularly the
XX antibody, is useful for inhibiting undesired angiogenesis, treating
XX cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
XX 2 activity, modulating vascular permeability or plasma leakage, or
XX treating a disease (e.g. ocular neovascular disease, obesity,
XX haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
XX inflammatory disorders, atherosclerosis, endometriosis, neoplastic
XX disease, bone-related disease, or psoriasis) in a mammal. The present
XX sequence represents a heavy chain variable region of an anti-Ang-2
XX antibody
XX
XX Sequence 122 AA;
XX
XX Query Match 87.8%; Score 72; DB 6; Length 122;
XX Best Local Similarity 86.7%; Pred. No. 0.00022;
XX Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 INPNSGNTDYAQKFQ 15
XX DB 51 MNPNSGNTGYAQKFQ 65
XX :|||||
XX
XX RESULT 15
XX ABO04846
XX ID ABO04846 standard; protein; 149 AA.
XX AC ABO04846;
XX
XX DT 12-AUG-2003 (first entry)
XX DE Human epidermal growth factor receptor (EGF-r) antibody #19.
XX
XX Human; epidermal growth factor receptor; EGF-r; antibody; cytostatic;
XX antiinflammatory; immunosuppressive; tyrosine phosphorylation; EGF-2;
XX EGF-r degradation; vascular endothelial cell growth factor; VEGF; tumour;
XX endothelial cell; threonine phosphorylation; autoimmune disease; colon;
XX inflammation; lung; cancer.
XX
XX OS Homo sapiens.
XX
XX PN US2002173629-A1.
XX
XX PD 21-NOV-2002.
XX
XX PF 05-NOV-1998; 98US-00187693.
XX
XX PR 05-MAY-1997; 97US-00851362.
XX PR 29-SEP-1998; 98US-00162280.
XX
XX PA (JAKO/) JAKOBOWITS A.
XX PA (YANG/) YANG X.
XX PA (GALL/) GALLO M.
XX PA (JIAK/) JIA X.
XX
XX PI Jakobovits A, Yang X, Gallo M, Jia X;
XX WPI; 2003-328430/31.
XX

DR N-PSDB; ACD10930.
XX Fully human monoclonal antibodies that bind to epidermal growth factor
XX receptors, useful in cancer therapy.
XX
XX Example 3; Fig 59; 100pp; English.
XX
XX The invention relates to an antibody that binds to an epidermal growth
XX factor receptor (EGF-r) and exhibits inhibition of tyrosine
XX phosphorylation of EGF-2, the degradation of EGF-r, the EGF induced
XX degradation of EGF-r, vascular endothelial cell growth factor (VEGF)
XX production by tumour cells (by greater than 50%) and endothelial cells
XX (by greater than 40%) and also protects threonine phosphorylation of EGF-
XX r and a 63KD protein. The antibody is internalised with EGF-r. The
XX antibody may be used for treating tumours such as lung tumours and colon
XX tumours and for treating inflammation and autoimmune diseases. Sequences
XX ABO04824-ABO04859 represent human EGF-r receptor antibodies of the
XX invention
XX
XX Sequence 149 AA;
XX
XX Query Match 87.8%; Score 72; DB 6; Length 149;
XX Best Local Similarity 86.7%; Pred. No. 0.00027;
XX Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 INPNSGNTDYAQKFQ 15
XX DB 39 MNPNSGNTGYAQKFQ 53
XX :|||||
XX
XX Search completed: April 21, 2004, 17:33:10
XX Job time : 61 secs

Sequence 53, Appl
Sequence 55, Appl
Sequence 56, Appl
Sequence 58, Appl
Sequence 5, Appl
Sequence 127, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 19, Appl
Sequence 28, Appl
Sequence 42, Appl
Sequence 19, Appl

28 60 73.2 128 5 PCT-US95-08743-53
29 60 73.2 128 5 PCT-US95-08743-55
30 60 73.2 128 5 PCT-US95-08743-56
31 60 73.2 137 3 US-08-513-968-38
32 59 72.0 110 4 US-09-899-896-5
33 59 72.0 117 3 US-08-545-809A-127
34 59 72.0 128 1 US-08-276-852-58
35 59 72.0 128 1 US-08-899-575-58
36 59 72.0 128 1 PCT-US95-08743-58
37 59 72.0 137 3 US-08-444-644-17
38 58 70.7 137 4 US-08-232-246A-17
39 58 70.7 233 3 US-08-444-644-33
40 58 70.7 233 4 US-08-232-246A-33
41 58 70.7 235 3 US-08-444-644-19
42 58 70.7 235 3 US-08-444-644-28
43 58 70.7 235 3 US-08-444-644-42
44 58 70.7 235 4 US-08-232-246A-19
45 58 70.7 235 4

ALIGNMENTS

RESULT 1
US-09-025-769B-22
; Sequence 22, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-22

Query Match 93.9%; Score 77; DB 4; Length 117;
Best Local Similarity 93.3%; Pred. No. 9.2e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: April 21, 2004, 17:28:28 ; Search time 18.0435 Seconds
(without alignments)
42.918 Million cell updates/sec

Title: SEQ2
Perfect score: 82
Sequence: 1 lnpsngtdyagkfq 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCITUS_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 77 | 93.9 | 117 | 4 | US-09-025-769B-22 |
| 2 | 72 | 87.8 | 117 | 3 | US-08-545-809A-96 |
| 3 | 71 | 86.6 | 117 | 4 | US-09-424-712-21 |
| 4 | 71 | 86.6 | 117 | 3 | US-08-545-809A-90 |
| 5 | 71 | 86.6 | 120 | 4 | US-09-025-769B-36 |
| 6 | 71 | 86.6 | 120 | 4 | US-09-025-769B-59 |
| 7 | 71 | 86.6 | 123 | 1 | US-08-477-877B-94 |
| 8 | 71 | 86.6 | 123 | 2 | US-08-472-881A-94 |
| 9 | 71 | 86.6 | 123 | 2 | US-08-477-989B-94 |
| 10 | 67 | 81.7 | 119 | 1 | US-08-478-039-65 |
| 11 | 67 | 81.7 | 119 | 1 | US-08-476-349A-65 |
| 12 | 62 | 75.6 | 97 | 2 | US-08-290-592E-16 |
| 13 | 62 | 75.6 | 97 | 5 | PCT-US95-10053-13 |
| 14 | 62 | 75.6 | 97 | 5 | PCT-US96-09448-16 |
| 15 | 62 | 75.6 | 117 | 3 | US-08-545-809A-128 |
| 16 | 60 | 73.2 | 118 | 1 | US-08-491-845-6 |
| 17 | 60 | 73.2 | 118 | 1 | US-08-491-845-14 |
| 18 | 60 | 73.2 | 119 | 4 | US-09-438-954-4 |
| 19 | 60 | 73.2 | 128 | 1 | US-08-276-852-53 |
| 20 | 60 | 73.2 | 128 | 1 | US-08-276-852-55 |
| 21 | 60 | 73.2 | 128 | 1 | US-08-276-852-56 |
| 22 | 60 | 73.2 | 128 | 1 | US-08-899-575-53 |
| 23 | 60 | 73.2 | 128 | 1 | US-08-899-575-55 |
| 24 | 60 | 73.2 | 128 | 1 | US-08-899-575-56 |
| 25 | 60 | 73.2 | 128 | 1 | US-08-899-575-53 |
| 26 | 60 | 73.2 | 128 | 1 | US-08-899-575-55 |
| 27 | 60 | 73.2 | 128 | 1 | US-08-899-575-56 |

QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNSGNTNYAQKFQ 65

RESULT 2

US-08-545-809A-96
; Sequence 96, Application US/08545809A

; Patent No. 6096878

; GENERAL INFORMATION:

; APPLICANT: Honjo, Tasuku

; APPLICANT: Matsuda, Fumihiko

; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

; NUMBER OF SEQUENCES: 145

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/545,809A

; FILING DATE: 27-MAR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP93/00603

; FILING DATE: 10-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29,066

; REFERENCE/DOCKET NUMBER: 06501/004001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 96:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 117 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-545-809A-96

Query Match 87.8%; Score 72; DB 3; Length 117;
Best Local Similarity 86.7%; Pred. No. 6.4e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 70 MNPNSGNTGYAQKFQ 84

RESULT 3

US-09-424-712-21

; Sequence 21, Application US/09424712

; Patent No. 6620587

; GENERAL INFORMATION:

; APPLICANT: TAUSIG, Michael John

; APPLICANT: HE, Mingyue

; TITLE OF INVENTION: RIBOSOME COMPLEXES AS SELECTION PARTICLES FOR IN VITRO DISPLAY AN

; TITLE OF INVENTION: EVOLUTION OF PROTEINS

; FILE REFERENCE: 37945-0017

; CURRENT APPLICATION NUMBER: US/09/424,712

; CURRENT FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/GB98/01564

; PRIOR FILING DATE: 1998-05-28

; PRIOR APPLICATION NUMBER: GB 9804195.7
; PRIOR FILING DATE: 1998-02-28
; PRIOR APPLICATION NUMBER: GB 9724850.4
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: GB 9710829.4
; PRIOR FILING DATE: 1997-05-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-712-21

Query Match 86.6%; Score 71; DB 4; Length 117;
Best Local Similarity 86.7%; Pred. No. 1.2e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 2 INPNSGNTNYAQKFQ 16

RESULT 4

US-08-545-809A-90

; Sequence 90, Application US/08545809A

; Patent No. 6096878

; GENERAL INFORMATION:

; APPLICANT: Honjo, Tasuku

; APPLICANT: Matsuda, Fumihiko

; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

; NUMBER OF SEQUENCES: 145

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/545,809A

; FILING DATE: 27-MAR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP93/00603

; FILING DATE: 10-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29,066

; REFERENCE/DOCKET NUMBER: 06501/004001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 90:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 117 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-545-809A-90

Query Match 86.6%; Score 71; DB 3; Length 117;
Best Local Similarity 86.7%; Pred. No. 9.5e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 1 INPNSGNTNYAQKFQ 15

Db 70 INPNSGGTNYAQKFQ 84

RESULT 5

US-09-025-769B-36
; Sequence 36, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-36

Query Match 86.6%; Score 71; DB 4; Length 120;
Best Local Similarity 86.7%; Pred. No. 9.8e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 INPNSGGTNYAQKFQ 15
Db 51 INPNSGGTNYAQKFQ 65

RESULT 6

US-09-025-769B-59
; Sequence 59, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-59

Query Match 86.6%; Score 71; DB 4; Length 120;
Best Local Similarity 86.7%; Pred. No. 9.8e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 INPNSGGTNYAQKFQ 15
Db 51 INPNSGGTNYAQKFQ 65

RESULT 7

US-08-477-877B-94
; Sequence 94, Application US/08477877B
; Patent No. 5730979
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,877B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008

```
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable region.
; US-08-477-877B-94

Query Match      86.6%; Score 71; DB 1; Length 123;
Best Local Similarity 86.7%; Pred. No. 0.0001;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 INPNSGNTDYAQKFQ 15
        |||||..|..|..|..|
Db      51 INPNSGGTNYAQKFQ 65

RESULT 8
US-08-472-281A-94
; Sequence 94, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,281A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable
; TYPE: amino acid
; STRANDEDNESS:
; US-08-477-877B-94
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; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable region.
; US-08-472-281A-94

Query Match      86.6%; Score 71; DB 2; Length 123;
Best Local Similarity 86.7%; Pred. No. 0.0001;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 INPNSGNTDYAQKFQ 15
        |||||..|..|..|..|
Db      51 INPNSGGTNYAQKFQ 65

RESULT 9
US-08-477-989B-94
; Sequence 94, Application US/08477989B
; Patent No. 5951983
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,989B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable
; TYPE: amino acid
; STRANDEDNESS:
; US-08-477-989B-94
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Query Match      86.6%; Score 71; DB 2; Length 123;
Best Local Similarity 86.7%; Pred. No. 0.0001;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 INPNSGNTDYAQKFQ 15
      |||||:|||||
DB      51 INPNSGGTNYAQKFQ 65

RESULT 10
US-08-478-039-65
; Sequence 65, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: clone 1-14
US-08-478-039-65
Query Match      81.7%; Score 67; DB 1; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.00046;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 INPNSGNTDYAQKFQ 15
      |||||:|||||
DB      51 INPNSGGTNYAQKFQ 65

RESULT 12
US-08-476-349A-65
; Sequence 65, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: clone 1-14
US-08-476-349A-65
Query Match      81.7%; Score 67; DB 1; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.00046;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 INPNSGNTDYAQKFQ 15
      |||||:|||||
DB      51 INPNSGGTNYAQKFQ 65

RESULT 12
US-08-290-592B-16
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Sequence 16, Application US/08290592E
Patent No. 5824307
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
TITLE OF INVENTION: Respiratory Syncytical Virus
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &
ADDRESSEE: OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,592E
FILING DATE: August 15, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 469201-257
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-290-592E-15

Query Match 75.6%; Score 62; DB 2; Length 97;
Best Local Similarity 73.3%; Pred. No. 0.0026;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFQ 15
Db 51 INPSGGSTSYAQKFQ 65

RESULT 13
PCT-US95-10053-13
Sequence 13, Application PC/TUS9510053
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against Respiratory Syncytica
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10053

FILING DATE: Concurrently
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,592
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 469201-274
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-10053-13

Query Match 75.6%; Score 62; DB 5; Length 97;
Best Local Similarity 73.3%; Pred. No. 0.0026;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFQ 15
Db 51 INPSGGSTSYAQKFQ 65

RESULT 14
PCT-US96-09448-16
Sequence 16, Application PC/TUS9609448
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against Respiratory Syncytica
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09448
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,592
FILING DATE: August 15, 1994
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: HERRON, CHARLES J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 469201-257
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 AMINO ACIDS
TYPE: AMINO ACID

STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US96-09448-16

Query Match 75.6%; Score 62; DB 5; Length 97;
Best Local Similarity 73.3%; Pred. No. 0.0026; 2; Indels 0; Gaps 0;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKRFQ 15
Db 51 INPSSGGSYAKRFQ 65

RESULT 15
US-08-545-809A-128
Sequence 128, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Horjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-128

Query Match 75.6%; Score 62; DB 3; Length 117;
Best Local Similarity 73.3%; Pred. No. 0.0031; 2; Indels 0; Gaps 0;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKRFQ 15
Db 70 INPSSGGSYAKRFQ 84

Search completed: April 21, 2004, 17:40:03
Job time : 18.0435 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:37:29 ; Search time 45,2174 Seconds
(without alignments)
91.715 Million cell updates/sec

Title: SEQ2

Perfect score: 82

Sequence: 1 inpsngntdyakfq 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 82 | 100.0 | 125 | 14 | US-10-041-860-48 |
| 2 | 82 | 100.0 | 125 | 14 | US-10-041-860-200 |
| 3 | 82 | 100.0 | 125 | 14 | US-10-041-860-237 |
| 4 | 82 | 100.0 | 125 | 14 | US-10-041-860-372 |
| 5 | 79 | 96.3 | 98 | 14 | US-10-041-860-373 |
| 6 | 77 | 93.9 | 248 | 10 | US-09-880-748-1381 |
| 7 | 77 | 93.9 | 248 | 12 | US-10-293-418-1381 |
| 8 | 75 | 91.5 | 98 | 14 | US-10-041-860-374 |
| 9 | 75 | 91.5 | 241 | 10 | US-09-880-748-1948 |
| 10 | 75 | 91.5 | 241 | 12 | US-10-293-418-1948 |
| 11 | 75 | 91.5 | 249 | 10 | US-09-880-748-1891 |
| 12 | 75 | 91.5 | 249 | 12 | US-10-293-418-1891 |
| 13 | 72 | 87.8 | 17 | 14 | US-10-148-844-40 |
| 14 | 72 | 87.8 | 92 | 9 | US-09-864-761-47202 |
| 15 | 72 | 87.8 | 96 | 14 | US-10-194-975-3 |

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|----|----|------|-----|----|-------------------|-------------------|
| 16 | 72 | 87.8 | 98 | 12 | US-10-029-926B-45 | Sequence 45, Appl |
| 17 | 72 | 87.8 | 98 | 14 | US-10-041-860-289 | Sequence 289, App |
| 18 | 72 | 87.8 | 98 | 14 | US-10-041-860-290 | Sequence 290, App |
| 19 | 72 | 87.8 | 98 | 14 | US-10-041-860-295 | Sequence 295, App |
| 20 | 72 | 87.8 | 98 | 14 | US-10-041-860-296 | Sequence 296, App |
| 21 | 72 | 87.8 | 98 | 14 | US-10-041-860-342 | Sequence 342, App |
| 22 | 72 | 87.8 | 98 | 14 | US-10-041-860-344 | Sequence 344, App |
| 23 | 72 | 87.8 | 98 | 14 | US-10-041-860-348 | Sequence 348, App |
| 24 | 72 | 87.8 | 98 | 14 | US-10-041-860-361 | Sequence 361, App |
| 25 | 72 | 87.8 | 98 | 15 | US-10-032-037B-45 | Sequence 45, Appl |
| 26 | 72 | 87.8 | 98 | 15 | US-10-029-988B-45 | Sequence 45, Appl |
| 27 | 72 | 87.8 | 98 | 15 | US-10-032-423A-45 | Sequence 1, Appli |
| 28 | 72 | 87.8 | 99 | 14 | US-10-041-860-1 | Sequence 1, Appli |
| 29 | 72 | 87.8 | 122 | 14 | US-10-269-805-61 | Sequence 61, Appl |
| 30 | 72 | 87.8 | 125 | 14 | US-10-041-860-38 | Sequence 38, Appl |
| 31 | 72 | 87.8 | 125 | 14 | US-10-041-860-203 | Sequence 203, App |
| 32 | 72 | 87.8 | 125 | 14 | US-10-041-860-238 | Sequence 238, App |
| 33 | 72 | 87.8 | 125 | 14 | US-10-041-860-240 | Sequence 240, App |
| 34 | 72 | 87.8 | 125 | 14 | US-10-041-860-343 | Sequence 343, App |
| 35 | 72 | 87.8 | 126 | 14 | US-10-041-860-19 | Sequence 19, Appl |
| 36 | 72 | 87.8 | 126 | 14 | US-10-041-860-21 | Sequence 21, Appl |
| 37 | 72 | 87.8 | 126 | 14 | US-10-041-860-37 | Sequence 37, Appl |
| 38 | 72 | 87.8 | 126 | 14 | US-10-041-860-199 | Sequence 199, App |
| 39 | 72 | 87.8 | 126 | 14 | US-10-041-860-201 | Sequence 201, App |
| 40 | 72 | 87.8 | 126 | 14 | US-10-041-860-202 | Sequence 202, App |
| 41 | 72 | 87.8 | 126 | 14 | US-10-041-860-236 | Sequence 236, App |
| 42 | 72 | 87.8 | 126 | 14 | US-10-041-860-239 | Sequence 239, App |
| 43 | 72 | 87.8 | 126 | 14 | US-10-041-860-288 | Sequence 288, App |
| 44 | 72 | 87.8 | 126 | 14 | US-10-041-860-294 | Sequence 294, App |
| 45 | 72 | 87.8 | 149 | 9 | US-09-187-693-57 | Sequence 57, Appl |

ALIGNMENTS

RESULT 1
US-10-041-860-48
; Sequence 48, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-48

Query Match 100.0%; Score 82; DB 14; Length 125;
Best local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKQFK 15
DB 51 INPNSGNTDYAKQFK 65

RESULT 2
US-10-041-860-200
; Sequence 200, Application US/10041860

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; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-200

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```

Query Match 100.0%; Score 82; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 INPNSGNTDYAQKFQ 15
| | | | | | | | | | | | | | |
Db 51 INPNSGNTDYAQKFQ 65

```

```

RESULT 3
US-10-041-860-237
; Sequence 237, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-237

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```

Query Match 100.0%; Score 82; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 INPNSGNTDYAQKFQ 15
| | | | | | | | | | | | | | |
Db 51 INPNSGNTDYAQKFQ 65

```

```

RESULT 4
US-10-041-860-372
; Sequence 372, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.

```

```

; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-372

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```

Query Match 100.0%; Score 82; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 INPNSGNTDYAQKFQ 15
| | | | | | | | | | | | | | |
Db 51 INPNSGNTDYAQKFQ 65

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RESULT 5
US-10-041-860-373
; Sequence 373, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-373

```

```

Query Match 96.3%; Score 79; DB 14; Length 98;
Best Local Similarity 93.3%; Pred. No. 8.4e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 INPNSGNTDYAQKFQ 15
| | | | | | | | | | | | | | |
Db 51 MNPNSGNTDYAQKFQ 65

```

```

RESULT 6
US-09-880-748-1381
; Sequence 1381, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
; FILE REFERENCE: PP523
; CURRENT APPLICATION NUMBER: US/09/880,748

```



```

; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1381
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1381

Query Match          93.9%; Score 77; DB 10; Length 248;
Best Local Similarity 93.3%; Pred. No. 5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNSGNTNYAQKFQ 65

RESULT 7
US-10-293-418-1381
; Sequence 1381, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1381
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1381

Query Match          93.9%; Score 77; DB 12; Length 248;
Best Local Similarity 93.3%; Pred. No. 5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNSGNTNYAQKFQ 65

RESULT 8
US-10-041-860-374
; Sequence 374, Application US/10041860

```

```

; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Biryam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX-051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 374
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 59, 73, 97
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 59, 73, 97
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-374

Query Match          91.5%; Score 75; DB 14; Length 98;
Best Local Similarity 93.3%; Pred. No. 4.1e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNSGNTXYAQKFQ 65

RESULT 9
US-09-880-748-1948
; Sequence 1948, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1948
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1948

Query Match          91.5%; Score 75; DB 10; Length 241;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15

```

```
Db      51  INPNSGNTGYAQRKQ 65
|||||
Query Match      91.5%; Score 75; DB 12; Length 249;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 10
US-10-293-418-1948
; Sequence 1948, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1948
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1948

Query Match      91.5%; Score 75; DB 12; Length 241;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  INPNSGNTGYAQRKQ 15
|||||
Db      51  INPNSGNTGYAQRKQ 65

RESULT 11
US-09-880-748-1891
; Sequence 1891, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1891
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1891

Query Match      91.5%; Score 75; DB 12; Length 249;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  INPNSGNTGYAQRKQ 15
|||||
Db      51  INPNSGNTGYAQRKQ 65

RESULT 12
US-10-293-418-1891
; Sequence 1891, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1891
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1891

Query Match      91.5%; Score 75; DB 12; Length 249;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  INPNSGNTGYAQRKQ 15
|||||
Db      51  INPNSGNTGYAQRKQ 65

RESULT 13
US-10-148-844-40
; Sequence 40, Application US/10148844
; Publication No. US20030096403A1
; GENERAL INFORMATION:
; APPLICANT: Hyo-Jeong Hong
; APPLICANT: Keun-Soo Kim
; TITLE OF INVENTION: A HUMANIZED ANTIBODY TO SURFACE ANTIGEN S OF HEPATITIS B
; FILE REFERENCE: 118.15-US-WO
; CURRENT APPLICATION NUMBER: US/10/148,844
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: KR 2000-57891
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: KR 2001-60966
; PRIOR FILING DATE: 2001-09-29
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-148-844-40

Query Match      87.8%; Score 72; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 2e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
Db 2 MNFNSGNTGYAQKFQ 16

RESULT 14
US-09-864-761-47202
; Sequence 47202, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47202
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
```

```
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62
; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUATE 2.00e-39
; OTHER INFORMATION: EST_HUMAN HIT: AW405627.1, EVALUATE 8.00e-48
US-09-864-761-47202
```

```
Query Match      87.8%; Score 72; DB 9; Length 92;
Best Local Similarity 86.7%; Pred. No. 0.00012;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 INPNSGNTDYAQKFQ 15
Db 42 MNFNSGNTGYAQKFQ 56
```

```
RESULT 15
US-10-194-975-3
; Sequence 3, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-3
```

```
Query Match      87.8%; Score 72; DB 14; Length 96;
Best Local Similarity 86.7%; Pred. No. 0.00013;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 INPNSGNTDYAQKFQ 15
Db 49 MNFNSGNTGYAQKFQ 63
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Search completed: April 21, 2004, 18:02:05
Job time : 45.2174 secs
```

| Result No. | Score | Query Match | Length | DB | ID | Description | |
|------------|-------|-------------|--------|----|-----------|-------------|--|
| | | | | | | | |
| 1 | 62.5 | 64.4 | 143 | 6 | AAE37203 | Human AB- | |
| 2 | 59 | 60.8 | 146 | 5 | AAAM51172 | Human rec | |
| 3 | 57 | 58.8 | 112 | 6 | ABRA41574 | Human DIT | |
| 4 | 56.5 | 58.2 | 21 | 5 | ABPA46758 | Human BLY | |
| 5 | 56.5 | 58.2 | 257 | 5 | ABPA45542 | Human BLY | |
| 6 | 56 | 57.7 | 124 | 5 | ABGG77138 | Anti-IGF- | |
| 7 | 56 | 57.7 | 170 | 4 | AAAT79672 | Human pro | |
| 8 | 56 | 57.7 | 384 | 4 | AAAM24101 | Human EST | |
| 9 | 56 | 57.7 | 470 | 5 | ABGT77157 | Amino aci | |
| 10 | 56 | 57.7 | 590 | 4 | AAAM78688 | Human pro | |
| 11 | 55 | 56.7 | 44 | 5 | ABG31313 | Human pro | |
| 12 | 55 | 56.7 | 128 | 6 | ADAA89202 | Human ant | |
| 13 | 55 | 56.7 | 145 | 6 | ABPS7367 | Anti-trAI | |
| 14 | 54 | 55.7 | 157 | 6 | ABO04856 | Human epi | |
| 15 | 53.5 | 55.2 | 18 | 5 | AAU70375 | Mouse hea | |
| 16 | 53 | 54.6 | 19 | 5 | ABPA46976 | Human BLY | |
| 17 | 53 | 54.6 | 125 | 5 | ABGG77142 | ABG463976 | |
| 18 | 53 | 54.6 | 146 | 5 | AAAM51170 | Human rec | |
| 19 | 53 | 54.6 | 146 | 5 | AAAM51171 | Human rec | |
| 20 | 53 | 54.6 | 146 | 5 | AAAM51168 | Human rec | |
| 21 | 53 | 54.6 | 254 | 5 | ABPA45614 | Human BLY | |
| 22 | 53 | 54.6 | 470 | 5 | ABGG77158 | Germline | |
| 23 | 52.5 | 54.1 | 24 | 5 | ABPA46915 | Human BLY | |
| 24 | 52.5 | 54.1 | 145 | 6 | AAE37205 | Human AB- | |
| 25 | 52.5 | 54.1 | 260 | 5 | ABPA45447 | Human AB- | |

CC carcinoma, lung cancer including non-small cell lung carcinoma, kidney
 CC cancer including conventional renal cell carcinoma, sarcoma including
 CC soft tissue sarcoma, breast cancer including breast carcinoma, brain
 CC cancer including glioblastoma multiforme, neuroendocrine carcinoma, colon
 CC cancer including colonic carcinoma, testicular cancer including
 CC testicular embryonal carcinoma, or melanoma including malignant melanoma.
 CC The invention is useful also for inhibiting or enhancing folate hydrolase
 CC activity of a folate hydrolase polypeptide, N-acetylated alpha-linked
 CC acidic dipeptidase (NAALADase) activity of a NAALADase polypeptide,
 CC dipeptidyl dipeptidase IV activity of a dipeptidyl dipeptidase IV
 CC polypeptide, gamma-glutamyl hydrolase activity of a gamma-glutamyl
 CC hydrolase polypeptide. The present sequence is human PSMA antibody heavy
 CC chain variable region (VH)
 XX
 XX
 SQ Sequence 143 AA;
 Query Match 64.4%; Score 62.5; DB 6; Length 143;
 Best Local Similarity 73.3%; Pred. No. 0.23;
 Matches 11; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
 Qy 3 GYSVNYDY-YGMDV 16
 Db 118 GYNWNEYHYGMDV 132
 RESULT 2
 ID AAMS1172 standard; protein; 146 AA.
 XX
 AC AAMS1172;
 XX
 DT 10-JUN-2002 (first entry)
 XX
 DE Human recombinant mAb TNV196 heavy chain variable region.
 XX
 KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
 KW complementarity determining region; antirheumatic; antiarthritic;
 KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antischling;
 KW antidiabetic; antiatherosclerotic; antiatherosclerotic; vasotropic;
 KW antidiagonal; cardiant; antibacterial; virucide; fungicide; antileprotic;
 KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
 KW human; diagnosis; therapy; TNV196; monoclonal antibody; mAb.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Signal peptide
 FT /note= "amino acids 1-7 are PCR primer-encoded and may
 FT differ from the native sequence"
 FT Protein 20..146
 FT /label= Mature_protein
 FT Region 31..49
 FT /label= FR1
 FT Region 50..54
 FT /label= CDR1
 FT Region 55..68
 FT /label= FR2
 FT Region 69..85
 FT /label= CDR2
 FT Region 86..117
 FT /label= FR3
 FT Region 118..135
 FT /label= CDR3
 FT Misc-difference 126
 FT /note= "encoded by A"
 FT Region 136..146
 FT /label= J6
 XX
 XX WO200212502-A2.
 XX
 PD 14-FEB-2002.
 XX
 XX

PF 07-AUG-2001; 2001WO-US024785.
 XX
 PR 07-AUG-2000; 2000US-0223360P.
 PR 29-SEP-2000; 2000US-0236826P.
 PR 01-AUG-2001; 2001US-00920137.
 XX
 XX (CENZ) CENTOCOR INC.
 PA
 XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;
 PI WPI; 2002-217194/27.
 XX N-PSDB; ABL53512.
 XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
 PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
 PT angina pectoris, myocardial infarction, leprosy.
 XX
 PS Example 3; Fig 4; 131pp; English.
 XX
 CC The present sequence is that of the heavy chain variable region of anti-
 CC tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)
 CC TNV196. TNV196 was 1 of 8 human mAbs produced from a GentV fusion using
 CC spleen cells from a hybrid mouse containing human variable and constant
 CC region antibody transgenes that was immunised with human TNF alpha. The
 CC human mAbs bound immobilised human TNF alpha with high avidity and had a
 CC totally human IgG1, kappa isotype. They showed relatedness to each other
 CC and to the human germline DP-46 heavy chain sequence (see AAMS1167). The
 CC invention provides isolated human, primate, rodent, mammalian, chimeric,
 CC humanised and/or complementarity determining region (CDR)-grafted anti-
 CC TNF antibodies, immunoglobulins, cleavage products and other specified
 CC portions and variants, as well as anti-TNF antibody compositions,
 CC encoding or complementary nucleic acids, vectors, host cells,
 CC compositions, formulations, devices, transgenic animals, transgenic
 CC plants, and methods of making and using them. The anti-TNF antibody
 CC comprises at least a portion of an immunoglobulin molecule, especially
 CC the heavy chain and/or light chain variable regions given in the present
 CC sequence and in AAMS1165, or either all of the CDRs of the heavy chain
 CC (see AAMS1158-60) or all of the CDRs of the light chain (see AAMS1161-
 CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,
 CC inhibit TNF binding to receptor, or provide Arthritic Index improvement
 CC in a mouse model. They are useful for diagnosing or treating a TNF
 CC related condition in a cell, tissue, organ or animal (claimed) such as
 CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's
 CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such
 CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
 CC myocardial infarction, an infectious disease in a cell such as bacterial,
 CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
 CC lymphoma and multiple myeloma, or a neurological disease such as multiple
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
 CC Creutzfeldt-Jakob disease
 XX
 SQ Sequence 146 AA;
 Query Match 60.8%; Score 59; DB 5; Length 146;
 Best Local Similarity 68.8%; Pred. No. 0.76;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 GFGVSYNDYVYGMV 16
 Db 120 GIGAGNYVYVYGMV 135
 RESULT 3
 ID ABR41574 standard; protein; 112 AA.
 XX
 XX ABR41574;
 AC
 XX
 XX 02-JUN-2003 (first entry)
 DT
 XX Human DITHP antigen recognition protein.
 DE
 XX

| | |
|----|---|
| KW | Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis; |
| KW | cancer; cell proliferative disorder; autoimmune disorder; |
| KW | inflammatory disorder; infection; hormonal disorder; metabolic disorder; |
| KW | neurological disorder; gastrointestinal disorder; transport disorder; |
| KW | connective tissue disorder; drug screening; proteome analysis; |
| KW | gene therapy; antisense therapy; genotyping; transgenic animal; knock in; |
| KW | disease model; toxicological testing; transcript imaging; |
| KW | antigen recognition. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO200297031-A2. |
| XX | |
| PD | 05-DEC-2002. |
| XX | |
| PF | 27-MAR-2002; 2002WO-US010056. |
| XX | |
| PR | 28-MAR-2001; 2001US-0279619P. |
| PR | 29-MAR-2001; 2001US-0280067P. |
| PR | 29-MAR-2001; 2001US-0280068P. |
| PR | 16-MAY-2001; 2001US-0291280P. |
| PR | 17-MAY-2001; 2001US-0291829P. |
| PR | 17-MAY-2001; 2001US-0291849P. |
| PR | 13-JUN-2001; 2001US-0299428P. |
| PR | 20-JUN-2001; 2001US-029976P. |
| PR | 20-JUN-2001; 2001US-030001P. |
| XX | |
| PA | (INCY-) INCYTE GENOMICS INC. |
| XX | |
| PI | Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J; |
| PI | Dufour GB, Hillman JI, Yu JY, Tuason O, Yap PE, Amahey SR; |
| PI | Daughter SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH; |
| PI | Paralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B; |
| PI | Flores V, Marwaha R, Lo A, Lan RY, Uraehka ME; |
| XX | |
| DR | WPI; 2003-129518/12. |
| DR | N-PSDB; ACC46512. |
| XX | |
| PT | Novel human diagnostic and therapeutic polypeptide useful for identifying |
| PT | test compound which specifically binds to a polypeptide encoded by human |
| PT | diagnostic and therapeutic polynucleotide, and to induce antibodies. |
| XX | |
| PS | Claim 27; SEQ ID NO 1109; 591pp; English. |
| XX | |
| CC | The invention relates to novel human diagnostic and therapeutic |
| CC | polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded |
| CC | proteins (DITHP; ABR41136-ABR41812). The invention also relates to |
| CC | polynucleotide sequences at least 90% identical to the dithp cDNA |
| CC | sequences of the invention; recombinant vectors, host cells and |
| CC | transgenic organisms comprising a dithp nucleic acid sequence; the |
| CC | recombinant production of DITHP proteins; antibodies specific for DITHP |
| CC | proteins; microarrays comprising dithp nucleic acid sequences; methods of |
| CC | detecting dithp nucleotide and protein sequences; methods of screening |
| CC | for compounds which specifically bind a DITHP protein; and methods of |
| CC | assessing the toxicity of test compounds using a dithp hybridisation |
| CC | probe. Dithp nucleic acid sequences and DITHP proteins may be used in the |
| CC | diagnosis of a wide variety of conditions including cancer and other cell |
| CC | proliferative disorders; autoimmune or inflammatory disorders; bacterial, |
| CC | viral, fungal or parasitic infections; hormonal disorders; metabolic |
| CC | disorders; neurological disorders; gastrointestinal disorders; transport |
| CC | disorders; and connective tissue disorders. They may also be used to |
| CC | screen for modulators of protein activity or gene expression. DITHP |
| CC | proteins can additionally be used in analysis of the proteome of a tissue |
| CC | or cell type and to induce antibodies. The dithp nucleic acids are |
| CC | additionally useful in somatic or germline gene therapy of the disorders |
| CC | mentioned above, as a source of antisense sequences, as a source of |
| CC | probes and primers, in genotyping and identification of individuals, in |
| CC | the generation of transgenic animal models of human disease or knock in |
| CC | humanised animals, in toxicological testing and in transcript imaging. |
| CC | The present sequence represents a DITHP protein which has antigen |
| CC | recognition activity. Note: The sequence data for this parent did not |
| CC | form part of the printed specification, but was obtained in electronic |
| CC | format directly from WIPO at ftp.wipo.int/pub/published pct sequences |

SQ Sequence 21 AA;
 Query Match 58.2%; Score 56.5; DB 5; Length 21;
 Best Local Similarity 78.6%; Pred. No. 0.21; Mismatches 1; Indels 1; Gaps 1;
 Matches 11; Conservative 1;
 QY 3 GYSYNDYDYYGMDV 16
 |||:|||||
 Db 9 GY-YLWDYYGMDV 21
 |||:|||||

RESULT 5
 ABP45542
 ID ABP45542 standard; protein; 257 AA.
 XX
 AC ABP45542;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human BlyS binding scFv SEQ ID 1553.
 XX
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 FI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI; 2002-114799/15.
 XX
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 1; Page 2256-2257; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 257 AA;

Query Match 58.2%; Score 56.5; DB 5; Length 257;
 Best Local Similarity 78.6%; Pred. No. 3.2;
 Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 QY 3 GYSYNDYDYYGMDV 16
 |||:|||||
 Db 107 GY-YLWDYYGMDV 119
 |||:|||||

RESULT 6
 ABG77138
 ID ABG77138 standard; protein; 124 AA.
 XX
 AC ABG77138;
 XX
 DT 24-OCT-2002 (first entry)
 XX
 DE Anti-IGF-IR antibody (2.13.2) variable region heavy chain protein.
 XX
 KW Insulin-like growth factor I receptor; antibody; human; cytostatic;
 KW osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour;
 KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;
 KW acromegaly; gigantism; psoriasis; atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200253596-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-US051113.
 XX
 PR 05-JAN-2001; 2001US-0259927P.
 XX
 PA (PFIZ) PFIZER INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
 XX
 DR WPI; 2002-575410/61.
 DR N-PSDB; ABS62700.
 XX
 PT Novel humanized, chimeric monoclonal antibody that specifically binds to
 PT insulin-like growth factor I (IGF-I) receptor useful for inhibiting
 PT binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
 XX
 PS Claim 13; Page 127; 172pp; English.
 XX
 CC This invention relates to a novel humanised, chimeric or human monoclonal
 CC antibody or its antigen binding portion that specifically binds to
 CC insulin-like growth factor I receptor (IGF-IR). The antibodies of the
 CC invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-
 CC IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
 CC phosphorylation. The antibodies of the invention are useful for
 CC diagnosing the presence or location of an IGF-IR-expressing tumour in a
 CC subject. The antibody or its antigen-binding portion is also useful for
 CC treating cancer in a human. The method for this further involves an anti
 CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The
 CC antibodies may also be useful for increasing IGF-IR activity and thus
 CC restoring IGF-IR activity in a condition characterised by low IGF-IR
 CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
 CC also useful for inducing apoptosis of specific cells in a patient, and to
 CC treat non-cancerous states or disease, e.g. acromegaly, gigantism,
 CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
 CC minimise the immunogenic and allergic responses intrinsic to mouse or
 CC mouse-derived monoclonal antibodies and thus increase the efficacy
 CC and safety of the administered antibodies. The present sequence
 CC represents an anti-insulin-like growth factor I receptor antibody of the
 CC invention
 XX
 SQ Sequence 124 AA;

XX DT 24-OCT-2002 (first entry)

XX DE Amino acid sequence of anti-IGF-1R antibody 2.13.2 Vh domain.

XX KW Insulin-like growth factor I receptor; antibody; human; cytostatic;

XX KW osteopathic; antiatherosclerotic; antipsoriatic; IGF-1R; tumour;

XX KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;

XX KW acromegaly; gigantism; psoriasis; atherosclerosis.

XX OS Homo sapiens.

XX PN WO200253596-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-US051113.

XX PR 05-JAN-2001; 2001US-0259927P.

XX PR (PFIZ) PFIZER INC.

XX PA (ABGE-) ABGENIX INC.

XX PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;

XX PI WPI; 2002-575410/61.

XX DR Novel humanized, chimeric monoclonal antibody that specifically binds to

XX PT insulin-like growth factor I (IGF-I) receptor useful for inhibiting

XX PT binding of IGF-I or IGF-II to receptor and for treating cancer in humans.

XX PS Claim 16; Fig 19B; 172pp; English.

XX CC This invention relates to a novel humanised, chimeric or human monoclonal

XX CC antibody or its antigen binding portion that specifically binds to

XX CC insulin-like growth factor I receptor (IGF-IR). The antibodies of the

XX CC invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-

XX CC IR and can inhibit in vivo tumour growth and IGF-IR tyrosine

XX CC phosphorylation. The antibodies of the invention are useful for

XX CC diagnosing the presence or location of an IGF-IR-expressing tumour in a

XX CC subject. The antibody or its antigen-binding portion is also useful for

XX CC treating cancer in a human. The method for this further involves an anti

XX CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The

XX CC antibodies may also be useful for increasing IGF-IR activity and thus

XX CC restoring IGF-IR activity in a condition characterised by low IGF-IR

XX CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is

XX CC also useful for inducing apoptosis of specific cells in a patient, and to

XX CC treat non-cancerous states or disease, e.g. acromegaly, gigantism,

XX CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies

XX CC minimise the immunogenic and allergic responses intrinsic to mouse or

XX CC mouse-derived monoclonal antibodies and thus increase the efficacy

XX CC and safety of the administered antibodies. The present sequence

XX CC represents an anti-insulin-like growth factor I receptor antibody of the

XX CC invention

XX SQ Sequence 470 AA;

Query Match 57.7%; Score 56; DB 5; Length 470;

Best Local Similarity 71.4%; Pred. No. 7.4;

Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 GVSVDYVYGVMDV 16

DB 120 GWSDSYVYVGVMDV 133

RESULT 10

ID AAM78688

XX AC AAM78688 standard; protein; 590 AA.

XX AC AAM78688;

XX DT 06-NOV-2001 (first entry)

XX DE Human protein SEQ ID NO 1350.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;

XX KW nervous system disorder; arthritis; inflammation.

XX OS Homo sapiens.

XX PN WO200157190-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US004098.

XX PR 03-FEB-2000; 2000US-00496914.

XX PR 27-APR-2000; 2000US-00560875.

XX PR 20-JUN-2000; 2000US-00598075.

XX PR 19-JUL-2000; 2000US-00620325.

XX PR 01-SEP-2000; 2000US-00854936.

XX PR 15-SEP-2000; 2000US-00863561.

XX PR 20-OCT-2000; 2000US-00693325.

XX PR 30-NOV-2000; 2000US-00728422.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

XX PI Ma F, Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

XX PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX DR WPI; 2001-476283/51.

XX DR N-PSDB; AAK51821.

XX PT Nucleic acids encoding polypeptides with cytokine-like activities, useful

XX PT in diagnosis and gene therapy.

XX PS Claim 20; Page 3595-3596; 622pp; English.

XX CC The invention relates to polynucleotides (AAK51456-AAK53435) and the

XX CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity relating to

XX CC cytokine, cell proliferation or cell differentiation or which may induce

XX CC production of other cytokines in other cell populations. The

XX CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

XX CC peptide therapy. The polypeptides have various cytokine-like activities,

XX CC e.g. stem cell growth factor activity, haematopoiesis regulating

XX CC activity, tissue growth factor activity, immunomodulatory activity and/or

XX CC activin/inhibin activity and may be useful in the diagnosis and/or

XX CC treatment of cancer, leukaemia, nervous system disorders, arthritis and

XX CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111

XX CC (AAK52582) and 3666 (AAM8020) are omitted as the relevant pages from the

XX CC sequence listing were missing at the time of publication

XX SQ Sequence 590 AA;

Query Match 57.7%; Score 56; DB 4; Length 590;

Best Local Similarity 72.7%; Pred. No. 9.5;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSYNDYVYVGM 14

DB 155 YNYGFDYVYGM 165

RESULT 11

ABG31313

ID ABG31313 standard; protein; 44 AA.

XX AC ABG31313;

XX AC ABG31313;

XX DT 21-OCT-2002 (first entry)

XX DE Human heavy chain CDR3 variable region from patient #1.

XX Human; immune response; chronic B-lymphoproliferative disorder; CDR3;
KW complementarity determining region 3; hypervariable region; B-cell;
KW immunoglobulin heavy chain; VH-CDR3; idiotypic immunoglobulin;
KW cytostatic; hairy cell leukaemia.
XX
OS Homo sapiens.
XX
PN WO200255559-A1.
XX
PD 18-JUL-2002.
XX
PF 15-JAN-2001; 2001WO-IT000014.
XX
PP 15-JAN-2001; 2001WO-IT000014.
XX
PR (FAZI/) FAZIO V M.
PA (SAGLI/) SAGLIO G.
XX
XX Fazio VM, Saglio G;
PI NPI; 2002-583654/62.
XX
XX N-PSDB; ABK90003.
DR
DR
XX
XX Use of DNA sequences coding for hypervariable region (VH- complementarity
PT determining region 3 (CDR3)) of idiotypic immunoglobulin expressed on B-
PT cells of chronic B- lymphoproliferative disorders, as therapeutic
PT vaccine.
XX
XX Disclosure; Fig 2; 30pp; English.
XX
XX The present invention relates to a method for inducing an immune response
CC against B-lymphoproliferative disorders. The method comprises DNA
CC sequences encoding for the complementarity determining region 3 (CDR3)
CC hypervariable region of immunoglobulin heavy chain (VH-CDR3) alone or in
CC combination with at least another immunomodulating sequence. The DNA
CC sequences are useful as therapeutic vaccines for chronic B-
CC lymphoproliferative disorders in mammals, preferably humans. A
CC recombinant plasmid expression vector containing a DNA sequence of the
CC invention is useful as a therapeutic vaccine or for the manufacture of a
CC vaccine effective against chronic B-lymphoproliferative disorders
CC expressing the surface idiotypic immunoglobulin on B-cells in mammals,
CC preferably humans. An efficient, safe and easily reproducible DNA-based
CC immune response against B-lymphoproliferative pathologies can be
CC achieved. The present sequence representing human CDR3 variable region is
CC isolated from a hairy cell leukaemia patient
XX
SQ Sequence 44 AA;
Query Match 56.7%; Score 55; DB 5; Length 44;
Best Local Similarity 76.9%; Pred. NO. 0.76;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4 YSYNYDYIYGMVDV 16
Db 21 YISNYIYIYGMVDV 33
RESULT 12
ADAR89202
ID ADA89202 standard; protein; 128 AA.
XX
XX ADA89202;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human antibody 2F1 heavy chain amino acid sequence SEQ ID NO:46.
XX
XX immunoglobulin; Ig; heavy chain variable domain;
KW light chain variable domain; major histocompatibility complex; MHC;
KW gp100; MUC1; TAX; hTERT; cytostatic; Gene therapy; cancerous disorder;
KW cancer.
XX

OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070752-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005128.
XX
XX 20-FEB-2002; 2002US-0358994P.
XX
XX (DYAX-) DYAX CORP.
PA (TECR) TECHNION RES & DEV FOUND LTD.
XX
XX Hoogenboom HRJM, Reiter Y;
PI WPI; 2003-663847/62.
XX
XX N-PSDB; ADA89201.
DR
DR
XX
XX New protein comprising an immunoglobulin heavy chain variable (VH) domain
PT and an immunoglobulin light chain variable (VL) domain, useful for
PT preparing a composition for treating or preventing a cancerous disorder.
XX
XX Disclosure; Fig 10B; 224pp; English.
XX
XX The present invention describes a protein comprising an immunoglobulin
CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC domain. The protein binds a complex comprising a major histocompatibility
CC complex (MHC) and a peptide, does not substantially bind the MHC in the
CC absence of the bound peptide, and does not substantially bind the peptide
CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC MUC1, TAX or hTERT. ALSO described: (1) a pharmaceutical composition
CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
CC comprising one or more nucleic acids for expressing the Ig that binds a
CC complex having an MHC and a peptide, does not substantially bind the MHC
CC in the absence of the bound peptide, and does not substantially bind the
CC peptide in the absence of the MHC; (3) an isolated nucleic acid
CC comprising a first segment that encodes the Ig variable domain; (4) a
CC host cell comprising heterologous nucleic acid sequences that encodes the
CC novel protein; (5) a transgenic animal whose genome includes heterologous
CC nucleic acid sequences that encode the protein; (6) identifying the
CC protein that specifically binds the MHC-peptide complex; (7) expressing
CC an antigen-binding protein; (8) ablating or killing a target cell that
CC displays a peptide on a surface MHC molecule; (9) treating or preventing
CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
CC complex in a sample. A protein of the invention has cytostatic activity,
CC and can be used in gene therapy. The protein is useful for preparing a
CC composition for treating or preventing a cancerous disorder. The present
CC sequence represents the heavy chain of an antibody which binds to an MHC-
CC peptide complex where the peptide component in as peptide fragment of
CC gp100.
XX
SQ Sequence 128 AA;
Query Match 56.7%; Score 55; DB 6; Length 128;
Best Local Similarity 83.3%; Pred. NO. 2.5;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5 SYNYDYIYGMVDV 16
Db 106 SYPYIYIYGMVDV 117
RESULT 13
ABP57367
ID ABP57367 standard; protein; 145 AA.
XX
XX ABP57367;
XX
XX 22-APR-2003 (first entry)
XX
XX Anti-TRAIL-R antibody related clone 0304 protein SEQ ID NO:29.
XX

KW Human; TRAIL-R1; TRAIL-R2; antibody; cytostatic; apoptotic; tumour;
 KW antibody therapy.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200294880-A1.
 XX 28-NOV-2002.
 XX 17-MAY-2002; 2002WO-JP004816.
 XX 18-MAY-2001; 2001JP-00150213.
 PR 09-AUG-2001; 2001JP-00243040.
 PR 11-OCT-2001; 2001JP-00314489.
 XX (KIRI) KIRIN BEER KK.
 XX Mori E, Kataoka S;
 DR WPI; 2003-120790/11.
 DR N-PSDB; ABZ59698.
 XX New anti-TRAIL-R antibodies with activity of inducing apoptosis of cancer
 PT cells and without exerting an effect on normal cells expressing TRAIL-Rs
 PT nor inducing injury to hepatocytes, for use in therapy of malignant
 PT tumor.
 XX Claim 54; Page 62; 92pp; Japanese.
 PS The present invention describes antibodies or their functional fragments
 XX that bind to TRAIL-R1 and/or TRAIL-R2. TRAIL-R1 and TRAIL-R2 antibodies
 CC have cytostatic and apoptotic activities, and can be used in antibody
 CC therapy. The antibodies can be applied as remedies and preventives of
 CC diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful
 CC in the therapy of malignant tumours. Remedies produced with the
 CC antibodies are highly safe, and avoid hepatotoxicity. The present
 CC sequence represents an anti-TRAIL-R antibody amino acid sequence from the
 XX present invention
 XX Sequence 145 AA;
 SQ Query Match 56.7%; Score 55; DB 6; Length 145;
 Best Local Similarity 83.3%; Pred. No. 2.8;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 SYNDYDYGGMDV 16
 || |||||
 DB 123 SYRDYDYGGMDV 134
 RESULT 14
 ABO04856
 ID ABO04856 standard; protein; 157 AA.
 XX ABO04856;
 AC 12-AUG-2003 (first entry)
 XX Human epidermal growth factor receptor (EGF-r) antibody #29.
 DE Human; epidermal growth factor receptor; EGF-r; antibody; cytostatic;
 XX antiinflammatory; immunosuppressive; tyrosine phosphorylation; EGF-2;
 KW EGF-r degradation; vascular endothelial cell growth factor; VEGF; tumour;
 KW endothelial cell; threonine phosphorylation; autoimmune disease; colon;
 KW inflammation; lung; cancer.
 XX Homo sapiens.
 OS US2002173629-A1.
 XX 21-NOV-2002.
 PD 21-NOV-2002.
 XX

PF 05-NOV-1998; 98US-00187693.
 XX 05-MAY-1997; 97US-00851362.
 PR 29-SEP-1998; 98US-00162280.
 XX (JAKO/) JAKOBOWITS A.
 PA (YANG/) YANG X.
 PA (GALL/) GALLO M.
 PA (JIA/) JIA X.
 XX Jakobovits A, Yang X, Gallo M, Jia X;
 PI WPI; 2003-328430/31.
 DR N-PSDB; ACD10940.
 DR Fully human monoclonal antibodies that bind to epidermal growth factor
 PT receptors, useful in cancer therapy.
 XX Example 3; Fig 69; 100pp; English.
 XX The invention relates to an antibody that binds to an epidermal growth
 CC factor receptor (EGF-r) and exhibits inhibition of tyrosine
 CC phosphorylation of EGF-2, the degradation of EGF-r, the EGF induced
 CC degradation of EGF-r, vascular endothelial cell growth factor (VEGF)
 CC production by tumour cells (by greater than 50%) and endothelial cells
 CC (by greater than 40%) and also protects threonine phosphorylation of EGF-
 CC r and a 63KD protein. The antibody is internalised with EGF-r. The
 CC antibody may be used for treating tumours such as lung tumours and colon
 CC tumours and for treating inflammation and autoimmune diseases. Sequences
 CC ABO04824-ABO04859 represent human EGF-r receptor antibodies of the
 CC invention
 XX Sequence 157 AA;
 SQ Query Match 55.7%; Score 54; DB 6; Length 157;
 Best Local Similarity 64.3%; Pred. No. 4.3;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GYSYDYDYGGMDV 16
 || |||||
 DB 87 GQKWSYDYGGMDV 100
 RESULT 15
 AAU70375
 ID AAU70375 standard; peptide; 18 AA.
 XX AAU70375;
 AC 14-FEB-2002 (first entry)
 XX Mouse heavy chain I CDR 3.
 DE Immunoglobulin; antibody; light chain; heavy chain; CDR; PR;
 XX complementarity determining region; framework region; IGBP;
 KW transgenic plant; immunoglobulin binding protein array; IGM; IGA;
 KW IGD; IGE; IGV; IGM; Kappa; lambda; CHBP.
 XX Mus musculus.
 OS WO200183806-A1.
 XX 08-NOV-2001.
 PD 02-MAY-2001; 2001WO-US014349.
 PF 02-MAY-2000; 2000US-00563222.
 XX (EPIC-) EPICYTE PHARM INC.
 XX Hiatt AC, Hein MB;
 PI WPI; 2002-055482/07.
 DR

XX Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Page 15; 129pp; English.
XX
XX The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds to
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 18 AA;

Query Match 55.2%; Score 53.5; DB 5; Length 18;
Best Local Similarity 62.5%; Pred. No. 0.47;
Matches 10; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 GFGYS-YNYDYGGMD 15
|:|:|:|:|:|:|
Db 2 GYGYYDYDYFFD 17

Search completed: April 21, 2004, 17:33:12
Job time : 66 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:37:29 ; Search time 48.2319 Seconds
(without alignments)

91.715 Million cell updates/sec

Title: SEQ3

Perfect score: 97

Sequence: 1 gfgysnydydygmav 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 97 | 100.0 | 125 | 14 | US-10-041-860-48 |
| 2 | 97 | 100.0 | 125 | 14 | US-10-041-860-200 |
| 3 | 97 | 100.0 | 125 | 14 | US-10-041-860-237 |
| 4 | 97 | 100.0 | 125 | 14 | US-10-041-860-372 |
| 5 | 83 | 85.6 | 125 | 14 | US-10-041-860-38 |
| 6 | 83 | 85.6 | 125 | 14 | US-10-041-860-203 |
| 7 | 83 | 85.6 | 125 | 14 | US-10-041-860-240 |
| 8 | 83 | 85.6 | 125 | 14 | US-10-041-860-343 |
| 9 | 62.5 | 64.4 | 143 | 12 | US-10-395-894-19 |
| 10 | 59.5 | 61.3 | 126 | 14 | US-10-041-860-25 |
| 11 | 59.5 | 61.3 | 126 | 14 | US-10-041-860-210 |
| 12 | 59.5 | 61.3 | 126 | 14 | US-10-041-860-246 |
| 13 | 59.5 | 61.3 | 126 | 14 | US-10-041-860-306 |
| 14 | 56.5 | 58.2 | 21 | 10 | US-09-880-748-2769 |
| 15 | 56.5 | 58.2 | 21 | 12 | US-10-293-418-2769 |

16 56.5 58.2 257 10 US-09-880-748-1553 Sequence 1553, Ap
17 56.5 58.2 257 12 US-10-293-418-1553 Sequence 1553, Ap
18 55 56.7 128 12 US-10-371-942-46 Sequence 46, Appl
19 54 55.7 157 9 US-09-187-693-67 Sequence 67, Appl
20 53.5 55.2 18 10 US-09-563-222-55 Sequence 55, Appl
21 53 54.6 19 10 US-09-880-748-2387 Sequence 2387, Ap
22 53 54.6 19 12 US-10-293-418-2387 Sequence 2387, Ap
23 53 54.6 254 10 US-09-880-748-1625 Sequence 1625, Ap
24 53 54.6 254 12 US-10-293-418-1625 Sequence 1625, Ap
25 52.5 54.1 24 10 US-09-880-748-2926 Sequence 2926, Ap
26 52.5 54.1 24 12 US-10-293-418-2926 Sequence 23, Appl
27 52.5 54.1 145 12 US-10-395-894-23 Sequence 23, Appl
28 52.5 54.1 260 10 US-09-880-748-1458 Sequence 1458, Ap
29 52.5 54.1 260 12 US-10-293-418-1458 Sequence 1458, Ap
30 52 53.6 17 10 US-09-880-748-2836 Sequence 2836, Ap
31 52 53.6 17 12 US-10-293-418-2836 Sequence 2836, Ap
32 52 53.6 19 10 US-09-880-748-2735 Sequence 2735, Ap
33 52 53.6 19 12 US-10-293-418-2735 Sequence 2735, Ap
34 52 53.6 24 9 US-09-891-064A-4 Sequence 4, Appl
35 52 53.6 252 10 US-09-880-748-1415 Sequence 1415, Ap
36 52 53.6 252 12 US-10-293-418-1415 Sequence 1415, Ap
37 52 53.6 254 10 US-09-880-748-1259 Sequence 1259, Ap
38 52 53.6 254 12 US-10-293-418-1259 Sequence 1259, Ap
39 52 53.6 255 10 US-09-880-748-1271 Sequence 1271, Ap
40 52 53.6 255 10 US-09-880-748-1284 Sequence 1284, Ap
41 52 53.6 255 12 US-10-293-418-1271 Sequence 1271, Ap
42 52 53.6 255 12 US-10-293-418-1284 Sequence 1284, Ap
43 52 53.6 257 10 US-09-880-748-1283 Sequence 1283, Ap
44 52 53.6 257 12 US-10-293-418-1283 Sequence 1283, Ap
45 52 53.6 522 9 US-09-891-064A-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-041-860-48
; Sequence 48, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-48

Query Match 100.0%; Score 97; DB 14; Length 125;
Best Local Similarity 100.0%; Pred.No. 3.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYSNYDYDYGMV 16

Db 99 GFGYSNYDYDYGMV 114

RESULT 2

US-10-041-860-200
; Sequence 200, Application US/10041860

Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 200
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-200

Query Match 100.0%; Score 97; DB 14; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYGMDV 16
 |||||
 DB 99 GFGYSYNDYYGMDV 114

RESULT 3
 US-10-041-860-237
 ; Sequence 237, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 237
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-237

Query Match 100.0%; Score 97; DB 14; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYGMDV 16
 |||||
 DB 99 GFGYSYNDYYGMDV 114

RESULT 4
 US-10-041-860-372
 ; Sequence 372, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.

APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 372
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-372

Query Match 100.0%; Score 97; DB 14; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYGMDV 16
 |||||
 DB 99 GFGYSYNDYYGMDV 114

RESULT 5
 US-10-041-860-38
 ; Sequence 38, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-38

Query Match 85.6%; Score 83; DB 14; Length 125;
 Best Local Similarity 87.5%; Pred. No. 0.00029;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYGMDV 16
 |||||
 DB 99 GFGYSYNDYYGMDV 114

RESULT 6
 US-10-041-860-203
 ; Sequence 203, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-203

Query Match 85.6%; Score 83; DB 14; Length 125;
Best Local Similarity 87.5%; Pred. No. 0.00029;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GFGYSYNDYIYGMVDV 16
Db 99 GSGYSYGYDIYIYGMVDV 114

RESULT 7
US-10-041-860-240
; Sequence 240, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-240

Query Match 85.6%; Score 83; DB 14; Length 125;
Best Local Similarity 87.5%; Pred. No. 0.00029;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GFGYSYNDYIYGMVDV 16
Db 99 GSGYSYGYDIYIYGMVDV 114

RESULT 8
US-10-041-860-343
; Sequence 343, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-343

Query Match 85.6%; Score 83; DB 14; Length 125;
Best Local Similarity 87.5%; Pred. No. 0.00029;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GFGYSYNDYIYGMVDV 16
Db 99 GSGYSYGYDIYIYGMVDV 114

RESULT 9
US-10-395-894-19
; Sequence 19, Application US/10395894
; Publication No. US2004003229A1
; GENERAL INFORMATION:
; APPLICANT: MADDON, Paul J.
; APPLICANT: DONOVAN, Gerald P.
; APPLICANT: OLSON, William C.
; APPLICANT: SCHLKE, No. US2004003229A1bert
; APPLICANT: GARDNER, Jason
; APPLICANT: MA, Dangshe
; TITLE OF INVENTION: FSMA ANTIBODIES AND PROTEIN MULTIMERS
; FILE REFERENCE: P00741.70005.US
; CURRENT APPLICATION NUMBER: US/10/395,894
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: PCT/US02/33944
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/335,215
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/362,747
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/412,618
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 19
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-395-894-19

Query Match 64.4%; Score 62.5; DB 12; Length 143;
Best Local Similarity 73.3%; Pred. No. 0.24;
Matches 11; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
Qy 3 GYSYNDY-YIYGMVDV 16
Db 118 GYNWYEVHYIYGMVDV 132

RESULT 10
US-10-041-860-25
; Sequence 25, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-25

Query Match 61.3%; Score 59.5; DB 14; Length 126;
Best Local Similarity 80.0%; Pred. No. 0.54;
Matches 12; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 3 GYSYNDYY-YGMDV 16
||||| |||||
DB 101 GYSYGVVYDYGMDV 115

RESULT 11
US-10-041-860-210
; Sequence 210, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-210

Query Match 61.3%; Score 59.5; DB 14; Length 126;
Best Local Similarity 80.0%; Pred. No. 0.54;
Matches 12; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 3 GYSYNDYY-YGMDV 16
||||| |||||
DB 101 GYSYGVVYDYGMDV 115

RESULT 12
US-10-041-860-246
; Sequence 246, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-246

Query Match 61.3%; Score 59.5; DB 14; Length 126;
Best Local Similarity 80.0%; Pred. No. 0.54;
Matches 12; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 3 GYSYNDYY-YGMDV 16
||||| |||||
DB 101 GYSYGVVYDYGMDV 115

RESULT 13
US-10-041-860-306
; Sequence 306, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 306
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-306

Query Match 61.3%; Score 59.5; DB 14; Length 126;
Best Local Similarity 80.0%; Pred. No. 0.54;
Matches 12; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 3 GYSYNDYY-YGMDV 16
||||| |||||
DB 101 GYSYGVVYDYGMDV 115

RESULT 14
US-09-880-748-2769
; Sequence 2769, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2769
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2769

Query Match 58.2%; Score 56.5; DB 10; Length 21;
Best Local Similarity 78.6%; Pred.No. 0.23;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 3 GYSYNDYVYGMV 16
|||:|||||
Db 9 GY-YLWDYVYGMV 21

RESULT 15
US-10-293-418-2769
; Sequence 2769, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/275,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2769
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2769

Query Match 58.2%; Score 56.5; DB 12; Length 21;
Best Local Similarity 78.6%; Pred.No. 0.23;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 3 GYSYNDYVYGMV 16
|||:|||||
Db 9 GY-YLWDYVYGMV 21

Search completed: April 21, 2004, 18:02:06
Job time : 49.2319 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:48 ; Search time 8.11594 Seconds
(without alignments)
102.653 Million cell updates/sec

Title: SEQ3
Perfect score: 97
Sequence: 1 gfgysnydyrygmdiv 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|---------------|---------------------|
| 1 | 56 | 57.7 | 591 | 1 ARSF_HUMAN | P54793 homo sapien |
| 2 | 52 | 53.6 | 522 | 1 OCLN_HUMAN | Q16625 homo sapien |
| 3 | 52 | 53.6 | 733 | 1 PTK_ACIJO | O52788 acinetobact |
| 4 | 50 | 51.5 | 733 | 1 HEXA_BIADI | Q17127 blaberrus di |
| 5 | 49 | 50.5 | 59 | 1 CUTEA_LIMPO | P83360 limulus pol |
| 6 | 48 | 49.5 | 146 | 1 HV21_HUMAN | P06331 homo sapien |
| 7 | 48 | 49.5 | 312 | 1 RYLY_MOUSE | P064012 mus musculu |
| 8 | 48 | 49.5 | 521 | 1 OCLN_CANFA | Q28269 canis fami |
| 9 | 47 | 48.5 | 504 | 1 OCLN_CHICK | Q91049 gallus gall |
| 10 | 47 | 48.5 | 719 | 1 FRBA_YEAST | P53746 saccharomyc |
| 11 | 47 | 48.5 | 1048 | 1 YC81_METUA | Q58677 methanococc |
| 12 | 46 | 47.4 | 201 | 1 YK00_YEAST | P38099 saccharomyc |
| 13 | 46 | 47.4 | 633 | 1 ROR_HUMAN | Q43390 homo sapien |
| 14 | 46 | 47.4 | 646 | 1 NA95_HUMAN | Q9ulx6 homo sapien |
| 15 | 45 | 46.4 | 321 | 1 VG74_HSVSA | Q01035 herpesvirus |
| 16 | 45 | 46.4 | 394 | 1 OMS1_SALTI | Q56110 salmonella |
| 17 | 45 | 46.4 | 397 | 1 YEOS_ECOLI | P76335 escherichia |
| 18 | 45 | 46.4 | 1312 | 1 DPOL_PRRSD | Q51334 pyrococcus |
| 19 | 44.5 | 45.9 | 435 | 1 YIYO_BACSU | P37489 bacillus su |
| 20 | 44.5 | 45.9 | 722 | 1 YC06_KLEPN | Q8452 klebsiella |
| 21 | 44.5 | 45.9 | 1326 | 1 BCC2_ACEXY | O82861 acetobacter |
| 22 | 44 | 45.4 | 59 | 1 CUTEA_LIMPO | P83359 limulus pol |
| 23 | 44 | 45.4 | 59 | 1 CUTEA_LIMPO | P83361 limulus pol |
| 24 | 44 | 45.4 | 147 | 1 HVLC_HUMAN | P01744 homo sapien |
| 25 | 44 | 45.4 | 183 | 1 DERM_BOVIN | P19427 bos taurus |
| 26 | 44 | 45.4 | 201 | 1 DERM_HUMAN | Q07507 homo sapien |
| 27 | 44 | 45.4 | 631 | 1 ADAS_DROME | Q9v778 drosophila |
| 28 | 44 | 45.4 | 642 | 1 NA95_MOUSE | Q9r017 mus musculu |
| 29 | 44 | 45.4 | 772 | 1 LP1G_DROME | P11997 drosophila |
| 30 | 44 | 45.4 | 789 | 1 LP1A_DROME | P11995 drosophila |
| 31 | 43.5 | 44.8 | 726 | 1 AMSA_ERWAN | Q46631 erwinia amy |
| 32 | 43.5 | 44.8 | 1302 | 1 ACSC_ACEXY | P37718 acetobacter |
| 33 | 43 | 44.3 | 316 | 1 Y034_METUA | Q60349 methanococc |

RESULT 1

| ID | ARSF_HUMAN | STANDARD; | PRT; | 591 AA. |
|----|--|-----------|------|---------|
| AC | P54793; | | | |
| DT | 01-OCT-1996 (Rel. 34, Created) | | | |
| DT | 15-JUL-1999 (Rel. 38, Last sequence update) | | | |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update) | | | |
| DE | Arylsulfatase F precursor (EC 3.1.6.-) (ASF). | | | |
| GN | ARSF. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Fetal brain; | | | |
| RX | MEDLINE=97336043; PubMed=9192838; | | | |
| RA | Puca A.A., Zolli M., Repetto M., Andolfi G., Guffanti A., Simon G., | | | |
| RA | Ballabio A., Franco B.; | | | |
| RT | "Identification by shotgun sequencing, genomic organization, and | | | |
| RT | functional analysis of a fourth arylsulfatase gene (ARSF) from the | | | |
| RT | Xp22.3 region." | | | |
| RL | Genomics 42:192-199(1997). | | | |
| RN | [2] | | | |
| RP | SEQUENCE OF 370-423 FROM N.A. | | | |
| RC | TISSUE=Kidney; | | | |
| RX | MEDLINE=95236447; PubMed=7720070; | | | |
| RA | Franco B., Meroni G., Parenti G., Leveilliers J., Bernard L., | | | |
| RA | Gebbia M., Cox L., Maroteaux P., Sheffield L., Rappold G.A., | | | |
| RA | Andria G., Pettit C., Ballabio A.; | | | |
| RT | "A cluster of sulfate genes on Xp22.3: mutations in | | | |
| RT | chondrodysplasia punctata (CDPX) and implications for warfarin | | | |
| RT | embryopathy." | | | |
| RL | Cell 81:15-25(1995). | | | |
| CC | -1- ENZYME REGULATION: Not inhibited by DHEAS or warfarin. | | | |
| CC | -1- MISCELLANEOUS: Optimum pH is 8. | | | |
| CC | -1- SIMILARITY: Belongs to the sulfatase family. | | | |
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| CC | or send an email to license@isb-sib.ch). | | | |
| CC | ----- | | | |
| DR | EMBL; X97868; CAA66462.1; -. | | | |
| DR | PIR; A56217; A56217. | | | |
| DR | HSSP; P15848; 1FSU. | | | |
| DR | Genew; HGNC:721; ARSF. | | | |
| DR | MIM; 300003; -. | | | |
| DR | GO; GO:0004085; P:arylsulfatase activity; TAS. | | | |
| DR | InterPro; IPR000917; Sulfatase. | | | |
| DR | Pfam; PF00884; Sulfatase; 1. | | | |
| DR | PROSITE; PS00523; SULFATASE_1; 1. | | | |
| DR | PROSITE; PS00149; SULFATASE_2; 1. | | | |

| | | | | | | |
|----|------|------|------|---|------------|--------------------|
| 34 | 43 | 44.3 | 667 | 1 | EM70 YEAST | P32802 saccharomyc |
| 35 | 42 | 43.3 | 214 | 1 | YB41 METUA | Q58541 methanococc |
| 36 | 42 | 43.3 | 306 | 1 | RALY_HUMAN | Q9ukm9 homo sapien |
| 37 | 42 | 43.3 | 369 | 1 | OMPF_YENNE | Q56828 xenorhabdus |
| 38 | 42 | 43.3 | 461 | 1 | FUCO_DICDI | P10901 dictyosteli |
| 39 | 42 | 43.3 | 687 | 1 | AKA8_RAT | Q63014 rattus norv |
| 40 | 42 | 43.3 | 826 | 1 | VILI_CHICK | P02640 gallus gall |
| 41 | 41.5 | 42.8 | 330 | 1 | SLEB_BACHD | Q9kce0 bacillus ha |
| 42 | 41.5 | 42.8 | 429 | 1 | AST1_YEAST | P35183 saccharomyc |
| 43 | 41.5 | 42.8 | 1325 | 1 | BCC3_ACEXY | Q9wx63 acetobacter |
| 44 | 41 | 42.3 | 102 | 1 | YAS9_HAEIN | P44112 haemophilus |
| 45 | 41 | 42.3 | 130 | 1 | C14A_LIMPO | P83354 limulus pol |

ALIGNMENTS


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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tyrosine-protein kinase ptk (EC 2.7.1.112).
GN PTK.
OS Acinetobacter johnsonii.
OC Bacteri; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=40214;
RN [1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP MEDLINE=98094281; PubMed=9434192;
RA Grangease C., Doublet P., Vaganay E., Vincent C., Deleage G.,
RA Duclos B., Cozzone A.J.;
RT "Characterization of a bacterial gene encoding an autophosphorylating
RT protein tyrosine kinase."
RL Gene 204:259-265(1997).
RN [2]
RN CHARACTERIZATION.
RX MEDLINE=96266486; PubMed=8683591;
RA Duclos B., Grangease C., Vaganay E., Riberty M., Cozzone A.J.;
RT "Autophosphorylation of a bacterial protein at tyrosine."
RL J. Mol. Biol. 259:891-895(1996).
RN [3]
RN MUTAGENESIS OF LYS-436; LYS-549; SER-550 AND ASP-651.
RX MEDLINE=99166918; PubMed=10069388;
RA Doublet P., Vincent C., Grangease C., Cozzone A.J., Duclos B.;
RT "On the binding of ATP to the autophosphorylating protein, Ptk, of the
RT bacterium Acinetobacter johnsonii."
RL FEBS Lett. 445:137-143(1999).
CC -1- FUNCTION: May be involved in the production and the transport of
CC exopolysaccharides.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- COFACTOR: Magnesium or manganese (Probable).
CC -1- PATHWAY: Exopolysaccharide biosynthesis.
CC -1- SUBCELLULAR LOCATION: Inner membrane.
CC -1- PTM: Autophosphorylated on several Tyr residues. Dephosphorylated
CC by pcp.
CC -1- SIMILARITY: BELONGS TO THE ETK/WZC FAMILY.
CC
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CC EMBL; Y15162; CAA75431.1; -
CC Prosite; O52789; -
CC InterPro; IPR003856; LPS_Wzz_MPA.
CC Pfam; PF02706; wzz; 1.
CC
CC Transferase; Tyrosine-protein kinase; Phosphorylation;
CC Exopolysaccharide synthesis; Transmembrane; Inner membrane;
CC ATP-binding; Magnesium; Manganese
CC TRANSMEM 19 39 POTENTIAL.
CC TRANSMEM 438 458 POTENTIAL.
CC NP_BIND 542 550 ATP (POTENTIAL).
CC MUTAGEN 436 436 K->M: NO LOSS OF AUTOPHOSPHORYLATION.
CC MUTAGEN 549 549 K->M: LOSS OF AUTOPHOSPHORYLATION.
CC MUTAGEN 550 550 S->C: LOSS OF AUTOPHOSPHORYLATION.
CC MUTAGEN 651 651 D->N: LOSS OF AUTOPHOSPHORYLATION.
CC SEQUENCE 733 AA; 82362 MW; EF31482AF7B954 CRC64;
Query Match 53.6%; Score 52; DB 1; Length 733;
Best Local Similarity 66.7%; Pred. No. 3.9;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GFGYSYNDYY 12
Db 715 GYGYNAYAY 726

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RESULT 4
HEXA BLADI
ID HEXA BLADI STANDARD; PRT; 733 AA.
AC Q17127;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hexamerin precursor.
DE Hexamerin discoidalis (Tropical cockroach).
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Blaberidae; Blaberus.
OX NCBI_TaxID=6981;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Fat body;
RC Jamroz R.C., Beintema J.J., Stam W.T., Bradfield J.Y.;
RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Larval storage protein (LSP) which may serve as a store
CC of amino acids for synthesis of adult proteins (By similarity).
CC -1- SUBUNIT: Homohexamer (Potential).
CC -1- SUBCELLULAR LOCATION: Extracellular (By similarity).
CC -1- SIMILARITY: TO ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.
CC
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CC
CC EMBL; U13128; AAA74579.1; -
CC HSSP; P04253; LOXY.
CC InterPro; IPR008922; Di-copper_centre.
CC InterPro; IPR008096; Hemocyanin.
CC InterPro; IPR005203; Hemocyanin_C.
CC InterPro; IPR005204; hemocyanin_N.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00372; hemocyanin; 1.
CC Pfam; PF03723; hemocyanin_C; 1.
CC Pfam; PF03722; hemocyanin_N; 1.
CC PRINTS; PR00187; HAEMOCYANIN.
CC PROSITE; PS00209; HEMOCYANIN_1; FALSE NEG.
CC PROSITE; PS00210; HEMOCYANIN_2; FALSE NEG.
CC Signal; Storage protein; Glycoprotein.
CC SIGNAL 1 17 POTENTIAL.
CC CHAIN 18 733 HEXAMERIN.
CC FT CARBOHYD 199 199 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 234 234 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 431 431 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 733 AA; 87813 MW; 083DF739DD65729 CRC64;
Query Match 51.5%; Score 50; DB 1; Length 733;
Best Local Similarity 53.3%; Pred. No. 7.6;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 2 FGYSYNDYYGMDV 16
Db 345 XYSTEHDYYYPEDL 359

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RESULT 5
CUTB LIMPO
ID CUTB LIMPO STANDARD; PRT; 59 AA.
AC P83360;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cuticle protein 7 isoform b (LpCp7b).
DE Limulus polyphemus (Atlantic horseshoe crab).
OS Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;

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OC Limulidae; Limulus.
OX NCBI_TaxID=8650;
RN
RP SEQUENCE, MASS SPECTROMETRY, AND PYRROLIDONE CARBOXYLIC ACID.
RC TISSUE=Carapace cuticle;
RA MEDLINE=22515710; PubMed=12628379;
RX Ditzel N., Andersen S.O., Hoejrup P.;
RT "Cuticular proteins from the horseshoe crab, Limulus polyphemus.";
RL Comp. Biochem. Physiol. 134B:489-497(2003).
CC -1- MASS SPECTROMETRY: MW=6970; METHOD=WALDI.
CC -1- SIMILARITY: Contains 1 cuticle consensus domain.
DR InterPro: IPR000618; Insect cuticle.
DR PROSITE: PS00233; CUTICLE; FALSE NEG.
KW Structural protein; Cuticle; PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
SQ SEQUENCE 59 AA; 6987 MW; 9E05626F95A41B5 CRC64;

Query Match 50.5%; Score 49; DB 1; Length 59;
Best Local Similarity 61.5%; Pred. No. 0.86;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GFGYSYNYDYVG 13
Db 37 GFGFYPHYYPG 49

RESULT 6
HV2I HUMAN
ID HV2I HUMAN STANDARD; PRT; 146 AA.
AC P06331.
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A. (ISOFORM 1);
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region.";
RL Gene 33:181-189(1985).
DR PIR: A02101; GIH02.
DR HSP: P01825; 7FAB.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 117 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52B8218171F CRC64;

Query Match 49.5%; Score 48; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DYYGMDV 16
Db 128 DYYGMDV 135

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RESULT 7
RALLY MOUSE
ID RALLY MOUSE STANDARD; PRT; 312 AA.
AC Q64012; Q99K76; Q9CXH8; Q9QZX6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RNA-binding protein Raly (hnRNP associated with lethal yellow protein)
DE (Maternally expressed hnRNP C-related protein).
DE RALLY OR MERC.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A. (ISOFORM 1); TISSUE SPECIFICITY, AND DEVELOPMENTAL
RP STAGE.
RC TISSUE=Embryo;
RX MEDLINE=93307655; PubMed=8319910;
RA Michaud E.J., Bultman S.J., Stubbs L.J., Woychik R.P.;
RT "The embryonic lethality of homozygous lethal yellow mice (Ay/ay) is
RT associated with the disruption of a novel RNA-binding protein.";
RL Genes Dev. 7:1203-1213(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1);
RX MEDLINE=94326666; PubMed=8050375;
RA Dahl D.M., Stevens M.E., Vrieling H., Saxon P.J., Miller M.W.,
RA Epstein C.J., Barsh G.S.;
RT "Pleiotropic effects of the mouse lethal yellow (Ay) mutation
RT explained by deletion of a maternally expressed gene and the
RT simultaneous production of agouti fusion RNAs.";
RL Development 120:1695-1708(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1);
RC STRAIN=C57BL/6J; TISSUE=Embryonic head;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fiechmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1);
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Ruben G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schestz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullyah S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 100-135 FROM N.A. (ISOFORM 2).
RX MEDLINE=99431566; PubMed=10500250;
RA Khrutskova I., Kuklin A., Woychik R.P., Michaud E.J.;
RT "Alternative processing of the human and mouse raly genes.";
RL Biochim. Biophys. Acta 1447:107-112(1999).
CC -!- FUNCTION: Probable-RNA binding protein. Could be a heterogeneous
CC nuclear ribonucleoprotein (hnRNP).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=2;
CC IsoId=Q64012-1; Sequence=Displayed;
CC Name=1;
CC IsoId=Q64012-2; Sequence=VSP_005805;
CC -!- TISSUE SPECIFICITY: Widely expressed. Expressed in brain, testis,
CC lung, spleen and kidney. Weakly expressed in liver.
CC -!- DEVELOPMENTAL STAGE: Expressed in the unfertilized egg, in the
CC blastocyst, as well as in the developing embryo and fetus.
CC Expressed in developing skin.
CC -!- DISEASE: Defects in RALY are the cause of lethal yellow mutation
CC (A(y)), a dominant allele that cause embryonic lethality when
CC homozygous, and pleiotropic effects when heterozygous, including
CC yellow pelage, obesity, non-insulin dependent diabetes and
CC increased tumor susceptibility. A(y) is due to a 170 kb deletion
CC that removes all but the promoter and non-coding first exon of
CC RALY and links them to the ASIP/Agouti gene.
CC -!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC
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CC
CC EMBL; S72641; AAC60688.1; -;
CC EMBL; L17076; -; NOT ANNOTATED_CDS.
CC EMBL; AK014356; BAB29294.1; -;
CC EMBL; BC004851; AAH04851.1; -;
CC EMBL; BC016587; AAH16587.1; -;
CC EMBL; AF148458; AAF04488.1; -;
CC MGD; MGI:197850; Raly.
CC InterPro; IPR000504; RNA_rec_mot.
CC Pfam; PF00076; rrm; 1.
CC SMART; SM00360; RRM; 1.
CC PROSITE; PS50102; RRM; 1.
CC PROSITE; PS00030; RRM_RNP_1; 1.
CC Ribonucleoprotein; RNA-binding; Nuclear protein; Alternative splicing.
FT DOMAIN 21 92
FT VARSPIC 110 125
FT Missing (in isoform 1).
FT /FTid=VSP_005805.
FT CONFLICT 249 249
FT G -> S (IN REF. 2 AND 3).
FT CONFLICT 281 281
FT T -> I (IN REF. 1).
SQ SEQUENCE 312 AA; 33158 MW; BF68B0E8876BFC50 CRC64;

Query Match 49.5%; Score 48; DB 1; Length 312;
Best Local Similarity 77.8%; Pred. No. 6.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYSYNDYY 11
| | | | |
Db 111 GYSFDYDY 119

RESULT 8
OCLN_CANFA STANDARD; PRT; 521 AA.
AC Q28269;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Occludin.
GN OCLN.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=96181089; PubMed=8601611;
RA Ando-Akatsuka Y., Saitou M., Hirase T., Kishi M., Sakakibara A.,
RA Itoh M., Yonemura S., Furuse M., Tsukita S.;
RT "Interspecies diversity of the occludin sequence: cDNA cloning of
RT human, mouse, dog, and rat-kangaroo homologues";
RL J. Cell Biol. 133:43-47(1996).
RN [2]
RP PHOSPHORYLATION.
RX MEDLINE=97327764; PubMed=9182670;
RA Sakakibara A., Furuse M., Saitou M., Ando-Akatsuka Y., Tsukita S.;
RT "Possible involvement of phosphorylation of occludin in tight junction
RT formation.";
RL J. Cell Biol. 137:1393-1401(1997).
CC -!- FUNCTION: May play a role in the formation and regulation of the
CC tight junction (TJ) paracellular permeability barrier. Interacts
CC with ZO-1.
CC -!- SUBUNIT: Interacts with VAPA (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC epithelial and endothelial cells.
CC -!- DOMAIN: The C-terminal is cytoplasmic and is important for
CC interaction with ZO-1. Necessary for the tight junction
CC localization. Involved in the regulation of the permeability
CC barrier function of the tight junction (By similarity).
CC -!- PTM: PHOSPHORYLATED. LESS PHOSPHORYLATED FORMS ARE FOUND IN
CC BASOLATERAL MEMBRANE, CYTOSOL AND TIGHT JUNCTION. MORE HEAVILY
CC PHOSPHORYLATED FORMS ARE CONCENTRATED EXCLUSIVELY IN TIGHT
CC JUNCTION.
CC -!- SIMILARITY: Belongs to the ELL / occludin family.
CC
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CC
CC EMBL; U49221; AAC48582.1; -;
CC InterPro; IPR008253; Marvel.
CC InterPro; IPR002958; Occludin.
CC Pfam; PF01284; MARVEL; 1.
CC PRINTS; PR01358; OCLUDIN.
CC Tight junction; Transmembrane; Coiled coil; Phosphorylation.
KW DOMAIN 1 66
KW TRANSMEM 67 89
FT DOMAIN 90 134
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 135 159
FT TRANSMEM 160 169
FT DOMAIN 170 194
FT TRANSMEM 170 194
FT DOMAIN 195 242
FT TRANSMEM 243 264
FT DOMAIN 265 521
FT DOMAIN 92 130
FT TYR/GLY-RICH.
FT DOMAIN 308 311
FT POLY-PRO.
FT DOMAIN 424 488
FT COILED COIL (POTENTIAL).

SQ SEQUENCE 521 AA; 59275 MW; 2875E59F8F0A1FFA CRC64;
 Query Match 49.5%; Score 48; DB 1; Length 521;
 Best Local Similarity 53.8%; Pred. No. 10;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 13
 Db 116 GYGFGYGYG 128

RESULT 9
 OCLN_CHICK STANDARD; PRT; 504 AA.
 AC Q91029;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Occludin.
 GN OCLN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic brain;
 RX MEDLINE=94103332; PubMed=8276896;
 RA Furuse M., Hirase T., Itoh M., Nagafuchi A., Yonemura S., Tsukita S.,
 RA Tsukita S.;
 RT "Occludin: a novel integral membrane protein localizing at tight
 RT junctions."
 RL J. Cell Biol. 123:1777-1788(1993).
 CC -!- FUNCTION: May play a role in the formation and regulation of the
 CC tight junction (TJ) paracellular permeability barrier. Interacts
 CC with ZO-1.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
 CC epithelial and endothelial cells. Highly expressed in lung and
 CC liver. Expressed at a lower level in brain.
 CC -!- DOMAIN: The C-terminal is cytoplasmic and is important for
 CC interaction with ZO-1. Necessary for the tight junction
 CC localization. Involved in the regulation of the permeability
 CC barrier function of the tight junction. The second extracellular
 CC domain may also be implicated in the permeability barrier function
 CC of the tight junction.
 CC -!- PTM: Phosphorylated (By similarity).
 CC -!- SIMILARITY: Belongs to the ELL / occludin family.

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 EMBL; D21837; BA04865.1; -
 PIR; A49467; A49467.
 InterPro; IPR008253; Marvel.
 InterPro; IPR002958; Occludin.
 Pfam; PF01284; MARVEL; 1.
 PRINTS; PR01258; OCLUDIN.
 Tight junction; Transmembrane; Coiled coil; Phosphorylation.
 DOMAIN 1 57 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 58 80 POTENTIAL.
 DOMAIN 81 123 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 124 148 POTENTIAL.
 DOMAIN 149 158 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 159 183 POTENTIAL.
 DOMAIN 184 227 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 228 249 POTENTIAL.

FT DOMAIN 250 504 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 82 119 TYR/GLY-RICH.
 FT DOMAIN 347 351 POLY-GLU.
 FT DOMAIN 363 370 POLY-ARG.
 FT DOMAIN 412 471 COILED COIL (POTENTIAL).
 SQ SEQUENCE 504 AA; 55863 MW; AD0352A45A0231FF CRC64;
 Query Match 48.5%; Score 47; DB 1; Length 504;
 Best Local Similarity 61.5%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 13
 Db 106 GLSYSYGYGYG 118

RESULT 10
 FRE4_YEAST STANDARD; PRT; 719 AA.
 AC P53746;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ferric reductase transmembrane component 4 precursor (EC 1.16.1.7)
 DE (Ferric-chelate reductase 4).
 DE (Ferric-chelate reductase 4).
 GN FRE4 OR YNR060W OR N3518.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Duasterhoef A., Floeth M., Fritz C., Heuss-Neitzel D.,
 RA Hilbert H., Moestl D.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: NADH + 2 Fe(3+) = NAD(+) + 2 Fe(2+).
 CC -!- COPACITOR: FAD (Probable).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the FRE / CVBB family.

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 EMBL; Z71675; CA96342.1; -
 PIR; S63392; S63392.
 GerMOnline; 143405; -
 SGD; S0005343; FRE4.
 GO; GO:0005886; C:plasma membrane; IMP.
 GO; GO:0000293; F:ferric-chelate reductase activity; IMP.
 GO; GO:0015892; P:iron-siderochrome transport; IMP.
 InterPro; IPR002916; Ferric_reduct.
 Pfam; PF01794; Ferric_reduct; 1.
 Oxidoreductase; Electron transport; Transmembrane; Iron transport;
 KW FAD; NAD; Glycoprotein; Signal; Multigene family.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 719 FERRIC REDUCTASE TRANSMEMBRANE COMPONENT
 FT NP_BIND 472 478 FAD (POTENTIAL).
 FT TRANSMEM 157 177 POTENTIAL.
 FT TRANSMEM 229 249 POTENTIAL.
 FT TRANSMEM 268 288 POTENTIAL.
 FT TRANSMEM 347 367 POTENTIAL.
 FT TRANSMEM 375 395 POTENTIAL.
 FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 647 647 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 696 696 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 719 AA; 82015 MW; 9CA91F1F890AF1F9 CRC64;

Query Match 48.5%; Score 47; DB 1; Length 719;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 2 GYSYNYD--YYG 13
DB 147 YGYNNHDIPIYFEG 160

RESULT 11
YC81.METJA STANDARD; PRT; 1048 AA.
AC Q58677;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Hypothetical protein MJ1281.
GN Mj1281.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=868087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073 (1996).
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CC -----
DR EMBL; U67568; AAB99287.1; -.
DR TIGR; MJ1281; -.
KW Hypothetical protein; Complete proteome.
FT DOMAIN 598 601 POLY-GLU.
SQ SEQUENCE 1048 AA; 121014 MW; 14138CFDCE6A8A76 CRC64;

Query Match 48.5%; Score 47; DB 1; Length 1048;
Best Local Similarity 72.7%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GYSYNYDYTG 13
DB 419 GYSYNEEYGG 429

RESULT 12
YK00.YEAST STANDARD; PRT; 201 AA.
ID YK00.YEAST
AC P36099;

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DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical 23.0 kDa protein in YXR1-TPA1 intergenic region.
GN YKL030W OR YKL243.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-180 FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94262309; PubMed=82031146;
RA Purnelle B., Skala J., van Dyck L., Goffeau A.;
RT "Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new
RT tRNA gene and four new open reading frames including a leucine zipper
RT protein and a homologue to the yeast mitochondrial regulator ABF2."
RL Yeast 10:125-130 (1994).
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CC -----
DR EMBL; Z28029; CAA81864.1; -.
DR EMBL; X71622; -. NOT ANNOTATED_CDS.
DR PIR; S37847; S37847.
DR GEMOnline; 139786; -.
DR SGD; S0001513; YKL030W.
KW Hypothetical protein.
SQ SEQUENCE 201 AA; 22956 MW; AF7B9798DFA88459 CRC64;

Query Match 47.4%; Score 46; DB 1; Length 201;
Best Local Similarity 72.7%; Pred. No. 7.8;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSYNYDYGYG 14
DB 25 YYYYYGYGYG 35

RESULT 13
ROR_HUMAN STANDARD; PRT; 633 AA.
AC O43390;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heterogeneous nuclear ribonucleoprotein R (hnRNP R).
GN hnRNP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98083170; PubMed=9421497;
RA Hassfeld W., Chan E.K.L., Mathison D.A., Portman D., Dreyfuss G.,
RA Steiner G., Tan E.M.;
RT "Molecular definition of heterogeneous nuclear ribonucleoprotein R
RT (hnRNP R) using autoimmune antibody: immunological relationship with
RT hnRNP P."
RL Nucleic Acids Res. 26:439-445 (1998).
CC -!- FUNCTION: Component of ribonucleosomes, which are complexes of at
CC least 20 other different heterogeneous nuclear ribonucleoproteins
CC (hnRNP). hnRNP play an important role in processing of precursor

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CC mRNA in the nucleus.
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleoplasm.
CC -!- SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.
CC -----
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CC -----
CC EMBL: AF000364; AAC39540.1; -.
CC PIR: T02673; T02673.
CC DR HSP: P09651; IHA1.
CC DR Genew: HGNC:5047; HNRPR.
CC DR GK: O43390; -.
CC DR MIM: 607201; -.
CC DR GO: GO:0005634; C:nucleus; TAS.
CC DR GO: GO:0008436; F:heterogeneous nuclear ribonucleoprotein; TAS.
CC DR GO: GO:0003723; F:RNA binding; TAS.
CC DR GO: GO:0006397; P:RNA processing; TAS.
CC DR InterPro: IPR006535; hRNP_R_Q.
CC DR InterPro: IPR000504; RNA_rec_mot.
CC DR Pfam: PF00076; rrm; 3.
CC DR SMART: SM00360; RRM; 3.
CC DR TIGRFAMs: TIGR01648; hRNP-R-Q; 1.
CC DR PROSITE: PS00102; RRM; 3.
CC DR PROSITE: PS00030; RRM_RNP; 1.
CC DR Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat.
CC DOMAIN 1 153 ASP/GLU-RICH (ACIDIC).
CC FT DOMAIN 1 418 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT DOMAIN 2 244 RNA-BINDING (RRM) 1.
CC FT DOMAIN 3 328 RNA-BINDING (RRM) 2.
CC FT DOMAIN 341 411 RNA-BINDING (RRM) 3.
CC FT DOMAIN 447 567 RNA-BINDING (RRM-BOX).
CC FT DOMAIN 462 497 G-Y-D-Y-H-D-Y.
CC FT REPEAT 462 471 1 (APPROXIMATE).
CC FT REPEAT 472 482 2 (APPROXIMATE).
CC FT REPEAT 488 497 3 (APPROXIMATE).
CC FT REPEAT 579 633 GLN/ASN-RICH DOMAIN.
CC SQ SEQUENCE 633 AA; 70943 MW; 088341F6465ED46F CRC64;
Query Match 47.4%; Score 46; DB 1; Length 633;
Best Local Similarity 57.1%; Pred No; 25;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 2 FGYSYNDYDYYGMD 15
Db 465 YGEDYDYYDYYGD 478
RESULT 14
NA95 HUMAN STANDARD; PRT; 646 AA.
AC Q9ULX6; Q94792; Q96J58; Q9NRQ0; Q9UGM0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neighbor of A-kinase anchoring protein 95 (Homologous to AKAP95
DE protein) (HA95) (Helicase A-binding protein 95) (HAP95) (HRIHP2018).
GN NAKAP95.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=20163068; PubMed=10697960;
RA Seki N., Ueki N., Yano K., Saito T., Masuho Y., Muramatsu M.-A.;
RT "CDNA cloning of a novel human gene NAKAP95, neighbor of A-kinase

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RT anchoring protein 95 (AKAP95) on chromosome 19p13.11-pl3.12 region." ;
RL J. Hum. Genet. 45:31-37(2000).
RP SEQUENCE FROM N.A.
RX MEDLINE=2022332; PubMed=10761695;
RA Orstavik S., Eide T., Collas P., Han I.O., Tasken K., Kieff E.,
RA Jansen I., Skalhogg B.S.;
RT "Identification, cloning and characterization of a novel nuclear
RT protein, HA95, homologous to A-kinase anchoring protein 95." ;
RL Biol. Cell 92:27-37(2000).
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta; and T-cell lymphoma;
RX MEDLINE=20347256; PubMed=10748171;
RA Westberg C., Yang J.-P., Tang H., Reddy T.R., Wong-Staal F.;
RT "A novel shuttle protein binds to RNA helicase A and activates the
RT retroviral constitutive transport element." ;
RL J. Biol. Chem. 275:21396-21401(2000).
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska J., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE OF 1-358 FROM N.A., AND SUBCELLULAR LOCATION.
RC TISSUE=Fetal brain;
RX MEDLINE=99068504; PubMed=9853615;
RA Ueki N., Oda T., Kondo M., Yano K., Noguchi T., Muramatsu M.-A.;
RT "Selection system for genes encoding nuclear-targeted proteins." ;
RL Nat. Biotechnol. 16:1338-1342(1998).
CC -!- FUNCTION: Could play a role in constitutive transport element
CC (CTE)-mediated gene expression. Does not seem to be implicated in
CC the binding of regulatory subunit II of PKA.
CC -!- SUBUNIT: Binds to the C-terminal of RNA helicase A.
CC -!- SUBCELLULAR LOCATION: Nuclear at steady state but shuttles between
CC the nucleus and cytoplasm.
CC -----
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CC -----
CC EMBL: AB025905; BAA5003.1; -.
CC DR EMBL: AJ243467; CAB65092.1; -.
CC DR EMBL: AF199414; AAF86048.1; -.
CC DR EMBL: BC000713; AAH00713.1; -.
CC DR EMBL: AB015332; BAA34791.1; ALT_INIT.
CC DR GO: GO:0005634; C:nucleus; TAS.
CC DR GO: GO:0017151; F:DEAD/H-box RNA helicase binding; TAS.
CC DR InterPro: IPR007071; AKAP95.
CC DR InterPro: IPR007087; Znf_C2H2.

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DR Pfam; PF04988; AKAP95; 1.
DR SMART; SM00355; Znf_C2H2; 1.
KW Nuclear protein; Zinc-finger.
FT DOMAIN 274 279 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 362 364 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT ZN_FING 391 413 C2H2-TYPE.
FT ZN_FING 484 507 C2H2-TYPE.
FT DOMAIN 41 52 TYR/GLY-RICH.
FT DOMAIN 602 608 PRO-RICH.
FT DOMAIN 589 597 PRO-RICH.
FT DOMAIN 100 100 D -> N (IN REF. 3).
FT CONFLICT 189 189 S -> N (IN REF. 3).
FT CONFLICT 351 358 ALTTQDEN -> BFSWAGC (IN REF. 4).
FT CONFLICT 458 458 O -> H (IN REF. 1).
FT CONFLICT 554 596 EEEKQEEAEAGALDEGAAGEAGISGEAGCVPAQPPVPE
FT EEEKQEEAEAGALDEGAAGEAGISGEAGCVPAQPPVPE
FT LFCPSQSP (IN REF. 3).
FT EEEGAVPLLGALQRIQIRGLDVEDDEE -> GGGGGR
FT RGPWEGRCNARSASRASTWTRTKK (IN REF. 3).
SQ SEQUENCE 646 AA; 71640 MW; CBC265BF25996BA2 CRC64;

Query Match 47.4%; Score 46; DB 1; Length 646;
Best Local Similarity 45.0%; Pred. No. 25;
Matches 9; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 1 GFGYSYNY-----DYTYGM 14
DB 44 GYGYGYGQDNTNYGYGM 63

RESULT 15
VG74_HSVSA
ID VG74_HSVSA STANDARD; PRT; 321 AA.
AC Q01035;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE G-protein coupled receptor homolog ECRF3.
GN 74 OR ECRF3.
OS Herpesvirus saimiri (strain 11).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10383;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92333688; PubMed=131287;
RA Albrecht J.-C.; Nicholas J.; Biller D.; Cameron K.R.; Biesinger B.;
RA Newman C.; Wittmann S.; Craxton M.A.; Coleman H.; Fleckenstein B.;
RA Honess R.W.;
RT "Primary structure of the herpesvirus saimiri genome.";
RL J. Virol. 66:5047-5058(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92230228; PubMed=1314457;
RA Nicholas J.; Cameron K.R.; Coleman H.; Newman C.; Honess R.W.;
RT "Analysis of nucleotide sequence of the rightmost 43 kbp of
RT herpesvirus saimiri (HVS) L-DNA: general conservation of genetic
RT organization between HVS and Epstein-Barr virus.";
RL Virology 188:296-310(1992).
RN [3]
RP SIMILARITY TO G-PROTEIN COUPLED RECEPTORS.
RX MEDLINE=92115001; PubMed=1309943;
RA Nicholas J.; Cameron K.R.; Honess R.W.;
RT "Herpesvirus saimiri encodes homologues of G protein-coupled
RT receptors and cyclins.";
RL Nature 355:362-365(1992).
CC -!- FUNCTION: MAY BE HIGHLY RELEVANT TO THE PROCESS OF CELLULAR
CC TRANSFORMATION AND RAPID T-CELL PROLIFERATION EFFECTED BY HVS
CC DURING LATENT INFECTIONS OF T-CELLS IN SUSCEPTIBLE HOSTS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S76368; AB21117.1; --
DR EMBL; X64346; CAA45697.1; --
DR EMBL; M86409; AAA46150.1; --
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 51 1 (POTENTIAL).
FT DOMAIN 52 76 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 77 93 2 (POTENTIAL).
FT DOMAIN 94 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 141 3 (POTENTIAL).
FT DOMAIN 142 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 166 4 (POTENTIAL).
FT DOMAIN 167 196 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 197 215 5 (POTENTIAL).
FT DOMAIN 216 234 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 235 251 6 (POTENTIAL).
FT DOMAIN 252 286 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 287 303 7 (POTENTIAL).
FT DOMAIN 304 321 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 18 18 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 321 AA; 37132 MW; 9C4F4C760B962003 CRC64;

Query Match 46.4%; Score 45; DB 1; Length 321;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 4 YSYNY--DYTYG 13
DB 15 YSYNSGDIYTG 26

Search completed: April 21, 2004, 17:33:58
Job time : 9.11594 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:26:23 ; Search time 42.6667 Seconds

(without alignments)
118.319 Million cell updates/sec

Title: SEQ3

Perfect score: 97

Sequence: 1 gfgysynydygmdv 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 58 | 59.8 | 205 | 16 Q9A419 | Q9A419 caulobacter |
| 2 | 56 | 57.7 | 590 | 4 Q8ICC5 | Q8tc5 homo sapien |
| 3 | 55 | 56.7 | 825 | 3 Q07834 | Q07834 saccharomyc |
| 4 | 52 | 53.6 | 152 | 5 Q86EL6 | Q86el6 schistosoma |
| 5 | 52 | 53.6 | 779 | 16 Q8ABP9 | Q8abp9 bacteroides |
| 6 | 52 | 53.6 | 3519 | 5 Q8IE65 | Q8ie65 plasmodium |
| 7 | 51 | 52.6 | 726 | 2 Q9RMD9 | Q9rmd9 acinetobact |
| 8 | 50 | 51.5 | 386 | 10 Q8SLT9 | Q8slt9 oryza sativ |
| 9 | 50 | 51.5 | 753 | 5 Q8ILQ8 | Q8ilq8 plasmodium |
| 10 | 50 | 51.5 | 770 | 17 Q8U3D2 | Q8u3d2 pyrococcus |
| 11 | 50 | 51.5 | 1089 | 16 Q8RE37 | Q8ree7 fusobacteri |
| 12 | 49.5 | 51.0 | 171 | 9 Q8SCT5 | Q8sct5 pseudomonas |
| 13 | 49 | 50.5 | 1044 | 16 Q97GN9 | Q97gn9 clostridium |
| 14 | 49 | 50.5 | 1781 | 5 Q8ILK7 | Q8ilk7 plasmodium |
| 15 | 48 | 49.5 | 380 | 11 Q8GCB8 | Q8gcb8 mus musculu |
| 16 | 48 | 49.5 | 560 | 6 Q9N0W3 | Q9n0w3 canis famil |

| | | | | | |
|----|------|------|------|-----------|--------------------|
| 17 | 48 | 49.5 | 560 | 13 Q802X5 | Q802x5 brachydanio |
| 18 | 48 | 49.5 | 785 | 11 Q8CBY3 | Q8cb3 mus musculu |
| 19 | 48 | 49.5 | 795 | 4 Q8EPV6 | Q8epv6 homo sapien |
| 20 | 48 | 49.5 | 800 | 4 Q8IZ27 | Q8iz27 homo sapien |
| 21 | 48 | 49.5 | 812 | 16 Q8AA51 | Q8aa51 bacteroides |
| 22 | 48 | 49.5 | 1159 | 5 Q8IIN6 | Q8iin6 plasmodium |
| 23 | 48 | 49.5 | 2900 | 5 Q8IEI2 | Q8iei2 plasmodium |
| 24 | 47.5 | 49.0 | 105 | 16 Q9PLS4 | Q9pls4 chlamydia m |
| 25 | 47 | 48.5 | 70 | 16 Q9KCW8 | Q9kcw8 bacillus ha |
| 26 | 47 | 48.5 | 126 | 11 Q8C3P0 | Q8c3p0 mus musculu |
| 27 | 47 | 48.5 | 142 | 5 Q9VC22 | Q9vc22 drosophila |
| 28 | 47 | 48.5 | 345 | 12 Q67G63 | Q67g63 garlic late |
| 29 | 47 | 48.5 | 1816 | 5 Q97275 | Q97275 plasmodium |
| 30 | 46.5 | 47.9 | 91 | 17 Q8TP77 | Q8tp77 methanosarc |
| 31 | 46 | 47.4 | 95 | 16 Q822E5 | Q822e5 chlamydophi |
| 32 | 46 | 47.4 | 101 | 16 Q8XWFS | Q8xwf5 ralstonia s |
| 33 | 46 | 47.4 | 132 | 16 Q8Y9W5 | Q8y9w5 listeria mo |
| 34 | 46 | 47.4 | 210 | 16 Q9AAZ0 | Q9aaz0 caulobacter |
| 35 | 46 | 47.4 | 243 | 4 Q7Z334 | Q7z334 homo sapien |
| 36 | 46 | 47.4 | 307 | 11 Q8BL32 | Q8bl32 mus musculu |
| 37 | 46 | 47.4 | 483 | 17 Q980U1 | Q980u1 sulfolobus |
| 38 | 46 | 47.4 | 537 | 8 Q9B8W3 | Q9b8w3 taenia cras |
| 39 | 46 | 47.4 | 539 | 8 Q955Z6 | Q955z6 taenia soli |
| 40 | 46 | 47.4 | 539 | 8 Q956A0 | Q956a0 taenia soli |
| 41 | 46 | 47.4 | 539 | 8 Q955Z5 | Q955z5 taenia soli |
| 42 | 46 | 47.4 | 539 | 8 Q955Z9 | Q955z9 taenia soli |
| 43 | 46 | 47.4 | 539 | 8 Q955Z7 | Q955z7 taenia soli |
| 44 | 46 | 47.4 | 539 | 8 Q955Z8 | Q955z8 taenia soli |
| 45 | 46 | 47.4 | 539 | 8 Q956A1 | Q956a1 taenia soli |

ALIGNMENTS

RESULT 1

Q9A419 PRELIMINARY; PRT; 205 AA.
AC Q9A419
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein CC3024.
GN CC3024.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Fockea I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Hart D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RA "Complete genome sequence of Caulobacter crescentus";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005965; AA024986.1; -.
DR PIR; F87623; F87623.
DR TIGR; CC3024; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 205 AA; 22665 MW; C03B0E4FC08908E8 CRC64;

Query Match 59.8%; Score 58; DB 16; Length 205;

Best Local Similarity 58.8%; Pred. No. 1.3;

Matches 10; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

OY 1 GFGYSYNYDY----YYG 13

DB 165 GYGGYDYDYAPRPYVG 181

| | | | | |
|--|--|-----------------|-----------|--|
| QY | 1 | GFGYSTNYDY 12 | : : : : : | |
| DB | 795 | GYGYTEYDY 806 | : : : : : | |
| RESULT 4 | | | | |
| Q86EL6 | PRELIMINARY; | PRT; 152 AA. | | |
| ID | Q86EL6 | | | |
| AC | Q86EL6; | | | |
| DT | 01-JUN-2003 (TrEMBLrel. 24, Created) | | | |
| DT | 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) | | | |
| DT | 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) | | | |
| DE | Clone ZD208 mRNA sequence. | | | |
| OS | Schistosoma japonicum (Blood fluke). | | | |
| OC | Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; | | | |
| OC | Schistosomatidae; Schistosomatidae; Schistosoma. | | | |
| OX | NCBI_TaxID=6182; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Liu F., Hu W., Yan Q., Xu X., Zhu Z., Zhang X., Wang J., Sun J., | | | |
| RA | Xu X., Wang Z., Zeng L., Rong Y., Wu X., Qu J., Xu Z., Huang J., | | | |
| RA | Ma Y., Wang S., Wang Z., Xue C., Feng Z., Chen Z., Han Z., | | | |
| RT | "The full-length cDNA of S. japonicum genes"; | | | |
| RL | Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; AY223200; AAP06221.1; - | | | |
| SQ | SEQUENCE 152 AA; 17239 MW; FC6B629092B0E878 CRC64; | | | |
| Query Match 53.6%; Score 52; DB 5; Length 152; | | | | |
| Best Local Similarity 61.5%; Pred. No. 6.9; 2; Indels 0; Gaps 0; | | | | |
| Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0; | | | | |
| QY | 4 | YSYNDYDYGM 16 | : : : : : | |
| DB | 126 | YSYHQYYDIDV 138 | : : : : : | |
| RESULT 5 | | | | |
| Q8ABP9 | PRELIMINARY; | PRT; 779 AA. | | |
| ID | Q8ABP9 | | | |
| AC | Q8ABP9; | | | |
| DT | 01-JUN-2003 (TrEMBLrel. 24, Created) | | | |
| DT | 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) | | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | | | |
| DE | Putative tyrosine-protein kinase ptk. | | | |
| GN | BT0061. | | | |
| OS | Bacteroides thetaiotaomicron. | | | |
| OC | Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales; | | | |
| OC | Bacteroidaceae; Bacteroides. | | | |
| OX | NCBI_TaxID=818; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=VPI-5482 / ATCC 29148; | | | |
| RC | MEDLINE=22550858; PubMed=12663928; | | | |
| RA | Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K., | | | |
| RA | Chiang H.C., Hooper L.V., Gordon J.I., | | | |
| RT | "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."; | | | |
| RL | Science 299:2074-2076 (2003). | | | |
| DR | EMBL; AE016926; AA075168.1; - | | | |
| DR | GO; GO:0009279; C:external outer membrane (sensu Gram-negativ. .; IEA. | | | |
| DR | GO; GO:0003793; P:defense/immunity protein activity; IEA. | | | |
| DR | GO; GO:0016301; P:kinase activity; IEA. | | | |
| DR | GO; GO:0006952; P:defense response; IEA. | | | |
| DR | GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA. | | | |
| DR | InterPro; IPR001800; Lipoprotein_6. | | | |
| DR | InterPro; IPR003856; LPS_Wzz_MPA. | | | |
| DR | Pfam; PF02706; wzz; 1. | | | |
| DR | ProDom; PD001149; Lipoprotein_6; 1. | | | |
| KW | Kinase; Complete proteome. | | | |
| SQ | SEQUENCE 779 AA; 87242 MW; FF30209278D8F430 CRC64; | | | |
| Query Match 53.6%; Score 52; DB 16; Length 779; | | | | |
| Best Local Similarity 61.5%; Pred. No. 39; | | | | |
| Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0; | | | | |

QY 1 GFGYSYNDYYG 13
 :|||:|
 Db 757 GYGYGYGYG 769

RESULT 6

Q8IE65 PRELIMINARY; PRT; 3519 AA.
 AC Q8IE65;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Hypothetical malaria antigen.
 GN M26-32-10.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
 RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
 RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrall B.,
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL844509; CAD52401.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 3519 AA; 419077 MW; 15C47FF2C08C5393 CRC64;

Query Match 53.6%; Score 52; DB 5; Length 3519;
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYGMD 15
 :|||:|

Db 1027 GKGYNYNYNDD 1041

RESULT 7

Q9RMD9 PRELIMINARY; PRT; 726 AA.
 AC Q9RMD9;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Protein tyrosine kinase.
 GN WZC.
 OS Acinetobacter lwoffii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=28090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Nakar D., Gutnick D.L.;
 RC STRAIN=RAG-1;
 RT "Genomic organization of the wce region of Acinetobacter lwoffii RAG-1
 required for emulsan biosynthesis."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RA Nakar D., Gutnick D.L.;
 RC STRAIN=RAG-1;
 RT "A protein tyrosine kinase of Acinetobacter lwoffii RAG-1 is involved
 in emulsan biosynthesis."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ243431; CAB57193.1; -
 DR PIR; T44825; T44825.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0009103; F:kinase activity; IEA.
 DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
 DR InterPro; IPR003856; IFS_Wzz_MPA.
 DR Pfam; PF02706; wzz; 1.
 KW Kinase.
 SQ SEQUENCE 726 AA; 81609 MW; 845BDEDD73E09C0E CRC64;

Query Match 52.6%; Score 51; DB 2; Length 726;
 Best Local Similarity 75.0%; Pred. No. 50;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFGYSYNDYY 12
 :|||:|

Db 709 GAGSYNYAYAY 720

RESULT 8

Q8S1T9 PRELIMINARY; PRT; 386 AA.
 AC Q8S1T9;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE P0506B12.3 protein (P0460C04.23 protein).
 GN P0506B12.3 OR P0460C04.23.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 clone P0506B12."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RA STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 clone P0460C04."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003271; BAB89731.1; -
 DR EMBL; AP004366; BAB92930.1; -
 DR Gramene; Q8S1T9; -
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR004314; DUF239.
 DR Pfam; PF03080; DUF239; 1.
 SQ SEQUENCE 386 AA; 42354 MW; DD4AED7939404EFD CRC64;

Query Match 51.5%; Score 50; DB 10; Length 386;
 Best Local Similarity 57.1%; Pred. No. 36;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 GYSYNDYYGMDV 16
 :|||:|

Db 66 GYEMNSQYYGIEV 79

RESULT 9

Q8I1Q8 PRELIMINARY; PRT; 753 AA.
 AC Q8I1Q8;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN PF00845W.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
 RA Muncall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,

RESULT 13

```

Q97GN9          PRELIMINARY;          PRT; 1044 AA.
ID Q97GN9;
AC Q8ILK7;
DT 01-MAR-2003 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Glycosyltransferase domain containing protein.
GN CAC327.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusev R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AB007733; AAK80283.1; -.
DR PIR; H97186; H97186.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR001296; Glyco_transf_1.
DR InterPro; IPR001173; Glyco_transf_2.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Transferrase; Complete proteome.
SQ SEQUENCE 1044 AA; 121349 MW; C1F2F27E651C39F2 CRC64;

Query Match          50.5%; Score 49; DB 16; Length 1044;
Best Local Similarity 64.3%; Pred. No. 1.4e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 GYSYNYDYVYGMVDV 16
DB 143 GYGYQYD--YGMDI 154
||| ||| ||| |||
||| ||| ||| |||

RESULT 14
Q8ILK7          PRELIMINARY;          PRT; 1781 AA.
ID Q8ILK7;
AC Q8ILK7;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
GN PF14_0236.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.M.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Aguioli S.,
RA Partea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL; AB014819; AAN36849.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.

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DR InterPro; IPR000571; Znf_CCH.
DR Pfam; PF00642; zf-CCCH; 2.
DR SMART; SM00356; Znf_C3H1; 2.
KW Hypothetical protein.
SQ SEQUENCE 1781 AA; 211749 MW; E4E19022A14C46F0 CRC64;

Query Match          50.5%; Score 49; DB 5; Length 1781;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 FGYSYNYDYVYGMVD 15
DB 1114 YNYNYNYNYAYD 1127
||| ||| ||| |||
||| ||| ||| |||

RESULT 15
Q8CGB8          PRELIMINARY;          PRT; 360 AA.
ID Q8CGB8;
AC Q8CGB8;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Similar to hypothetical protein 9330175N02.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041775; AAH41775.1; -.
KW Hypothetical protein.
SQ SEQUENCE 360 AA; 39183 MW; DA00242A347C7709 CRC64;

Query Match          49.5%; Score 48; DB 11; Length 360;
Best Local Similarity 46.7%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 FGYSYNYDYVYGMVDV 16
DB 94 YNYAYPYSYYPMSM 108
||| ||| ||| |||
||| ||| ||| |||

Search completed: April 21, 2004, 17:37:16
Job time : 44.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 16:59:07 ; Search time 32.9099 Seconds
(without alignments)
1035.433 Million cell updates/sec

Title: US-10-041-860-49
Perfect score: 558
Sequence: 1 EIVLTQSPGTLISLPSGERAT.....CQVGSPPCSFGQTKLEIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL.25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 518 | 92.8 | 109 | 4 Q9UL78 | Q9ul78 homo sapien |
| 2 | 504 | 90.3 | 109 | 4 Q9UL86 | Q9ul86 homo sapien |
| 3 | 435.5 | 78.0 | 108 | 4 Q9UL83 | Q9ul83 homo sapien |
| 4 | 426 | 76.3 | 109 | 4 Q9UL85 | Q9ul85 homo sapien |
| 5 | 398.5 | 71.4 | 108 | 4 Q9UL79 | Q9ul79 homo sapien |
| 6 | 390.5 | 70.0 | 108 | 4 Q9UL77 | Q9ul77 homo sapien |
| 7 | 386.5 | 69.3 | 108 | 4 Q9UL70 | Q9ul70 homo sapien |
| 8 | 384 | 68.8 | 114 | 11 Q8K1F1 | Q8klf1 mus musculu |
| 9 | 383.5 | 68.7 | 131 | 11 Q811C3 | Q811c3 mus musculu |
| 10 | 382.5 | 68.5 | 236 | 4 Q7Z3Y4 | Q7z3y4 homo sapien |
| 11 | 381 | 68.3 | 107 | 4 Q96SA9 | Q96sa9 homo sapien |
| 12 | 378.5 | 67.8 | 234 | 4 Q7Z473 | Q7z473 homo sapien |
| 13 | 364.5 | 65.3 | 237 | 13 Q7SZ36 | Q7sz36 xenopus lae |
| 14 | 364 | 65.2 | 239 | 4 Q8NEK0 | Q8nek0 homo sapien |
| 15 | 362 | 64.9 | 107 | 4 Q9UL81 | Q9ul81 homo sapien |
| 16 | 362 | 64.9 | 112 | 11 Q8K1F2 | Q8klf2 mus musculu |

| | | | | | |
|----|-------|------|-----|-----------|--------------------|
| 17 | 361 | 64.7 | 112 | 11 Q8K1E3 | Q8klf3 mus musculu |
| 18 | 358.5 | 64.2 | 111 | 11 Q920E9 | Q920e9 mus musculu |
| 19 | 358 | 64.2 | 106 | 5 Q9U410 | Q9u410 schistosoma |
| 20 | 356.5 | 63.9 | 111 | 11 Q811U6 | Q811u6 mus musculu |
| 21 | 355 | 63.6 | 238 | 11 Q99M37 | Q99m37 mus musculu |
| 22 | 347 | 62.2 | 238 | 11 Q8VCI6 | Q8vci6 mus musculu |
| 23 | 345.5 | 61.9 | 107 | 11 Q9ERZ9 | Q9erz9 mus musculu |
| 24 | 343.5 | 61.6 | 234 | 11 Q8R062 | Q8r062 mus musculu |
| 25 | 343 | 61.5 | 134 | 11 Q8VDD0 | Q8vdd0 mus musculu |
| 26 | 341.5 | 61.2 | 236 | 11 Q7TMK3 | Q7tmk3 mus musculu |
| 27 | 341 | 61.1 | 239 | 4 Q8TCD0 | Q8tcd0 homo sapien |
| 28 | 340 | 60.9 | 239 | 11 Q8VC55 | Q8vc55 mus musculu |
| 29 | 339.5 | 60.8 | 108 | 11 Q8VIJ0 | Q8vij0 mus musculu |
| 30 | 338.5 | 60.7 | 99 | 11 Q9JL74 | Q9jl74 mus musculu |
| 31 | 338 | 60.6 | 235 | 11 Q9LW12 | Q9lw12 mus musculu |
| 32 | 337.5 | 60.5 | 233 | 11 Q9LWS9 | Q9lws9 mus musculu |
| 33 | 334.5 | 59.9 | 109 | 11 Q920E6 | Q920e6 mus musculu |
| 34 | 334.5 | 59.9 | 214 | 11 Q9RIAS | Q9rias mus musculu |
| 35 | 334 | 59.9 | 112 | 11 Q8K1F0 | Q8klf0 mus musculu |
| 36 | 333.5 | 59.8 | 116 | 4 Q96PF6 | Q96pf6 homo sapien |
| 37 | 333.5 | 59.8 | 234 | 11 Q8VCP0 | Q8vcp0 mus musculu |
| 38 | 333.5 | 59.8 | 298 | 11 Q9QYF0 | Q9qyf0 mus musculu |
| 39 | 333 | 59.7 | 235 | 11 Q7TMK0 | Q7tmk0 mus musculu |
| 40 | 331.5 | 59.4 | 101 | 11 Q9JL78 | Q9jl78 mus musculu |
| 41 | 329.5 | 59.1 | 114 | 4 Q9UL80 | Q9ul80 homo sapien |
| 42 | 329.5 | 59.1 | 236 | 11 Q7TS98 | Q7ts98 mus musculu |
| 43 | 328.5 | 58.9 | 234 | 11 Q9LWF8 | Q9lwf8 mus musculu |
| 44 | 323 | 57.9 | 104 | 11 Q9JL82 | Q9jl82 mus musculu |
| 45 | 322.5 | 57.8 | 107 | 11 Q9JL84 | Q9jl84 mus musculu |

ALIGNMENTS

RESULT 1
Q9UL78 PRELIMINARY; PRT; 109 AA.
ID Q9UL78 AC Q9UL78; 2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Marwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; --
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
DR PIR; C30607; C30607.
DR PIR; C30608; C30608.
DR PIR; D30601; D30601.
DR PIR; D30607; D30607.
DR PIR; D30608; D30608.
DR PIR; F30607; F30607.
DR PIR; F30608; F30608.
DR PIR; G30601; G30601.
DR PIR; G30608; G30608.
DR PIR; H30607; H30607.
DR PIR; H30608; H30608.
DR PIR; I30601; I30601.


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DR PIR; PH0963; PH0963.
DR PIR; PH0965; PH0965.
DR PIR; S34096; S34096.
DR HSP; P80362; IWT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EB197 CRC64;

Query Match 92.8%; Score 518; DB 4; Length 109;
Best Local Similarity 93.5%; Pred. No. 3.2e-49;
Matches 101; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60

Qy 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPCFSGQGTKEIK 108
Db 61 DRFSGSGGTDFLTISRLEPEDCAVYCCQYGGSPFLTFGGTKVEIK 108

RESULT 2
Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR PIR; B30609; B30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSP; P80362; IWT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 78.0%; Score 435.5; DB 4; Length 108;
Best Local Similarity 79.6%; Pred. No. 3.7e-40;
Matches 86; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
Db 1 EIVNTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYCASTRATGIP 59

Qy 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPCFSGQGTKEIK 108
Db 60 ARFSGSGGTDFLTISRLEPEDFAVYCCQYHNNWFFTFGGTKVDIK 107

RESULT 4
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR PIR; D30609; D30609.
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RESULT 3
Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR PIR; B30609; B30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSP; P80362; IWT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 78.0%; Score 435.5; DB 4; Length 108;
Best Local Similarity 79.6%; Pred. No. 3.7e-40;
Matches 86; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
Db 1 EIVNTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYCASTRATGIP 59

Qy 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPCFSGQGTKEIK 108
Db 60 ARFSGSGGTDFLTISRLEPEDFAVYCCQYHNNWFFTFGGTKVDIK 107

RESULT 4
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR PIR; D30609; D30609.
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DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; F81E43E7C7AFAPACC CRC64;

Query Match 76.3%; Score 426; DB 4; Length 109;
Best Local Similarity 78.0%; Pred. No. 4.2e-39;
Matches 85; Conservative 11; Mismatches 11; Indels 2; Gaps 2;

Qy 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYATSSRATGIP 60
Db 1 EIVMTQSPATLSVSPGERATLSCWASQSISSN-LAWYQQKPGQAPRLIYATSSRATGIP 59

Qy 61 DRFSGSGGTDTFTLTISRLPEDFAVYYCQYGS-SPCSFGQTKLEIK 108
Db 60 ARFSGSGGTDTFTLTISLQSEDFAIHCQYNSWPLTFGGTKVEIK 108

RESULT 5
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 70.0%; Score 390.5; DB 4; Length 108;
Best Local Similarity 69.4%; Pred. No. 3.3e-35;
Matches 75; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYATSSRATGIP 60
Db 1 DIQMTQSPSLASVGDRTITCRASQSI-SYLAWYQQKPKAPRLIYATSSRATGIP 59

Qy 61 DRFSGSGGTDTFTLTISRLPEDFAVYYCQYGS-SPCSFGQTKLEIK 108
Db 60 SRPFGSGGTDTFTLTISLQSEDFAIYCCQSYSTWTFEGTKVEIK 107

RESULT 7
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; P0863; P0863.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 71.4%; Score 398.5; DB 4; Length 108;
Best Local Similarity 71.3%; Pred. No. 4.3e-36;
Matches 77; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYATSSRATGIP 60
Db 1 DIQMTQSPSLASVGDRTITCRMSQGI-SYLAWYQQKPKAPRLIYATSSRATGIP 59

Qy 61 DRFSGSGGTDTFTLTISRLPEDFAVYYCQYGS-SPCSFGQTKLEIK 108
Db 60 SRPFGSGGTDTFTLTISLQSEDFAIYCCQYSPPTTFGGTKVEIK 107

RESULT 6
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 70.0%; Score 390.5; DB 4; Length 108;
Best Local Similarity 69.4%; Pred. No. 3.3e-35;
Matches 75; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYATSSRATGIP 60
Db 1 DIQMTQSPSLASVGDRTITCRASQSI-SYLAWYQQKPKAPRLIYATSSRATGIP 59

Qy 61 DRFSGSGGTDTFTLTISRLPEDFAVYYCQYGS-SPCSFGQTKLEIK 108
Db 60 SRPFGSGGTDTFTLTISLQSEDFAIYCCQSYSTWTFEGTKVEIK 107

RESULT 7
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; P0863; P0863.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 71.4%; Score 398.5; DB 4; Length 108;
Best Local Similarity 71.3%; Pred. No. 4.3e-36;
Matches 77; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYATSSRATGIP 60
Db 1 DIQMTQSPSLASVGDRTITCRMSQGI-SYLAWYQQKPKAPRLIYATSSRATGIP 59

Qy 61 DRFSGSGGTDTFTLTISRLPEDFAVYYCQYGS-SPCSFGQTKLEIK 108
Db 60 SRPFGSGGTDTFTLTISLQSEDFAIYCCQYSPPTTFGGTKVEIK 107

RESULT 6
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;

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RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RW EMBL: BC005332; AAH05332.1; -.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7BFBE4ED23084BC6 CRC64;

Query Match 68.5%; Score 382.5; DB 4; Length 236;
Best Local Similarity 66.7%; Pred. No. 6.7e-34;
Matches 72; Conservative 16; Mismatches 19; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSVLAWYQQKPGAPRLIYATSSRATGIP 60
DB 23 DIQMTQSPSLASVGVDTIITCRASQDI-SNYLWFOQKPGKAPKSLIYGASSLQSGVQ 81
QY 61 DRPSGSGGTDFTLTISRLEPEDFAVYVYQQYSGSPCSFGQGTKEIK 108
DB 82 SRFGSGSGGTDFTLTISRLEPEDFAVYVYQQYSGSPCSFGQGTKEIK 129

RESULT 11
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RW EMBL: 98375893; PubMed=9712075;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL: U96396; AA868785.1; -.
DR EIR; B49047; B49047.
DR EIR; S34083; S34083.
DR PIR; S34086; S34086.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9CB577F16 CRC64;

Query Match 68.3%; Score 381; DB 4; Length 107;
Best Local Similarity 69.4%; Pred. No. 3.6e-34;
Matches 75; Conservative 14; Mismatches 17; Indels 2; Gaps 2;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSVLAWYQQKPGAPRLIYATSSRATGIP 60
DB 1 DIQMTQSPSLASVGVDTIITCRASQSI-SSYLNWYQKPGKAPKLLIYAASLQSGVP 59
QY 61 DRPSGSGGTDFTLTISRLEPEDFAVYVYQQYSGSPCSFGQGTKEIK 108
DB 60 SRFGSGSGGTDFTLTISRLEPEDFAVYVYQQYSGSPCSFGQGTKEIK 106

RESULT 12
Q7Z473 PRELIMINARY; PRT; 234 AA.
AC Q7Z473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

RC TISSUE=Whole;
RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";

```

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rana S.S., Iqbalan N.A., Peters G.J., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Strausberg R.;
RW EMBL: 98375893; PubMed=9712075;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL: U96396; AA868785.1; -.
DR EIR; B49047; B49047.
DR EIR; S34083; S34083.
DR PIR; S34086; S34086.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 67.8%; Score 378.5; DB 4; Length 234;
Best Local Similarity 67.3%; Pred. No. 1.8e-33;
Matches 72; Conservative 16; Mismatches 18; Indels 1; Gaps 1;

QY 2 IVLTQSPGTLSPGERATLSCRASQSVSSVLAWYQQKPGAPRLIYATSSRATGIP 61
DB 22 IRMTQSPSPSASTGDRVTITCRASQSI-GSYLWYQKPGKAPQLIYAASLQSGVPS 80
QY 62 RFSGSGSGTDFTLTISRLEPEDFAVYVYQQYSGSPCSFGQGTKEIK 108
DB 81 RFSGSGSGTDFTLTISRLEPEDFAVYVYQQYSGSPCSFGQGTKEIK 127

RESULT 13
Q7SZ36 PRELIMINARY; PRT; 237 AA.
AC Q7SZ36;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";

```

DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00335; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;
 Query Match 65.2%; Score 364; DB 4; Length 239;
 Best Local Similarity 62.5%; Pred. No. 7.4e-32;
 Matches 70; Conservative 20; Mismatches 18; Indels 4; Gaps 1;
 QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSS---VLAAYQKPGQAPRLIIYATSSRA 56
 Db 21 DIVMTQSPSLFVTPGEPAISICRSQSLHSDGYNLDWYQKPGQAPRLIIYLSNRA 80
 QY 57 TGPDPFSGSGGTDTLTISLPEDEFAVYVCOQYSGSPCSFGQGTLEIK 108
 Db 81 SGVPDFSGSGGTDTLTLSKVEAEDEVYCYMQGLQTPQTFGQGTKEIK 132
 RESULT 15
 Q9UL81 PRELIMINARY; PRT; 107 AA.
 ID Q9UL81
 AC Q9UL81
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035033; AAD56269.1; -;
 DR HSSP; P01607; IREI.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00335; IG_LIKE; 1.
 FT NON TER 107
 FT NON TER 107
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;
 Query Match 64.9%; Score 362; DB 4; Length 107;
 Best Local Similarity 65.7%; Pred. No. 4.4e-32;
 Matches 71; Conservative 16; Mismatches 19; Indels 2; Gaps 2;
 QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSVLAAYQKPGQAPRLIIYATSSRA 60
 Db 1 DIQMTQSPSLASVGRVITTCRASQSI-SNYLWYQKPGKAPNLLIYAASLSQSGVP 59
 QY 61 DRFGSGSGGTDTLTISLPEDEFAVYVCOQYSGSPCSFGQGTLEIK 108
 Db 60 SRFGSGSGGTDTLTISGLQAEDEPATYCCQ-SYSAITFGPTKVDIR 106
 Search completed: April 21, 2004, 17:03:47
 Job time : 33.9099 secs

RL Dev. Dyn. 225:384-391 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Datchenko L., Marusheva K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.N., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Klein S., Strausberg R.;
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC054155; AAH54155.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 237 AA; 26300 MW; 47B8D0D2639CB436 CRC64;
 Query Match 65.3%; Score 364.5; DB 13; Length 237;
 Best Local Similarity 64.0%; Pred. No. 6.4e-32;
 Matches 71; Conservative 16; Mismatches 21; Indels 3; Gaps 1;
 QY 1 EIVLTQSPGTLSPGERATLSCRASQSV---SSVLAAYQKPGQAPRLIIYATSSRA 57
 Db 21 QIVLTQSPDVSVSPGTEVTLTCKASSVAIGSTIYLHWYQKSGQVPEKLLIYLANTRHT 80
 QY 58 GIPDRSGSGGTDTLTISLPEDEFAVYVCOQYSGSPCSFGQGTLEIK 108
 Db 81 GTPERISGSGGTDTLTISLPEDEFAVYVCOQYSGSPCSFGQGTLEIK 131
 RESULT 14
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 ID Q9NEKO
 AC Q9NEKO
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC030814; AAH30814.1; -;
 DR PIR; S23638; S23638.
 DR PIR; S34091; S34091.
 DR PIR; S40357; S40357.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; IG MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 2.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 16:55:26 ; Search time 47.279 seconds
(without alignments)
645.427 Million cell updates/sec

Title: US-10-041-860-49
Perfect score: 558
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 535 | 95.9 | 129 | 2 | Aar38672 vk325-Jk2 |
| 2 | 533 | 95.5 | 130 | 6 | Abj36930 Anti-CD40 |
| 3 | 533 | 95.5 | 384 | 4 | Am24101 Human EST |
| 4 | 532 | 95.3 | 120 | 7 | Add40551 3E1/4G11 |
| 5 | 530 | 95.0 | 384 | 4 | Aau14462 Human nov |
| 6 | 530 | 95.0 | 384 | 4 | Aau14463 Human nov |
| 7 | 530 | 95.0 | 384 | 4 | Aau14461 Human nov |
| 8 | 530 | 95.0 | 384 | 4 | Aau14464 Human nov |
| 9 | 526 | 94.3 | 108 | 6 | Aae38059 Human 17G |
| 10 | 526 | 94.3 | 109 | 6 | Ada89268 Human ant |
| 11 | 525.5 | 94.2 | 131 | 6 | Abp57366 Anti-TBAI |
| 12 | 524.5 | 94.0 | 109 | 5 | Abg32514 Human VK |
| 13 | 524.5 | 94.0 | 226 | 4 | Aab99397 Human int |
| 14 | 524.5 | 94.0 | 226 | 4 | Aab99374 Human int |
| 15 | 524.5 | 94.0 | 226 | 4 | Aab75007 Anti-IL8 |
| 16 | 524.5 | 94.0 | 226 | 4 | Aab75030 Anti-IL8 |
| 17 | 524 | 93.9 | 109 | 6 | Aae35209 Human IGE |
| 18 | 522.5 | 93.6 | 109 | 6 | Aaw84096 Human V k |
| 19 | 522 | 93.5 | 109 | 6 | Ada89220 Human ant |
| 20 | 522 | 93.5 | 131 | 5 | Abp62199 Human imm |
| 21 | 522 | 93.5 | 134 | 5 | Abp62186 Human imm |
| 22 | 521.5 | 93.5 | 109 | 5 | Abb07233 Anti-IL-4 |
| 23 | 521 | 93.4 | 131 | 5 | Abp62200 Human imm |
| 24 | 521 | 93.4 | 134 | 5 | Abp62207 Human imm |
| 25 | 521 | 93.4 | 134 | 5 | Abp62210 Human imm |

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|----|-------|------|-----|---|--------------------|
| 26 | 521 | 93.4 | 235 | 3 | AAy93702 The kappa |
| 27 | 521 | 93.4 | 235 | 3 | AAy93729 The kappa |
| 28 | 521 | 93.4 | 235 | 6 | AAe35884 Human 4.1 |
| 29 | 520.5 | 93.3 | 107 | 5 | Abb07229 Anti-IL-4 |
| 30 | 520.5 | 93.3 | 109 | 6 | ABE07229 Light cha |
| 31 | 520 | 93.2 | 108 | 6 | ABR54909 Kappa cha |
| 32 | 520 | 93.2 | 108 | 6 | ABR55800 Kappa cha |
| 33 | 519 | 93.0 | 108 | 4 | ABR55804 Kappa cha |
| 34 | 519 | 93.0 | 125 | 5 | ABp62770 Human HIV |
| 35 | 519 | 93.0 | 130 | 6 | ABp62228 Human imm |
| 36 | 518.5 | 92.9 | 109 | 6 | Ada43061 Human ant |
| 37 | 518.5 | 92.9 | 226 | 4 | ABr54907 Light cha |
| 38 | 518.5 | 92.9 | 226 | 4 | ABr54907 Human int |
| 39 | 518.5 | 92.9 | 236 | 5 | AAU74299 Anti-IL8 |
| 40 | 518 | 92.8 | 108 | 4 | AAU74299 Human ant |
| 41 | 518 | 92.8 | 108 | 6 | AAg93666 Human ant |
| 42 | 518 | 92.8 | 131 | 5 | ABO27473 Anti-Rh(D |
| 43 | 517.5 | 92.7 | 109 | 5 | ABp62197 Human imm |
| 44 | 516 | 92.5 | 108 | 5 | ABb07231 Anti-IL-4 |
| 45 | 516 | 92.5 | 108 | 5 | ABg69321 Antibody |
| | | | | | AAo21549 Antibody |

ALIGNMENTS

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ID AAR38672 standard; protein; 129 AA.

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| XX | XX | | | | |
| DT | 25-MAR-2003 | (revised) | | | |
| DT | 01-NOV-1993 | (first entry) | | | |
| XX | XX | | | | |
| DE | vk325-Jk2. | | | | |
| XX | XX | | | | |
| KW | Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS; CD4; | | | | |
| KW | receptor; hybridoma; polymerase chain reaction; PCR; heavy; light; chain; | | | | |
| KW | epitope; immune deficiency. | | | | |
| XX | Homo sapiens. | | | | |
| OS | | | | | |
| XX | Key | Location/Qualifiers | | | |
| FH | Region | 1..116 | | | |
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| FT | | /label= sig_peptide | | | |
| FT | Misc-difference | 1 | | | |
| FT | | /note= "Met encoded by ATC (sic)" | | | |
| FT | Protein | 21..129 | | | |
| FT | | /label= mat_protein | | | |
| FT | Misc-difference | 35 | | | |
| FT | | /note= "Pro encoded by GCA (sic)" | | | |
| FT | Region | 44..55 | | | |
| FT | | /label= CDR1 | | | |
| FT | Region | 71..77 | | | |
| FT | | /label= CDR2 | | | |
| FT | Misc-difference | 99 | | | |
| FT | | /note= "Leu encoded by GTG (sic)" | | | |
| FT | Region | 110..117 | | | |
| FT | | /label= CDR3 | | | |
| FT | Misc-difference | 113 | | | |
| FT | | /note= "Gly encoded by GAT (sic)" | | | |
| FT | Misc-difference | 114 | | | |
| FT | | /note= "Ser encoded by AAC (sic)" | | | |
| FT | Misc-difference | 116 | | | |
| FT | | /note= "Pro encoded by GTT (sic)" | | | |
| FT | Region | 117..129 | | | |
| FT | | /label= Jk2 | | | |
| XX | WO9312232-A1. | | | | |
| XX | 24-JUN-1993. | | | | |
| PD | | | | | |

```

XX 10-DEC-1992; 92WO-US010928.
XX 10-DEC-1991; 91US-00804652.
XX (DAND ) DANA FARBER CANCER INST INC.
XX (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
XX Marasco WA, Sodroski JG, Posner MR, Haseitine WA;
XX WPI; 1993-214174/26.
XX N-PSDB; AAQ42706.
XX DNA segments encoding monoclonal antibody - which binds to gp120 and
XX neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV
XX infection.
XX Disclosure; Page 74-75; 109pp; English.
XX The nucleotide sequence of F105 V $\kappa$  (AAQ42707 - sequence differs from
XX other F105 V $\kappa$  sequences given elsewhere in the specification) was
XX compared with germline gene HumvX325 (AAQ42706), showing 97.7%
XX similarity. By nucleotide sequence analysis, F105 appears to be derived
XX from a member of the V $\kappa$  III subgroup gene family. (Updated on 25-MAR-2003
XX to correct PN field.)
XX Sequence 129 AA;
SQ
Query Match 95.9%; Score 535; DB 2; Length 129;
Best Local Similarity 96.3%; Pred. No. 1.8e-33;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLLIYATSSRATGIP 60
DB 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLLIYATSSRATGIP 80
QY 61 DRFGSGSGTDTLTISRLEPEDFAVYVYCCQYGGSPCSFGQGTLEIK 108
DB 81 DRFGSGSGTDTLTISRLEPEDFAVYVYCCQYGGSPYTFGQGTLEIK 128
RESULT 2
ABJ36930
ID ABJ36930 standard; protein; 130 AA.
AC ABJ36930;
XX
XX 01-MAY-2003 (first entry)
XX Anti-CD40 monoclonal antibody related protein SEQ ID No 46.
XX Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;
XX human CD40; IL-12; LPS; lipopolysaccharide; IFN $\gamma$ ; interferon gamma;
XX dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;
XX immunoadjuvant; anti-tumour agent; immunosuppressant; allergy;
XX autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.
XX Unidentified.
XX WO200288186-A1.
XX
XX 07-NOV-2002.
XX
XX 26-APR-2002; 2002WO-JP004292.
XX
XX 27-APR-2001; 2001WO-US013672.
XX 11-MAY-2001; 2001JP-00142482.
XX 05-OCT-2001; 2001JP-00310535.
XX 26-OCT-2001; 2001US-00040244.
XX (KIRI ) KIRIN BEER KK.
XX Mikayama T, Yoshida H, Force WR, Chen X, Takahashi N;
PI

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XX WPI; 2003-120463/11.
XX N-PSDB; ABT31872.
XX Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,
XX or functional fragment, is useful in the treatment of e.g. autoimmune
XX diseases or cancer.
XX Claim 25; Page 51; 94pp; Japanese.
XX The invention relates to an antibody to human CD40, or its functional
XX fragment, has at least one of the following properties: acting on
XX dendritic cells to produce IL-12 in the presence of LPS
XX (lipopolysaccharide) and IFN $\gamma$  (interferon gamma); acting on dendritic
XX cells to activate maturity of the dendritic cells with high G28-5
XX antibody; and activating CD95 expression with high G28-5 antibody against
XX B cell line. Such antibodies or functional fragments can be used as
XX immunoadjuvants, anti-tumour agents, immunosuppressants, and as remedies
XX for autoimmune diseases, allergy or coagulation factor VIII inhibitors
XX syndrome. This sequence represents a protein relating to the anti-CD40
XX monoclonal antibody of the invention
XX Sequence 130 AA;
SQ
Query Match 95.5%; Score 533; DB 6; Length 130;
Best Local Similarity 95.4%; Pred. No. 2.5e-33;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLLIYATSSRATGIP 60
DB 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLLIYATSSRATGIP 80
QY 61 DRFGSGSGTDTLTISRLEPEDFAVYVYCCQYGGSPCSFGQGTLEIK 108
DB 81 DRFGSGSGTDTLTISRLEPEDFAVYVYCCQYGGSPYTFGQGTLEIK 128
RESULT 3
AAM24101
ID AAM24101 standard; protein; 384 AA.
XX
XX AAM24101;
XX
XX 12-OCT-2001 (first entry)
XX Human EST encoded protein SEQ ID NO: 1626.
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
XX gene therapy; nutrition.
XX Homo sapiens.
XX WO200154477-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US002687.
XX
XX 25-JAN-2000; 2000US-00491404.
XX 17-JUL-2000; 2000US-00617746.
XX 03-AUG-2000; 2000US-00631451.
XX 15-SEP-2000; 2000US-00663870.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX Cao Y, Drmanac RA, Zhang J, Werhman T;
XX WPI; 2001-476164/51.
XX N-PSDB; AAH98760.
XX

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PT Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use.
PS Claim 20; Page 1102-1103; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX
XX Sequence 384 AA;
SQ
Query Match 95.5%; Score 533; DB 4; Length 384;
Best Local Similarity 95.4%; Pred. No. 6.9e-33;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 167 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 226
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGVSSPCSFQGTKEIK 108
DB 227 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGVSSPTTFGGTKVEIK 274
RESULT 4
ADD40551
ID ADD40551 standard; protein; 120 AA.
XX
AC ADD40551;
XX
XX 15-JAN-2004 (first entry)
DE
DE 3E1/4G11 light chain variable region.
XX
XX Human; human Fas ligand; hFasL; antibody;
KW systemic inflammatory response syndrome; sepsis;
KW multiple organ dysfunction syndrome; acute respiratory distress syndrome;
KW trauma; graft-versus-host disease; organ rejection; multiple sclerosis;
KW idiopathic pulmonary fibrosis; osteoarthritis;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW acute myocardial infarction; cardiomyopathy; cardiac reperfusion injury;
KW diabetes; cancer; HIV infection; influenza virus; hepatic disorder;
KW renal disorder; anti-inflammatory; antibacterial; cardiant; osteopathic;
KW virucide; anti-HIV; cytostatic; antidiabetic; nephrotropic; hepatotropic;
KW immunosuppressive; vulnary; gene therapy; vaccine;
KW light chain variable region; 3E1; 4G11.
XX
XX Homo sapiens.
XX OS
XX WO2003079750-A2.
XX
XX
XX 02-OCT-2003.
XX
XX 12-MAR-2003; 2003WO-US006155.
XX PF
XX 21-MAR-2002; 2002US-0367054P.
XX PR
XX 10-SEP-2002; 2002US-0409768P.
XX
XX (ELIL) LILLY & CO ELI.
XX PA
XX Lancaster JS;
XX PI
XX WPI; 2003-876866/81.
XX DR
XX N-PSDB; ADD40550.
XX
XX New isolated anti-hFasL human antibody or its antigen-binding portion,
PT useful for preparing a composition for neutralizing hFasL activity for
PT treating or preventing a disorder in which hFasL activity is detrimental,

PT e.g. sepsis.
XX Claim 1; SEQ ID NO 2; 55pp; English.
XX
XX The present invention relates to anti-human Fas ligand (hFasL) antibodies
CC or their antigen-binding portion (I). (I) are useful for preparing a
CC composition for neutralizing FasL activity for treating or preventing a
CC disorder in which FasL activity is detrimental, e.g. systemic
CC inflammatory response syndrome, sepsis, multiple organ dysfunction
CC syndrome, acute respiratory distress syndrome, trauma, graft-versus-host
CC disease, organ rejection associated with organ transplant, multiple
CC sclerosis, idiopathic pulmonary fibrosis, osteoarthritis, inflammatory
CC bowel disease, Crohn's disease, ulcerative colitis, acute myocardial
CC infarction, cardiomyopathy, cardiac reperfusion injury, diabetes, cancer,
CC HIV infection, influenza virus infection, hepatic disorders including but
CC not limited to fulminant viral hepatitis B or C, chronic hepatitis C
CC virus, chronic hepatitis B virus, alcoholic hepatitis, hepatic cirrhosis
CC or renal disorders. The present sequence is a light chain variable region
CC (LCVR) of anti-FasL antibodies 3E1 or 4G11.
XX
XX Sequence 120 AA;
SQ
Query Match 95.3%; Score 532; DB 7; Length 120;
Best Local Similarity 95.4%; Pred. No. 2.8e-33;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGVSSPCSFQGTKEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGVSSPTTFGGTKVEIK 108
RESULT 5
AAU14462
ID AAU14462 standard; protein; 384 AA.
XX
AC AAU14462;
XX
XX 24-OCT-2001 (first entry)
DT
XX Human novel protein #333.
XX
XX Human; novel protein; Antianaemic; osteopathic; anti-inflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnary; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
XX Homo sapiens.
XX OS
XX WO200155437-A2.
XX
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US002623.
XX PF
XX 25-JAN-2000; 2000US-00491404.
XX PR
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-451939/48.
XX DR
XX N-PSDB; AAS22767.
XX
XX Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage.
PT

PS Example 4; Page 825-826; 894pp; English.

XX The invention relates to polynucleotides encoding novel human proteins or

CC their active domains. The polypeptides, polynucleotides and antibodies

CC raised against the polypeptides are used in a method of treatment of a

CC mammal and prevention of disorders caused by the aberrant protein

CC expression or activity. The polypeptides can be used as molecular weight

CC markers, food supplements, and in antibody production. The polypeptides

CC are used to identify compounds which bind to the polypeptides.

CC Polynucleotides of the invention are used as probes and primers, for

CC sequencing, for chromosome or gene mapping, in the production of

CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene

CC therapy. Polypeptides of the invention can be used to target drugs to a

CC tumour, in assays to determine biological activity, to raise

CC antibodies/ elicit an immune response, to determine quantitative protein

CC levels, as tissue markers, and to isolate receptors or ligands.

CC Polypeptides of the invention may also be useful in treating platelet

CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,

CC ligament and/or nerve tissue, wound healing, treating burns, promoting

CC the proliferation, differentiation and survival of stem cells, as a

CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,

CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral

CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or

CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-

CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory

CC diseases, nervous system disorders, and infection. The present sequence

XX represents a protein of the invention

SQ Sequence 384 AA;

Query Match 95.0%; Score 530; DB 4; Length 384;

Best Local Similarity 94.4%; Pred. No. 1.2e-32;

Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60

DB 170 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYAGSSRATGIP 229

QY 61 DRFSGSGGTDFLTISRLEPEDFAYVYCOQYSSPCSFQGTKEIK 108

DB 230 DRFSGSGGTDFLTISRLEPEDFAYVYCOQYSSPTTFQGTKEIK 277

RESULT 6

AAU14463

ID AAU14463 standard; protein; 384 AA.

AC AAU14463;

XX 24-OCT-2001 (first entry)

DE Human novel protein #334.

XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;

XX immunomodulatory; cytostatic; neuroprotective; vulnary; nootropic;

XX anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;

XX antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;

XX thrombolytic; immunogen; antibody; gene therapy; neurological disorder;

XX Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;

XX tissue regeneration; immune disorder.

OS Homo sapiens.

XX WO200155437-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US002623.

XX 25-JAN-2000; 2000US-00491404.

XX (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-451939/48.

XX N-PSDB; AAS22768.

XX Isolated polypeptides useful for treating anti-inflammatory diseases,

PT nervous system disorders, and for regenerating bone and cartilage.

PS Example 4; Page 826-827; 894pp; English.

XX The invention relates to polynucleotides encoding novel human proteins or

CC their active domains. The polypeptides, polynucleotides and antibodies

CC raised against the polypeptides are used in a method of treatment of a

CC mammal and prevention of disorders caused by the aberrant protein

CC expression or activity. The polypeptides can be used as molecular weight

CC markers, food supplements, and in antibody production. The polypeptides

CC are used to identify compounds which bind to the polypeptides.

CC Polynucleotides of the invention are used as probes and primers, for

CC sequencing, for chromosome or gene mapping, in the production of

CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene

CC therapy. Polypeptides of the invention can be used to target drugs to a

CC tumour, in assays to determine biological activity, to raise

CC antibodies/ elicit an immune response, to determine quantitative protein

CC levels, as tissue markers, and to isolate receptors or ligands.

CC Polypeptides of the invention may also be useful in treating platelet

CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,

CC ligament and/or nerve tissue, wound healing, treating burns, promoting

CC the proliferation, differentiation and survival of stem cells, as a

CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,

CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral

CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or

CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-

CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory

CC diseases, nervous system disorders, and infection. The present sequence

XX represents a protein of the invention

SQ Sequence 384 AA;

Query Match 95.0%; Score 530; DB 4; Length 384;

Best Local Similarity 94.4%; Pred. No. 1.2e-32;

Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60

DB 170 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYAGSSRATGIP 229

QY 61 DRFSGSGGTDFLTISRLEPEDFAYVYCOQYSSPCSFQGTKEIK 108

DB 230 DRFSGSGGTDFLTISRLEPEDFAYVYCOQYSSPTTFQGTKEIK 277

RESULT 7

AAU14461

ID AAU14461 standard; protein; 384 AA.

AC AAU14461;

XX 24-OCT-2001 (first entry)

DE Human novel protein #332.

XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;

XX immunomodulatory; cytostatic; neuroprotective; vulnary; nootropic;

XX anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;

XX antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;

XX thrombolytic; immunogen; antibody; gene therapy; neurological disorder;

XX Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;

XX tissue regeneration; immune disorder.

OS Homo sapiens.

XX WO200155437-A2.

XX

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PD 02-AUG-2001.
XX
XX
XX 25-JAN-2001; 2001WO-US002623.
XX
XX 25-JAN-2000; 2000US-00491404.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-451939/48.
XX
XX N-PSDB; AAS22765.
XX
XX Isolated polypeptides useful for treating anti-inflammatory diseases,
XX nervous system disorders, and for regenerating bone and cartilage.
XX
XX Example 4; Page 824-825; 894pp; English.
XX
XX The invention relates to polynucleotides encoding novel human proteins or
XX their active domains. The polypeptides, polynucleotides and antibodies
XX raised against the polypeptides are used in a method of treatment of a
XX mammal and prevention of disorders caused by the aberrant protein
XX expression or activity. The polypeptides can be used as molecular weight
XX markers, food supplements, and in antibody production. The polypeptides
XX are used to identify compounds which bind to the polypeptides.
XX Polynucleotides of the invention are used as probes and primers, for
XX sequencing, for chromosome or gene mapping, in the production of
XX recombinant proteins, and in generating anti-sense DNA or RNA and in gene
XX therapy. Polypeptides of the invention can be used to target drugs to a
XX tumour, in assays to determine biological activity, to raise
XX antibodies/ elicit an immune response, to determine quantitative protein
XX levels, as tissue markers, and to isolate receptors or ligands
XX Polypeptides of the invention may also be useful in treating platelet
XX disorders, stem cell disorders, regenerating bone, cartilage, tendon,
XX ligament and/or nerve tissue, wound healing, treating burns, promoting
XX the proliferation, differentiation and survival of stem cells, as a
XX contraceptive, treating osteoporosis and osteoarthritis, anaemia,
XX Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
XX sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
XX fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
XX versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
XX diseases, nervous system disorders, and infection. The present sequence
XX represents a protein of the invention
XX
XX Sequence 384 AA;
XX
XX Query Match 95.0%; Score 530; DB 4; Length 384;
XX Best Local Similarity 94.4%; Pred. NO. 1.2e-32;
XX Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPKQAPRLLIYATSSRATGIP 60
XX 170 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPKQAPRLLIYATSSRATGIP 229
XX
XX 61 DRFGSGSGTDFLTISRLEPEDFAVYQYQQYVSSPCSGFGQTKLEIK 108
XX 230 DRFGSGSGTDFLTISRLEPEDFAVYQYQQYVSSPCSGFGQTKVDIK 277
XX
XX RESULT 8
XX AAU14464
XX ID AAU14464 standard; protein; 384 AA.
XX
XX AAU14464;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human novel protein #335.
XX
XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
XX immunomodulatory; cycostatic; neuroprotective; vulnerary; nootropic;
XX anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
XX antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;

```

KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 KW tissue regeneration; immune disorder.

OS Homo sapiens.

PN WO200155437-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US002623.

XX 25-JAN-2000; 2000US-00491404.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-451939/48.

XX N-PSDB; AAS22765.

Isolated polypeptides useful for treating anti-inflammatory diseases,

nervous system disorders, and for regenerating bone and cartilage.

Example 4; Page 827; 894pp; English.

The invention relates to polynucleotides encoding novel human proteins or
 their active domains. The polypeptides, polynucleotides and antibodies
 raised against the polypeptides are used in a method of treatment of a
 mammal and prevention of disorders caused by the aberrant protein
 expression or activity. The polypeptides can be used as molecular weight
 markers, food supplements, and in antibody production. The polypeptides
 are used to identify compounds which bind to the polypeptides.

Polynucleotides of the invention are used as probes and primers, for
 sequencing, for chromosome or gene mapping, in the production of
 recombinant proteins, and in generating anti-sense DNA or RNA and in gene
 therapy. Polypeptides of the invention can be used to target drugs to a
 tumour, in assays to determine biological activity, to raise
 antibodies/ elicit an immune response, to determine quantitative protein
 levels, as tissue markers, and to isolate receptors or ligands.

Polypeptides of the invention may also be useful in treating platelet
 disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 ligament and/or nerve tissue, wound healing, treating burns, promoting
 the proliferation, differentiation and survival of stem cells, as a
 contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
 versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
 diseases, nervous system disorders, and infection. The present sequence
 represents a protein of the invention

Sequence 384 AA;

Query Match 95.0%; Score 530; DB 4; Length 384;
 Best Local Similarity 94.4%; Pred. NO. 1.2e-32;
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPKQAPRLLIYATSSRATGIP 60

170 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPKQAPRLLIYATSSRATGIP 229

61 DRFGSGSGTDFLTISRLEPEDFAVYQYQQYVSSPCSGFGQTKLEIK 108

230 DRFGSGSGTDFLTISRLEPEDFAVYQYQQYVSSPCSGFGQTKVDIK 277

RESULT 9

AAE38059

ID AAE38059 standard; protein; 108 AA.

XX AAE38059;

XX AAE38059;

DT 06-NOV-2003 (first entry)

DE Human 17G1 CD30 antibody light chain variable domain (VL) protein.

XX Human; antibody; CD30; tumour; autoimmune disease; rheumatoid arthritis;

XX systemic lupus erythematosus; systemic sclerosis; Grave's disease; ALCL;

XX atopic dermatitis; Hashimoto's thyroiditis; chronic renal failure; ALLD;

KW acute infectious mononucleosis; angioimmunoblastic lymphadenopathy; HIV;

KW Hodgkin's disease; Castleman's disease; Kaposi's sarcoma; lymphoma; ATL;

KW adult T cell lymphoma; human immunodeficiency virus; carcinoma; therapy;

KW Wegner's granulomatosis; anaplastic large cell lymphoma; Omen's syndrome;

XX light chain variable domain; VL.

XX Homo sapiens.

OS

XX

XX

PH Key Location/Qualifiers

FT 24. .35

FT /note= "Complementarity determining region (CDR) 1"

FT Region

FT 51. .57

FT /note= "Complementarity determining region (CDR) 2"

FT Region

FT 90. .98

FT /note= "Complementarity determining region (CDR) 3"

FT

FT

PN WO2003059282-A2.

XX

XX

XX

XX 24-JUL-2003.

XX

XX 07-JAN-2003; 2003WO-US000440.

XX

XX 09-JAN-2002; 2002US-0347649P.

PR 19-AUG-2002; 2002US-0404427P.

PR 06-DEC-2002; 2002US-0431684P.

XX

XX (MEDA-) MEDAREX INC.

XX

XX

XX Keler T, Graziano R, Tremel J;

XX

DR WPI; 2003-598476/56.

DR N-PSDB; AAD57371.

XX

XX New human monoclonal antibody that binds to human CD30, useful for

PT treating or preventing tumor or autoimmune disease, e.g., rheumatoid

PT arthritis.

PT

XX

XX Claim 18; Fig 8; 122pp; English.

XX

XX The invention relates to human monoclonal antibody that binds to human

CC CD30. The antibody is useful for treating or preventing tumour or

CC autoimmune disease e.g. rheumatoid arthritis, systemic lupus

CC erythematosus, systemic sclerosis, atopic dermatitis, Grave's disease,

CC Hashimoto's thyroiditis, Wegner's granulomatosis, Omen's syndrome,

CC chronic renal failure, acute infectious mononucleosis, herpes or HIV

CC (human immunodeficiency virus), virus-associated diseases. The antibody is

CC also useful for treating Hodgkin's disease, anaplastic large cell

CC lymphoma (ALCL), adult T cell lymphoma (ATL), angioimmunoblastic

CC lymphadenopathy (AILD)-like T cell lymphoma, HIV associated body cavity

CC based lymphomas, embryonal carcinomas, undifferentiated carcinomas of the

CC rhino-pharynx (e.g. Schmincke's tumour), Castleman's disease, Kaposi's

CC Sarcoma and other T-cell or B-cell lymphomas. The present sequence is

CC human CD30 antibody VL (light chain variable domain) protein

XX

SQ Sequence 108 AA;

Query Match 94.3%; Score 526; DB 6; Length 108;

Best Local Similarity 94.4%; Pred. No. 7,2e-33;

Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 EVILQSPGTLISLGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYATSRATGIP 60

DB 1 EVILQSPGTLISLGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYATSRATGIP 60

OY 61 DRFSGSGGTDFTLTISLLEPDAFYVYCCQYGGSSPWTGQTKVEIK 108

DB 61 DRFSGSGGTDFTLTISLLEPDAFYVYCCQYGGSSPWTGQTKVEIK 108

RESULT 10

ADA89268

ID ADA89268 standard; protein; 109 AA.

XX

AC ADA89268;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human antibody 3G3 light chain amino acid sequence SEQ ID NO:112.

XX

XX immunoglobulin; Ig; heavy chain variable domain;

KW light chain variable domain; major histocompatibility complex; MHC;

KW gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;

XX Cancer.

XX

OS Synthetic.

OS Homo sapiens.

XX

XX WO2003070752-A2.

XX

XX 28-AUG-2003.

PD

XX

XX 20-FEB-2003; 2003WO-US005128.

PF

XX

XX 20-FEB-2002; 2002US-0358994P.

PR

XX

XX (DYAX-) DYAX CORP.

PA (TECR) TECHNION RES & DEV FOUND LTD.

PA

XX

XX Hoogenboom HRJM, Reiter Y;

PI

XX

XX WPI; 2003-663847/62.

DR

DR N-PSDB; ADA89267.

XX

XX

PT New protein comprising an immunoglobulin heavy chain variable (VH) domain

PT and an immunoglobulin light chain variable (VL) domain, useful for

PT preparing a composition for treating or preventing a cancerous disorder.

XX

XX Disclosure; Fig 27A; 224pp; English.

XX

XX The present invention describes a protein comprising an immunoglobulin

CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)

CC domain. The protein binds a complex comprising a major histocompatibility

CC complex (MHC) and a peptide, does not substantially bind the MHC in the

CC absence of the bound peptide, and does not substantially bind the peptide

CC in the absence of the MHC. The peptide is a peptide fragment of gp100,

CC MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition

CC comprising the novel protein and a carrier; (2) a cytotoxic T cell

CC comprising one or more nucleic acids for expressing the Ig that binds a

CC complex having an MHC and a peptide, does not substantially bind the MHC

CC in the absence of the bound peptide, and does not substantially bind the

CC peptide in the absence of the MHC; (3) an isolated nucleic acid

CC comprising a first segment that encodes the Ig variable domain; (4) a

CC host cell comprising heterologous nucleic acid sequences that encodes the

CC novel protein; (5) a transgenic animal whose genome includes heterologous

CC nucleic acid sequences that encode the protein; (6) identifying the

CC protein that specifically binds the MHC-peptide complex; (7) expressing

CC an antigen-binding protein; (8) ablating or killing a target cell that

CC displays a peptide on a surface MHC molecule; (9) treating or preventing

CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide

CC complex in a sample. A protein of the invention has cytostatic activity,

CC and can be used in gene therapy. The protein is useful for preparing a

CC composition for treating or preventing a cancerous disorder. The present

CC sequence represents the light chain of an antibody which binds to an MHC-

CC peptide complex where the peptide component in as peptide fragment of

CC hTERT.

XX

SQ Sequence 109 AA;

Query Match 94.3%; Score 526; DB 6; Length 109;

Best Local Similarity 94.4%; Pred. No. 7.3e-33;
Matches 102; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYCOQKPGQAPRLIYATSSRATGIP 60
DB 1 ETTLTQSPGTLSPGERATLSCRASQSVSSSYLAAYCOQKPGQAPRLIYATSSRATGIP 60

QY 61 DRFGSGSGTDTLTISRLEPEDFAVYCCQYGGSSPCSFQGTKEIK 108
DB 61 DRFGSGSGTDTLTISRLEPEDFAVYCCQYGGSSPVTFGQGTKEIK 108

RESULT 11
ABP57366
ID ABP57366 standard; protein; 131 AA.
XX AC ABP57366;
XX DT 22-APR-2003 (first entry)
XX DE Anti-TRAIL-R antibody related clone H-48-2 protein SEQ ID NO:27.
XX KW Human; TRAIL-R1; TRAIL-R2; antibody; cytostatic; apoptotic; tumour;
XX KW antibody therapy.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200294880-A1.
XX PD 28-NOV-2002.
XX PF 17-MAY-2002; 2002WO-JP004816.
XX PR 18-MAY-2001; 2001JP-00150213.
XX PR 09-AUG-2001; 2001JP-00243040.
XX PR 11-OCT-2001; 2001JP-00314489.
XX PA (KIRI) KIRIN BEER KK.
XX PI Mori E, Kataoka S;
XX WPI; 2003-120790/11.
XX DR N-PSDB; ABZ59697.
XX PS Claim 54; Page 59; 92pp; Japanese.
XX CC The present invention describes antibodies or their functional fragments
XX CC that bind to TRAIL-R1 and/or TRAIL-R2. TRAIL-R1 and TRAIL-R2 antibodies
XX CC have cytostatic and apoptotic activities, and can be used in antibody
XX CC therapy. The antibodies can be applied as remedies and preventives of
XX CC diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful
XX CC in the therapy of malignant tumours. Remedies produced with the
XX CC antibodies are highly safe, and avoid hepatotoxicity. The present
XX CC sequence represents an anti-TRAIL-R antibody amino acid sequence from the
XX CC present invention
XX CC Sequence 131 AA;
SQ Query Match 94.2%; Score 525.5; DB 6; Length 131;
Best Local Similarity 95.4%; Pred. No. 9.4e-33;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYCOQKPGQAPRLIYATSSRATGIP 60
DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYCOQKPGQAPRLIYATSSRATGIP 80

QY 61 DRFGSGSGTDTLTISRLEPEDFAVYCCQYGGSSPCSFQGTKEIK 108

DB 81 DRFGSGSGTDTLTISRLEPEDFAVYCCQYGGSSPVTFGQGTKEIK 129

RESULT 12
ABG32514
ID ABG32514 standard; protein; 109 AA.
XX AC ABG32514;
XX DT 15-NOV-2002 (first entry)
XX DE Human VK region of monoclonal antibody for CD89, CD89 8.2 VK.
XX KW Human; monoclonal antibody; antibody; CD89; IGA receptor; Fcalpha;
XX KW light chain variable region; cancer; bacterial infection;
XX KW viral infection; parasitic infection; autoimmune disease; diabetes;
XX KW arthritis; multiple sclerosis; psoriasis; Crohn's disease; asthma;
XX KW allergies; chronic hepatitis; Henoch-Schonlein purpura; Berger's disease;
XX KW IGA-glomerulonephritis; CD89 8.2.
XX OS Homo sapiens.
XX PN WO200264634-A2.
XX PD 22-AUG-2002.
XX PF 11-FEB-2002; 2002WO-US004024.
XX PR 12-FEB-2001; 2001US-0268075P.
XX PR 05-NOV-2001; 2001US-0338956P.
XX PA (MEDA-) MEDAREX INC.
XX PI Hudson D, Van De Winkel J, Van Dijk MA;
XX WPI; 2002-643459/69.
XX DR N-PSDB; ABG52473.
XX PS New isolated human monoclonal antibody that binds to human CD89, useful
XX PT for in the treatment of diseases related to CD89 expression such as
XX PT cancer, bacterial, viral and parasitic infections and autoimmune
XX PT diseases.
XX PS Claim 10; Fig 4; 82pp; English.
XX CC The invention relates to an isolated human monoclonal antibody which
XX CC binds to human CD89 (an IGA receptor also called Fcalpha), comprising at
XX CC least one characteristic selected from: (i) a binding equilibrium
XX CC association constant (K_a) to human CD89 of at least about 10⁷ M⁻¹; or
XX CC (ii) a dissociation constant (K_d) from human CD89 of about 10⁻⁸ S⁻¹ or
XX CC less; (iii) absence of in vivo complement activation upon binding to
XX CC human CD89; (iv) the antibody binds to an epitope on human CD89 which
XX CC does not inhibit human IGA binding to the receptor; and (v) the antibody
XX CC comprises heavy chain and light chain components and their encoding
XX CC nucleic acids appearing as ABS2470-ABS53473 and ABS32511-ABS32514. The
XX CC human antibodies of the present invention that modulates CD89 level.
XX CC blocks or inhibits IGA binding to CD89 are useful in the treatment of
XX CC diseases related to CD89 expression or by circulating IGA-containing
XX CC complexes such as cancer, bacterial, viral and parasitic infections,
XX CC autoimmune diseases (diabetes, arthritis, multiple sclerosis, psoriasis,
XX CC Crohn's disease, asthma, and allergies), chronic hepatitis, Henoch-
XX CC Schonlein purpura, Berger's disease or IGA-glomerulonephritis. The
XX CC present sequence represents the light chain variable region of the
XX CC monoclonal antibody CD89 8.2
SQ Sequence 109 AA;

Query Match 94.0%; Score 524.5; DB 5; Length 109;
Best Local Similarity 95.4%; Pred. No. 9.5e-33;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYCOQKPGQAPRLIYATSSRATGIP 60

CC of target antigen in a sample in a semi-quantitative or relative sense.
CC Quantification of one or more target antigens in a sample can also be
CC carried out using (i). AAH41612 to AAH41686, and AAB99361 to AAB99399,
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 226 AA;

Query Match 94.0%; Score 524.5; DB 4; Length 226;
Best Local Similarity 95.4%; Pred. No. 1.9e-32;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQYQYSS-PCSFQGGTKLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQYQYSSPPYTFQGGTKLEIK 109

RESULT 15
AAB75007
ID AAB75007 standard; protein; 226 AA.
XX
XX AAB75007;
XX 19-JUL-2001 (first entry)
XX
XX Anti-IL8 monoclonal antibody protein fragment M1_23L.
XX Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW human antibody phage display library; immunisation; transgenic animal.
XX Homo sapiens.
OS Synthetic.
XX WO200125492-A1.
PN
XX 12-APR-2001.
XX
XX 02-OCT-2000; 2000WO-US027237.
XX
XX 02-OCT-1999; 99US-0157415P.
PR
XX 01-DEC-1999; 99US-00453234.
XX
XX (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
XX Buechler J, Valkirs G, Gray J, Lonberg N;
PI
XX WPI; 2001-335567/35.
DR
XX

PT Producing a human antibody phage display library comprises providing a
PT transgenic animal whose genome comprises human immunoglobulin genes and
PT isolating nucleic acids encoding antibody chains from lymphatic cells.
XX
XX Example 22; Page 98; 161pp; English.

XX The present invention describes a method (M1) for producing a human
XX antibody phage display library (I), comprising: (1) providing a nonhuman
XX transgenic animal (ii) whose genome comprises human immunoglobulin genes;
XX (2) isolating nucleic acids encoding human antibody chains (iii) from
XX lymphatic cells; and (3) forming a library of display packages whose
XX members comprise a nucleic acid encoding (iii) which is displayed from
XX the package. The method is used for producing a human antibody display
XX library, e.g., a Fab phage display library. The display method may be
XX used to screen nucleic acids encoding antibody chains obtained from
XX immunised nonhuman transgenic animals, and from this a population of
XX antibodies may be prepared. Production of a human monoclonal antibodies
XX display library using this method means there is no need to immunise
XX humans with antigens, and the difficulties faced with immortalising B
XX cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
XX represent sequences used in the exemplification of the present invention

XX
SQ Sequence 226 AA;
Query Match 94.0%; Score 524.5; DB 4; Length 226;
Best Local Similarity 95.4%; Pred. No. 1.9e-32;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQYQYSS-PCSFQGGTKLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQYQYSSPPYTFQGGTKLEIK 109

Search completed: April 21, 2004, 17:01:54
Job time : 49.279 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:03:52 ; Search time 35.691 Seconds
(without alignments)
836.607 Million cell updates/sec

Title: US-10-041-860-49

Perfect score: 558
Sequence: 1 EIVLTQSPGTLSSPGERAT.....CQQYSSPCFSGQGTGLEIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------------|-------------------|
| 1 | 558 | 100.0 | 108 | US-10-041-860-49 | Sequence 49, Appl |
| 2 | 558 | 100.0 | 108 | US-10-041-860-225 | Sequence 225, App |
| 3 | 558 | 100.0 | 108 | US-10-041-860-259 | Sequence 259, App |
| 4 | 558 | 100.0 | 108 | US-10-041-860-375 | Sequence 375, App |
| 5 | 532 | 95.3 | 108 | US-10-309-762-156 | Sequence 156, App |
| 6 | 532 | 95.3 | 108 | US-10-307-724-123 | Sequence 123, App |
| 7 | 532 | 95.3 | 215 | US-10-307-724-122 | Sequence 122, App |
| 8 | 530 | 95.0 | 384 | US-10-231-265-805 | Sequence 805, App |
| 9 | 530 | 95.0 | 384 | US-10-231-265-805 | Sequence 804, App |
| 10 | 530 | 95.0 | 384 | US-10-231-265-806 | Sequence 806, App |
| 11 | 530 | 95.0 | 384 | US-10-231-265-807 | Sequence 807, App |
| 12 | 529 | 94.8 | 108 | US-10-269-711-21 | Sequence 21, Appl |
| 13 | 528 | 94.6 | 108 | US-09-948-939-9 | Sequence 9, Appli |
| 14 | 526 | 94.3 | 108 | US-10-338-366-4 | Sequence 4, Appli |
| 15 | 526 | 94.3 | 109 | US-10-371-942-112 | Sequence 112, App |

| | | | | | | |
|----|-------|------|-----|----|--------------------|--------------------|
| 16 | 525 | 94.1 | 106 | 15 | US-10-309-762-163 | Sequence 163, App |
| 17 | 525 | 94.1 | 108 | 14 | US-10-127-890-150 | Sequence 150, App |
| 18 | 524.5 | 94.0 | 109 | 14 | US-10-073-644C-8 | Sequence 8, Appli |
| 19 | 524.5 | 94.0 | 226 | 10 | US-09-453-234-50 | Sequence 50, Appl |
| 20 | 524.5 | 94.0 | 226 | 10 | US-09-453-234-86 | Sequence 86, Appl |
| 21 | 524 | 93.9 | 108 | 15 | US-10-309-762-43 | Sequence 43, Appl |
| 22 | 523 | 93.7 | 108 | 12 | US-10-292-088-113 | Sequence 113, App |
| 23 | 522.5 | 93.6 | 109 | 14 | US-10-223-880-8 | Sequence 8, Appli |
| 24 | 522 | 93.5 | 108 | 12 | US-09-948-939-7 | Sequence 7, Appli |
| 25 | 522 | 93.5 | 109 | 12 | US-10-371-942-64 | Sequence 64, Appl |
| 26 | 521 | 93.4 | 235 | 14 | US-10-153-382-7 | Sequence 7, Appli |
| 27 | 520.5 | 93.3 | 109 | 12 | US-10-251-085B-135 | Sequence 135, App |
| 28 | 520 | 93.2 | 108 | 14 | US-10-269-805-32 | Sequence 32, Appl |
| 29 | 520 | 93.2 | 108 | 14 | US-10-269-805-36 | Sequence 36, Appl |
| 30 | 518.5 | 92.9 | 109 | 12 | US-10-251-085B-133 | Sequence 133, App |
| 31 | 518.5 | 92.9 | 226 | 10 | US-09-453-234-80 | Sequence 80, Appli |
| 32 | 518.5 | 92.9 | 236 | 9 | US-09-859-053-34 | Sequence 34, Appli |
| 33 | 518 | 92.8 | 108 | 10 | US-09-848-788-178 | Sequence 178, App |
| 34 | 516 | 92.5 | 109 | 14 | US-10-067-800-70 | Sequence 70, Appl |
| 35 | 514 | 92.1 | 109 | 12 | US-10-371-942-104 | Sequence 104, App |
| 36 | 513.5 | 92.0 | 236 | 9 | US-09-859-053-38 | Sequence 38, Appl |
| 37 | 513 | 91.9 | 108 | 12 | US-10-180-648-14 | Sequence 14, Appl |
| 38 | 513 | 91.9 | 235 | 12 | US-10-180-648-4 | Sequence 4, Appli |
| 39 | 512.5 | 91.8 | 108 | 12 | US-10-371-942-36 | Sequence 36, Appl |
| 40 | 512.5 | 91.8 | 226 | 10 | US-09-453-234-74 | Sequence 74, Appl |
| 41 | 512 | 91.8 | 108 | 15 | US-10-309-762-39 | Sequence 39, Appl |
| 42 | 511.5 | 91.7 | 226 | 10 | US-09-453-234-42 | Sequence 42, Appl |
| 43 | 511 | 91.6 | 307 | 15 | US-10-291-265-332 | Sequence 332, App |
| 44 | 511 | 91.6 | 312 | 15 | US-10-291-265-334 | Sequence 334, App |
| 45 | 510 | 91.4 | 108 | 14 | US-10-041-860-47 | Sequence 47, Appl |

ALIGNMENTS

RESULT 1

US-10-041-860-49
; Sequence 49, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadl
; APPLICANT: Weber, Richard
; APPLICANT: Bezaheh, Binyan
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-49

Query Match 100.0%; Score 558; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSSPGERATLSCRASQSVSSSYLAWYQKQCPARLLIYATSSRATGIP 60

Db 1 EIVLTQSPGTLSSPGERATLSCRASQSVSSSYLAWYQKQCPARLLIYATSSRATGIP 60

QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYTCQQYGGSPCSFGQGTGLEIK 108

Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYTCQQYGGSPCSFGQGTGLEIK 108

```

RESULT 2
US-10-041-860-225
; Sequence 225, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-225

Query Match 100.0%; Score 558; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVILTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
DB 1 EVILTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60

QY 61 DRFSGSGGTDTFTLTISRLEPEDFAVYCCQYGGSPGSGGTGKLEIK 108
DB 61 DRFSGSGGTDTFTLTISRLEPEDFAVYCCQYGGSPGSGGTGKLEIK 108

RESULT 3
US-10-041-860-259
; Sequence 259, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-259

Query Match 100.0%; Score 558; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVILTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
DB 1 EVILTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60

QY 61 DRFSGSGGTDTFTLTISRLEPEDFAVYCCQYGGSPGSGGTGKLEIK 108
DB 61 DRFSGSGGTDTFTLTISRLEPEDFAVYCCQYGGSPGSGGTGKLEIK 108

```

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QY 61 DRFSGSGGTDTFTLTISRLEPEDFAVYCCQYGGSPGSGGTGKLEIK 108
DB 61 DRFSGSGGTDTFTLTISRLEPEDFAVYCCQYGGSPGSGGTGKLEIK 108

RESULT 4
US-10-041-860-375
; Sequence 375, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-375

Query Match 100.0%; Score 558; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVILTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
DB 1 EVILTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60

QY 61 DRFSGSGGTDTFTLTISRLEPEDFAVYCCQYGGSPGSGGTGKLEIK 108
DB 61 DRFSGSGGTDTFTLTISRLEPEDFAVYCCQYGGSPGSGGTGKLEIK 108

RESULT 5
US-10-309-762-156
; Sequence 156, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT FILING DATE: 2002-12-02
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-156

Query Match 95.5%; Score 533; DB 15; Length 108;
Best Local Similarity 95.4%; Pred. No. 2.8e-41;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```


| | | | | |
|----|----|---|---|----|
| QY | 1 | EIVLTOSPGTILSLSPGERATL | SLCRASQSVSSVSLAWYQQKQPCGAPRLIIYATSSRATGIP | 60 |
| Db | 1 | EIVLTOSPGTILSLSPGERATL | SLCRASQSVSSVSLAWYQQKQPCAPRLIIYGNSSRATGIP | 60 |
| QY | 61 | DRFGSGSGTDFTLTISRLEPEDFAVYYCQYGSSPCSFQGTQLEIK | 108 | |
| Db | 61 | DRFGSGSGTDFTLTISRLEPEDFAVYYCQYGSSPITFGQTRLEIK | 108 | |

RESULT 6
US-10-307-724-123
; Sequence 123, Application US/10307724
; Publication No. US2003023297A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES

```

Query Match      95.3%; Score 532; DB 15; Length 108;
Best Local Similarity 95.4%; Pred.No. 3.5e-41;
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVLTQSPGTLISLFGGERATLSCRASQSVSSYLAWYQKPGQAPRLIYATSSRATGIP 60
Db 1 EVLTQSPGTLISLFGGERATLSCRASQSVSSYLAWYQKPGQAPRLIYATSSRATGIP 60

QY 61 DRFGSGSGGTFTLTISRLEPEDPAVYYCOQYGSSSPCSFGQTGLEIK 108
Db 61 DRFGSGSGGTFTLTISRLEPEDPAVYYCOYGGSSPWTGGQTKVEIK 108

```

RESULT 7
US-10-307-724-122
; Sequence 122, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2c1p
; CURRENT APPLICATION NUMBER: US/10/307,724
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
; LENGTH: 215
; TYPE: PR1
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antibody light chain
US-10-307-724-132

```

```

Query Match      95.3%; Score 532; DB 15; Length 215;
Best Local Similarity 95.4%; Pred. No. 7.1e-4;
Matches 103; Conservative 2; Mismatches 3; Indels 0

Cy 1 EVLTQSPGTTSLSPGERATISCRASQSVSSSYLAWYQQKPGQAPRLIIVAT
Db 1 EVLTQSPGTTSLSPGERATISCRASQSVSSSYLAWYQQKPGQAPRLIIVAT
Qy 61 DRFGSGGGSDPTLLISLRLPEDFAVYCYQYQSGSPCFGGTKLEIK 108
Db 61 DRFGSGGGSDPTLLISLRLPEDFAVYCYQYQSGSPFTFGGTVKVIK 108

```

```

RESULT 8
US-10-291-265-804
; Sequence 804, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: NO. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 804
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-804

```

```

RESULT 9
US-10-291-265-805
; Sequence 805, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al.
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21372-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291.265
; CURRENT FILING DATE: 2000-01-25

```

```
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-805

Query Match          95.0%; Score 530; DB 15; Length 384;
Best Local Similarity 94.4%; Pred. No. 2e-40;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIYATSSRATGIP 60
   |||||
Db 170 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIYATSSRATGIP 229
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKLEIK 108
   |||||
Db 230 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKVDIK 277
   |||||

RESULT 10
US-10-291-265-806
; Sequence 806, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20030232054A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 806
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-806

Query Match          95.0%; Score 530; DB 15; Length 384;
Best Local Similarity 94.4%; Pred. No. 2e-40;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIYATSSRATGIP 60
   |||||
Db 170 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIYATSSRATGIP 229
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKLEIK 108
   |||||
Db 230 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKVDIK 277
   |||||

RESULT 11
US-10-291-265-807
; Sequence 807, Application US/10291265
; Publication No. US20030232054A1
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; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20030232054A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 807
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-807

Query Match          95.0%; Score 530; DB 15; Length 384;
Best Local Similarity 94.4%; Pred. No. 2e-40;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIYATSSRATGIP 60
   |||||
Db 170 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIYATSSRATGIP 229
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKLEIK 108
   |||||
Db 230 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKVDIK 277
   |||||

RESULT 12
US-10-269-711-21
; Sequence 21, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; FILE REFERENCE: 6989. US.O1
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-21

Query Match          94.8%; Score 529; DB 12; Length 108;
Best Local Similarity 94.4%; Pred. No. 6.5e-41;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIYATSSRATGIP 60
   |||||
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIYATSSRATGIP 60
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKLEIK 108
   |||||
Db 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKVEIK 108
   |||||
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```
RESULT 13
US-09-948-939-9
; Sequence 9, Application US/09948939
; Publication No. US20020086014A1
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
; APPLICANT: Halk, Edward L.
; APPLICANT: Lomborg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/09/948,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 09/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: light chain variable region predicted sequence for
; OTHER INFORMATION: 4b6 from V $\kappa$  A-27
US-09-948-939-9

Query Match          94.6%; Score 528; DB 12; Length 108;
Best Local Similarity 94.4%; Pred. No. 8e-41;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGGSPCSFGQGTKLEIK 108
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGGSPWTFGGQTKVEIK 108

RESULT 14
US-10-338-366-4
; Sequence 4, Application US/10338366
; Publication No. US20040006215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Graziano, Robert
; APPLICANT: Trembl, John
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
; FILE REFERENCE: MXI-180
; CURRENT APPLICATION NUMBER: US/10/338,366
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/347649
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/404427
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/431684
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-366-4

Query Match          94.3%; Score 526; DB 15; Length 108;
Best Local Similarity 94.4%; Pred. No. 1.2e-40;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
```

```
DB 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGGSPCSFGQGTKLEIK 108
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGGSPWTFGGQTKVEIK 108

RESULT 15
US-10-371-942-112
; Sequence 112, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-112

Query Match          94.3%; Score 526; DB 12; Length 109;
Best Local Similarity 94.4%; Pred. No. 1.2e-40;
Matches 102; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGGSPCSFGQGTKLEIK 108
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGGSPWTFGGQTKLEIK 108

Search completed: April 21, 2004, 17:13:23
Job time : 36.691 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:00:06 ; Search time 15.2961 Seconds
(without alignments)
364.511 Million cell updates/sec

Title: US-10-041-860-49
Perfect score: 558
Sequence: 1 EIVLTQSPGTLSPGERAT.....CQQYGSFPCFGQTKLEIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.psp:*
6: /cgn2_6/ptodata/2/iaa/backfiles.psp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 530 | 95.0 | 108 | 2 | US-08-232-081B-42 |
| 2 | 529 | 94.8 | 109 | 4 | US-09-025-769B-16 |
| 3 | 525 | 94.1 | 108 | 1 | US-08-488-113B-150 |
| 4 | 525 | 94.1 | 108 | 1 | US-08-477-484B-150 |
| 5 | 525 | 94.1 | 108 | 2 | US-08-646-360-150 |
| 6 | 525 | 94.1 | 108 | 3 | US-08-839-765-150 |
| 7 | 525 | 94.1 | 108 | 3 | US-09-136-389-150 |
| 8 | 525 | 94.1 | 108 | 4 | US-09-610-838-150 |
| 9 | 525 | 94.1 | 108 | 4 | US-09-711-485-150 |
| 10 | 524.5 | 94.0 | 226 | 4 | US-09-456-090A-50 |
| 11 | 524.5 | 94.0 | 226 | 4 | US-09-456-090A-86 |
| 12 | 521 | 93.4 | 235 | 4 | US-09-472-087-14 |
| 13 | 521 | 93.4 | 235 | 4 | US-09-472-087-65 |
| 14 | 518.5 | 92.9 | 226 | 4 | US-09-456-090A-80 |
| 15 | 518 | 92.8 | 108 | 3 | US-09-240-274-178 |
| 16 | 512.5 | 91.8 | 226 | 4 | US-09-456-090A-74 |
| 17 | 511.5 | 91.7 | 226 | 4 | US-09-456-090A-42 |
| 18 | 511 | 91.6 | 129 | 2 | US-08-480-774A-4 |
| 19 | 508 | 91.0 | 108 | 1 | US-07-634-278-86 |
| 20 | 508 | 91.0 | 108 | 1 | US-08-477-728-86 |
| 21 | 508 | 91.0 | 108 | 1 | US-08-474-040-86 |
| 22 | 508 | 91.0 | 108 | 1 | US-08-487-200-86 |
| 23 | 508 | 91.0 | 108 | 3 | US-08-484-537-86 |
| 24 | 506.5 | 90.8 | 226 | 4 | US-09-456-090A-72 |
| 25 | 506 | 90.7 | 107 | 4 | US-08-635-109-7 |
| 26 | 505 | 90.5 | 150 | 3 | US-08-862-124-5 |
| 27 | 505 | 90.5 | 287 | 3 | US-08-862-124-17 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 505 | 90.5 | 304 | 3 | US-08-862-124-14 | Sequence 14, Appl |
| 29 | 504.5 | 90.4 | 107 | 1 | US-08-107-669D-14 | Sequence 14, Appl |
| 30 | 504.5 | 90.4 | 107 | 1 | US-08-472-789A-14 | Sequence 14, Appl |
| 31 | 504.5 | 90.4 | 107 | 2 | US-08-477-531B-14 | Sequence 14, Appl |
| 32 | 504.5 | 90.4 | 107 | 2 | US-08-082-842A-14 | Sequence 14, Appl |
| 33 | 504.5 | 90.4 | 226 | 4 | US-09-456-090A-38 | Sequence 38, Appl |
| 34 | 500.5 | 89.7 | 224 | 4 | US-09-456-090A-52 | Sequence 52, Appl |
| 35 | 499 | 89.4 | 141 | 4 | US-09-472-087-88 | Sequence 88, Appl |
| 36 | 497 | 89.1 | 108 | 1 | US-08-276-852-99 | Sequence 99, Appl |
| 37 | 497 | 89.1 | 108 | 1 | US-08-899-575-99 | Sequence 99, Appl |
| 38 | 497 | 89.1 | 108 | 1 | US-08-899-575-99 | Sequence 99, Appl |
| 39 | 497 | 89.1 | 108 | 5 | PCT-US95-08743-99 | Sequence 99, Appl |
| 40 | 495.5 | 88.8 | 234 | 4 | US-09-472-087-17 | Sequence 17, Appl |
| 41 | 495.5 | 88.8 | 234 | 4 | US-09-472-087-69 | Sequence 69, Appl |
| 42 | 495 | 88.7 | 108 | 1 | US-08-276-852-86 | Sequence 86, Appl |
| 43 | 495 | 88.7 | 108 | 1 | US-08-899-575-86 | Sequence 86, Appl |
| 44 | 495 | 88.7 | 108 | 1 | US-08-899-575-86 | Sequence 86, Appl |
| 45 | 495 | 88.7 | 108 | 5 | PCT-US95-08743-86 | Sequence 86, Appl |

ALIGNMENTS

RESULT 1
US-08-232-081B-42
; Sequence 42, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIJENES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-232-081B-42

Query Match 95.0%; Score 530; DB 2; Length 108;
Best Local Similarity 94.4%; Pred. No. 1,1e-42;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EIVLTQSPGTLSPGERATLSCRAQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRAQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFGSGSGTDTLTISRLPEDFAVYCCQYGGSSPCSFQGTGKLEIK 108
DB 61 DRFGSGSGTDTLTISRLPEDFAVYCCQYGGSSPLTFGGTKVEIK 108

RESULT 2

US-09-025-769B-16
; Sequence 16, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-16

Query Match 94.8%; Score 529; DB 4; Length 109;
Best Local Similarity 94.4%; Pred. No. 1.4e-42;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60
QY 61 DRFGSGSGTDTLTISRLPEDFAVYCCQYGGSSPCSFQGTGKLEIK 108
DB 61 DRFGSGSGTDTLTISRLPEDFAVYCCQYGGNSPYTFGGTKVEIK 108

RESULT 3

US-08-488-113B-150
; Sequence 150, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-150

Query Match 94.1%; Score 525; DB 1; Length 108;
Best Local Similarity 94.4%; Pred. No. 3.3e-42;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60
QY 61 DRFGSGSGTDTLTISRLPEDFAVYCCQYGGSSPCSFQGTGKLEIK 108
DB 61 DRFGSGSGTDTLTISRLPEDFAVYCCQYGGSSPYTFGGTKVEIK 108

RESULT 4

US-08-477-484B-150
; Sequence 150, Application US/08477484B
; Patent No. 5756599
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.

;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 169
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/477,484B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/425,336
;; FILING DATE: 18-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 150:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 108 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-477-484B-150

Query Match 94.1%; Score 525; DB 1; Length 108;
Best Local Similarity 94.4%; Pred. No. 3.3e-42;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSGRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTSPGTLSPGERATLSGRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPDPFAVYCCQYGSSPCSPFGQTKLEIK 108
Db 61 DRFSGSGGTDFTLTISRLEPDPFAVYCCQYGSSPXTFGQTKVEIK 108

RESULT 5
US-08-646-360-150
; Sequence 150, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 173
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,360
;; FILING DATE: 13-MAY-1996
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 150:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 108 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-646-360-150

Query Match 94.1%; Score 525; DB 2; Length 108;
Best Local Similarity 94.4%; Pred. No. 3.3e-42;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSGRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTSPGTLSPGERATLSGRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPDPFAVYCCQYGSSPCSPFGQTKLEIK 108
Db 61 DRFSGSGGTDFTLTISRLEPDPFAVYCCQYGSSPXTFGQTKVEIK 108

RESULT 6
US-08-839-765-150
; Sequence 150, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; NUMBER OF SEQUENCES: 169
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/839,765
 ; FILING DATE: 15-APR-1997
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/425,336
 ; FILING DATE: 18-APR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-8989
 ; TELEFAX: 312/707-9155
 ; TELEX: 650 388-1248
 ; INFORMATION FOR SEQ ID NO: 150:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 108 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-839-765-150

Query Match 94.1%; Score 525; DB 3; Length 108;
 Best Local Similarity 94.4%; Pred. No. 3.3e-42;
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
 DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
 QY 61 DRFGSGSGTDFLTISRLEPGDFAVYVYCOQYSGSPCFSGQTKLEIK 108
 DB 61 DRFGSGSGTDFLTISRLEPGDFAVYVYCOQYSGSPCFSGQTKLEIK 108

RESULT 7
 US-09-136-389-150
 ; Sequence 150, Application US/09136389
 ; Patent No. 6146850
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; NUMBER OF SEQUENCES: 173

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/136,389
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/646,360
 ; FILING DATE: 13-MAY-1996
 ; APPLICATION NUMBER: PCT/US94/05348
 ; FILING DATE: 12-MAY-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 200-70.P4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-8889
 ; TELEFAX: 312/707-9155
 ; TELEX: 650 388-1248
 ; INFORMATION FOR SEQ ID NO: 150:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 108 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-136-389-150

Query Match 94.1%; Score 525; DB 3; Length 108;
 Best Local Similarity 94.4%; Pred. No. 3.3e-42;
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
 DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
 QY 61 DRFGSGSGTDFLTISRLEPGDFAVYVYCOQYSGSPCFSGQTKLEIK 108
 DB 61 DRFGSGSGTDFLTISRLEPGDFAVYVYCOQYSGSPCFSGQTKLEIK 108

RESULT 8
 US-09-610-838-150
 ; Sequence 150, Application US/09610838
 ; Patent No. 6376217
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; NUMBER OF SEQUENCES: 173

; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8989
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-610-838-150

Query Match 94.1%; Score 525; DB 4; Length 108;
Best Local Similarity 94.4%; Pred. No. 3.3e-42;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPDAFYVYCCQYGSSPCSFQGTKEIK 108
DB 61 DRFSGSGGTDFLTISRLEPDAFYVYCCQYGSSPCSFQGTKEIK 108

RESULT 9
US-09-711-485-150
; Sequence 150, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-711-485-150

Query Match 94.1%; Score 525; DB 4; Length 108;
Best Local Similarity 94.4%; Pred. No. 3.3e-42;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPDAFYVYCCQYGSSPCSFQGTKEIK 108
DB 61 DRFSGSGGTDFLTISRLEPDAFYVYCCQYGSSPCSFQGTKEIK 108

RESULT 10
US-09-456-090A-50
; Sequence 50, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff

APPLICANT: Lonberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 50
LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M1-23L
US-09-456-090A-50

Query Match 94.0%; Score 524.5; DB 4; Length 226;
Best Local Similarity 95.4%; Pred. No. 8.3e-42;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQQYGSS-PCSFQGGTKLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQQYGSSPPYTFQGGTKLEIK 109

RESULT 11
US-09-456-090A-86
Sequence 86, Application US/09456090A
Patent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 86
LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-33L
US-09-456-090A-86

Query Match 94.0%; Score 524.5; DB 4; Length 226;
Best Local Similarity 95.4%; Pred. No. 8.3e-42;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQQYGSS-PCSFQGGTKLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQQYGSSPPYTFQGGTKLEIK 109

RESULT 12
US-09-472-087-14
Sequence 14, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY

APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 14
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-14
Query Match 93.4%; Score 521; DB 4; Length 235;
Best Local Similarity 91.7%; Pred. No. 1.8e-41;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60
DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 80
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQQYGSSPCSFQGGTKLEIK 108
DB 81 DRFSGSGGTDFLTISRLEPEDFAVYYCQQYGTSPTWTFQGGTKVEIK 128

RESULT 13
US-09-472-087-65
Sequence 65, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 65
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-65

Query Match 93.4%; Score 521; DB 4; Length 235;
Best Local Similarity 91.7%; Pred. No. 1.8e-41;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60
DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 80
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQQYGSSPCSFQGGTKLEIK 108
DB 81 DRFSGSGGTDFLTISRLEPEDFAVYYCQQYGTSPTWTFQGGTKVEIK 128

RESULT 14
US-09-456-090A-80
Sequence 80, Application US/09456090A
Patent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Joe

Search completed: April 21, 2004, 17:05:19
Job time : 16.2961 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 16:58:51 ; Search time 9.73391 Seconds
(without alignments)
577.731 Million cell updates/sec

Title: US-10-041-860-49
Perfect score: 558
Sequence: 1 EIVLTQSPGTLISLSPGERAT.....CQYGVSSPCSGQGTKLEIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 528 | 94.6 | 129 | 1 KV3L HUMAN | P18135 homo sapien |
| 2 | 526 | 94.3 | 129 | 1 KV3M HUMAN | P18136 homo sapien |
| 3 | 524 | 93.9 | 109 | 1 KV3D HUMAN | P01622 homo sapien |
| 4 | 521 | 93.4 | 109 | 1 KV3B HUMAN | P01620 homo sapien |
| 5 | 508 | 91.0 | 109 | 1 KV3E HUMAN | P01623 homo sapien |
| 6 | 503 | 90.1 | 108 | 1 KV3A HUMAN | P01621 homo sapien |
| 7 | 500 | 89.6 | 109 | 1 KV3G HUMAN | P04206 homo sapien |
| 8 | 466 | 83.5 | 100 | 1 KV3C HUMAN | P01619 homo sapien |
| 9 | 465.5 | 83.4 | 128 | 1 KV3K HUMAN | P06311 homo sapien |
| 10 | 446 | 79.9 | 109 | 1 KV3F HUMAN | P01624 homo sapien |
| 11 | 439 | 78.7 | 129 | 1 KV3H HUMAN | P04207 homo sapien |
| 12 | 420.5 | 75.4 | 115 | 1 KV3I HUMAN | P04433 homo sapien |
| 13 | 415.5 | 74.5 | 114 | 1 KV4A HUMAN | P01625 homo sapien |
| 14 | 414 | 74.2 | 116 | 1 KV3J HUMAN | P04434 homo sapien |
| 15 | 399.5 | 71.6 | 134 | 1 KV4C HUMAN | P06314 homo sapien |
| 16 | 397.5 | 71.2 | 108 | 1 KV1H HUMAN | P01600 homo sapien |
| 17 | 387 | 69.4 | 133 | 1 KV4B HUMAN | P06313 homo sapien |
| 18 | 382.5 | 68.5 | 108 | 1 KV1M HUMAN | P01605 homo sapien |
| 19 | 380.5 | 68.2 | 108 | 1 KV1P HUMAN | P01598 homo sapien |
| 20 | 379.5 | 68.0 | 108 | 1 KV1K HUMAN | P01603 homo sapien |
| 21 | 378.5 | 67.3 | 129 | 1 KV1W HUMAN | P04431 homo sapien |
| 22 | 374 | 67.0 | 113 | 1 KV2D HUMAN | P01617 homo sapien |
| 23 | 373.5 | 66.9 | 108 | 1 KV1N HUMAN | P01606 homo sapien |
| 24 | 373.5 | 66.9 | 108 | 1 KV1V HUMAN | P04430 homo sapien |
| 25 | 371.5 | 66.6 | 111 | 1 KV3M MOUSE | P01665 mus musculus |
| 26 | 370.5 | 66.4 | 108 | 1 KV1L HUMAN | P01604 homo sapien |
| 27 | 369.5 | 66.2 | 111 | 1 KV3N MOUSE | P01666 mus musculus |
| 28 | 369 | 66.1 | 107 | 1 KV1D HUMAN | P01596 homo sapien |
| 29 | 367.5 | 65.9 | 111 | 1 KV3O MOUSE | P01667 mus musculus |
| 30 | 366.5 | 65.7 | 111 | 1 KV3L MOUSE | P01664 mus musculus |
| 31 | 365.5 | 65.5 | 108 | 1 KV1R HUMAN | P01610 homo sapien |
| 32 | 365.5 | 65.5 | 111 | 1 KV3U MOUSE | P01673 mus musculus |
| 33 | 364.5 | 65.3 | 108 | 1 KV1Y HUMAN | P03622 homo sapien |

ALIGNMENTS

RESULT 1

KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.

AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kippes T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Antibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISASS: the protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.
CC PIR; P00022; K3HUHA.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0008955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 94.6%; Score 528; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 3.3e-48;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYATSSRATGIP 60

Db 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYATSSRATGIP 80

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGVSSPCSGQGTKLEIK 108

DB 81 DRFGSGSGTDFLTISRLEPEDFAVYQQYQYGSPTFTFGQGTKEIK 128
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RESULT 2

KV3M_HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RT J. Exp. Med. 167:840-852(1988).
CC -I- DISFASP: The protein is one of the surface immunoglobulin M
autoantibodies expressed in patients with chronic lymphocytic
leukemia.
CC PIR; P10021; K3HUHI.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
FT SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 94.3%; Score 526; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 5.3e-48;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSLAWYQQKPGQAPRLIYATSSRATGIP 60
DB 21 EIVLTSPGTLSPGERATLSCRASQSVSSSLAWYQQKPGQAPRLIYATSSRATGIP 80
QY 61 DRFGSGSGTDFLTISRLEPEDFAVYQQYQYGSPTFTFGQGTKEIK 108
DB 81 DRFGSGSGTDFLTISRLEPEDFAVYQQYQYGSPTFTFGQGTKEIK 128
|||||

RESULT 3

KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region T1.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
Ti). IV. The complete amino acid sequence and its significance for
the mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
CC PIR; A01895; K3HUHI.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
FT SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 93.9%; Score 524; DB 1; Length 109;
Best Local Similarity 92.6%; Pred. No. 7.1e-48;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSLAWYQQKPGQAPRLIYATSSRATGIP 60
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSSLAWYQQKPGQAPRLIYATSSRATGIP 60
QY 61 DRFGSGSGTDFLTISRLEPEDFAVYQQYQYGSPTFTFGQGTKEIK 108
DB 61 DRFGSGSGTDFLTISRLEPEDFAVYQQYQYGSPTFTFGQGTKEIK 108
|||||

RESULT 4

KV3B_HUMAN
ID KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
idiotypically cross-reactive human IGM anti-gamma-globulins of the Wa
group.";
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
CC PIR; A01892; K3HUHI.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.

| | | | |
|---------------|---|-----------------------------------|--|
| DT | 21-JUL-1986 | (Rel. 01, Created) | |
| DT | 21-JUL-1986 | (Rel. 01, Last sequence update) | |
| DT | 15-JUL-1999 | (Rel. 38, Last annotation update) | |
| DE | IG kappa chain V-III region B6. | | |
| OS | Homo sapiens (Human) | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| OX | NCBI_TaxID=9606; | | |
| RN | [1] | | |
| RP | SEQUENCE. | | |
| RA | Milstein C.; | | |
| RT | "The basic sequences of immunoglobulin kappa chains: sequence studies | | |
| RT | of Bence Jones proteins Rad, Pr4 and B6." | | |
| RL | PBS Lett. 2:301-304(1969). | | |
| CC | 1- MISCELLANEOUS: This is a Bence-Jones protein. | | |
| DR | PIR; A01891; K3HUB6. | | |
| DR | HSSP; P80362; 1WTL. | | |
| DR | InterPro; IPR007110; Ig-like. | | |
| DR | InterPro; IPR003596; Ig_V. | | |
| DR | Pfam; PF00047; Ig; 1. | | |
| DR | SMART; SMO0406; IGV; 1. | | |
| DR | PROSITE; PS50835; IG LIKE; 1. | | |
| KW | Immunoglobulin V region; Bence-Jones protein. | | |
| FT | DISULFID 23 89 | | |
| FT | NON TER 108 108 | | |
| SQL | SEQUENCE 108 AA; 11635 MW; 8BC14PF07A419E3D CRC64; | | |
| | Query Match 90.1%; Score 503; DB 1; Length 108; | | |
| | Best Local Similarity 86.1%; Pred. No. 1.le-45; | | |
| | Matches 93; Conservative 9; Mismatches 6; Indels 0; Gaps | | |
| Qy | 1 EIVLTSPGTLSPGERATLSCRAQSQSVSSYLAWYQKPGQAPRLLIYATSSRATGIP | | |
| Db | 1 ZIVLTSPGTLSPGZRAALSCRAQSLSGNLYAWYQKPGQAPRLIMYGVSRRATGIP | | |
| Qy | 61 DRFGSGSGTDFTLTISRLEPEDFAVYVCOQYGSSPCSPGQGTGLEIK 108 | | |
| Db | 61 DRFGSGSGADFTLTISRLEPEDFAVYVCOQYGSSPFTFGQSGKLEIK 108 | | |
| RESULT 7 | | | |
| KV3G HUMAN | | | |
| ID_KV3G_HUMAN | STANDARD; PRT; 109 AA. | | |
| AC | P04206; | | |
| DT | 20-MAR-1987 (Rel. 04, Created) | | |
| DT | 20-MAR-1987 (Rel. 04, Last sequence update) | | |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update) | | |
| DE | IG kappa chain V-III region GOL (Rheumatoid factor). | | |
| OS | Homo sapiens (Human) | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| OX | NCBI_TaxID=9606; | | |
| RN | [1] | | |
| RP | SEQUENCE. | | |
| RA | MEDLINE=86230578; PubMed=3086710; | | |
| EX | Newkirk M.; Chen P.P.; Carson D.A.; Posnett D.; Capra J.D.; | | |
| RT | "Amino acid sequence of a light chain variable region of a human | | |
| RT | rheumatoid factor of the wa idiotypic group, in part predicted by its | | |
| RT | reactivity with antipeptide antibodies." | | |
| RL | Mol. Immunol. 23:239-244(1986). | | |
| DR | PIR; A01893; K3HUGO. | | |
| DR | HSSP; P80362; 1WTL. | | |
| DR | GO; GO:0005576; C:extracellular; NAS. | | |
| DR | GO; GO:0003823; F:antigen binding; NAS. | | |
| DR | GO; GO:0006955; P:immune response; NAS. | | |
| DR | InterPro; IPR007110; Ig-like. | | |
| DR | InterPro; IPR003596; Ig_V. | | |
| DR | Pfam; PF00047; Ig; 1. | | |
| DR | SMART; SMO0406; IGV; 1. | | |
| DR | PROSITE; PS50835; IG LIKE; 1. | | |
| KW | Immunoglobulin V region. | | |
| FT | DISULFID 23 89 | | |
| FT | NON TER 109 109 | | |
| | BY SIMILARITY. | | |

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SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;
Query Match 89.6%; Score 500; DB 1; Length 109;
Best Local Similarity 89.8%; Pred. No. 2.3e-45;
Matches 97; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DQ 1 EIVLTQSPGTLSPGERATLSCRAALLSRGLAWYQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYSSPCSFQGTGLEIK 108
DQ 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYSSPCSFQGTGLEIK 108

RESULT 8
KV3K_HUMAN
ID KV3K_HUMAN STANDARD; PRT; 100 AA.
AC P01621;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region NG9 precursor (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093600; PubMed=6419127;
RA Bentley D.L.;
RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
a small family of germ-line V genes.";
RL Nature 307:77-80(1984).
CC -!- MISCELLANEOUS; THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR PIR; A01894; K3HUNG.
DR HSSP; P80362; 1WTI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0008955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; Hybridoma.
FT SIGNAL 1
FT CHAIN 1
FT DOMAIN 41
FT DISULFID 27
FT NON_TER 100
SQ SEQUENCE 100 AA; 10729 MW; 5D9AF363CC52632F CRC64;

Query Match 83.5%; Score 466; DB 1; Length 100;
Best Local Similarity 94.7%; Pred. No. 7.1e-42;
Matches 90; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DQ 5 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 64
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYSS 95
DQ 65 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYSS 99

RESULT 9
KV3K_HUMAN
ID KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Ig kappa chain V-III region IARC/BL41 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G.; Meindl A.; Combratio G.; Solomon A.; Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC EMBL; Z00021; CAA7316.1; -.
DR PIR; A01899; K3HU41.
DR HSSP; P01607; 1RE1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0008955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 1
FT DOMAIN 21
FT DOMAIN 44
FT DOMAIN 55
FT DOMAIN 70
FT DOMAIN 77
FT DOMAIN 109
FT DOMAIN 118
FT DISULFID 43
FT NON_TER 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 83.4%; Score 465.5; DB 1; Length 128;
Best Local Similarity 87.0%; Pred. No. 1.1e-41;
Matches 94; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DQ 21 EIVLTQSPGTLSPGERATLSCRASQSVSSN-LAWYQKRGQSPRLIIYATSSRANGIP 79
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYSSPCSFQGTGLEIK 108
DQ 80 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYSSPCSFQGTGLEIK 127

RESULT 10
KV3F_HUMAN
ID KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig kappa chain V-III region POM.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

```

```

RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
RT from two idiotypically cross reactive IGM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC PIR; A01897; K3HUPM.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT SIGNAL 1 20
FT CHAIN 21 129
FT DOMAIN 21 43
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 118
FT DOMAIN 119 129
FT DISULFID 43 108
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 11922 MW; 62821DDCGA8ABA86 CRC64;

Query Match 79.9%; Score 446; DB 1; Length 109;
Best Local Similarity 78.7%; Pred. No. 9.6e-40;
Matches 85; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCASQSVSSSYLAWYQQKPGQAPRLIYATSSRATGIP 60
DB 1 EIVTQSPVTLVSFGERATLSCASQSVSSSYLAWYQQKPGSFRLLIYGASTRATGIP 60
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGS-SPCSFGQGTKLEIK 108
DB 61 ARFSGSGSGTEFTLTISRLEQSDFAVYCCQYNNWPFVFGQGTVEIK 108

RESULT 11
KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curo J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene."
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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CC -----
CC EMBL; M12740; AA58992.1; -
CC HSP; P80362; IWL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.

QY 1 EIVLTQSPGTLISLSPGERATLSCASQSVSSSYLAWYQQKPGQAPRLIYATSSRATGIP 60
DB 1 EIVTQSPVTLVSFGERATLSCASQSVSSSYLAWYQQKPGSFRLLIYGASTRATGIP 60
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGS-SPCSFGQGTKLEIK 108
DB 61 ARFSGSGSGTEFTLTISRLEQSDFAVYCCQYNNWPFVFGQGTVEIK 108

RESULT 12
KV3I_HUMAN STANDARD; PRT; 115 AA.
AC P04333;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region VG precursor (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pach M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus."
RL Nucleic Acids Res. 12:9229-9236(1984).
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CC -----
CC EMBL; X01668; -; NOT_ANNOTATED_CDS.
CC PIR; A01900; K3HUVG.
CC HSP; P80362; IWL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 55 69
IG KAPPA CHAIN V-III REGION VG.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DB47CDA3A17D555 CRC64;

Query Match 75.4%; Score 420.5; DB 1; Length 115;
Best Local Similarity 88.5%; Pred. No. 4.7e-37;
Matches 85; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLISLSPGERATLSCRAQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 21 EIVLTQSPATLSLSPGERATLSCRAQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 79
QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSP 96
DB 80 ARFGSGSGTDFLTISRLEPEDFAVYCCQYGGSP 115

RESULT 13
KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1995 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
RT subgroup IV of the kappa type (Bence-Jones protein Len).";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA Salomon A.;
RL Submitted (AUG-1986) to Swiss-Prot.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB; 1EEQ; 01-FEB-01.
DR PDB; 1ESU; 03-FEB-01.
DR PDB; 1EFQ; 09-FEB-01.
DR PDB; 1EX3; 06-MAR-01.
DR PDB; 1LVE; 21-JAN-98.
DR PDB; 3LVE; 18-MAY-99.
DR PDB; 5LVE; 28-MAR-01.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 63 94 FRAMEWORK-3.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 113 FRAMEWORK-4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 74.5%; Score 415.5; DB 1; Length 114;

Best Local Similarity 70.8%; Pred. No. 1.5e-36;
Matches 80; Conservative 16; Mismatches 12; Indels 5; Gaps 1;

QY 1 EIVLTQSPGTLISLSPGERATLSCRAQSVSSSYLAWYQKPGQAPRLIIYATSSR 55
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNKNYLAWYQKPGQPKLLIWASTR 60
QY 56 ATGIDPRFSGSGTDFLTISRLEPEDFAVYCCQYGGSPFCQGTKLK 108
DB 61 ESGVPRFSGSGTDFLTISRLEPEDFAVYCCQYGGSPFCQGTKLK 113

RESULT 14
KV30_HUMAN STANDARD; PRT; 116 AA.
AC P04334;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region VH precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).
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CC -----
DR EMBL; X02725; -; NOT ANNOTATED_CDS.
DR PIR; A01901; K3HUHV.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;

Query Match 74.2%; Score 414; DB 1; Length 116;
Best Local Similarity 84.4%; Pred. No. 2.2e-36;
Matches 81; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRAQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 21 EIVMTQSPPTLSLSPGERVTLSCRAQSVSSSYLTWYQKPGQAPRLIIYGASTRATSI 80
QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSP 96
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Search completed: April 21, 2004, 17:02:35
Job time : 10.7339 secs

Db 81 ARFGSGSGTDTLTITSLQPEDFAVYCCQDHNL 116

RESULT 15

KV4C_HUMAN
ID KV4C_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe."
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; X02990; CAA26733.1; -.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0009555; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 220
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 71.6%; Score 399.5; DB 1; Length 134;
Best Local Similarity 66.4%; Pred. No. 8.6e-35;
Matches 75; Conservative 20; Mismatches 13; Indels 5; Gaps 1;

QY 1 EIVLTSPGTLSPGERATLSGRASQSV-----SSSYLAWYQQKPGQAPRLLIYATSSR 55

Db 21 DIWMTQSPDSLAVSLGERATINCKSSQSYLSDNKNYLAWYQQKPGQAPRLIYASTR 80

QY 56 ATGIPRFSGSGGTFTLTISRLEPEDFAVYCCQYSGSPCSFGCGTKLEIK 108

Db 81 ESGVPRFSGSGGTFTLTITSLQAEADVAVYCCQYINLPWTFGGTKVEIK 133

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OM protein - protein search, using sw model

Run on: April 21, 2004, 16:59:07 ; Search time 12.515 Seconds
(without alignments)
830.097 Million cell updates/sec

Title: US-10-041-860-49
Perfect score: 558
Sequence: 1 EIVLTQSPGTLSPGERAT.....CQQYGSFCSFGQGTKLEIK 108
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191536 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 535 | 95.9 | 108 | 2 | H30608 |
| 2 | 535 | 95.9 | 108 | 2 | H30601 |
| 3 | 535 | 95.7 | 109 | 2 | H30601 |
| 4 | 533 | 95.5 | 109 | 2 | H30601 |
| 5 | 531 | 95.2 | 109 | 2 | H30601 |
| 6 | 531 | 95.2 | 109 | 2 | H30601 |
| 7 | 530 | 95.0 | 109 | 2 | H30601 |
| 8 | 530 | 95.0 | 129 | 2 | S46369 |
| 9 | 530 | 95.0 | 134 | 2 | S38643 |
| 10 | 529 | 94.8 | 109 | 2 | H30601 |
| 11 | 529 | 94.8 | 129 | 2 | S49532 |
| 12 | 528 | 94.6 | 129 | 1 | K3HUBA |
| 13 | 527 | 94.4 | 128 | 2 | S20636 |
| 14 | 526 | 94.3 | 129 | 1 | K3HUBI |
| 15 | 524 | 93.9 | 109 | 1 | K3HUTI |
| 16 | 524 | 93.9 | 109 | 2 | H30601 |
| 17 | 523.5 | 93.8 | 114 | 2 | S46375 |
| 18 | 521 | 93.4 | 109 | 1 | K3HUSI |
| 19 | 520 | 93.2 | 109 | 2 | H30608 |
| 20 | 515 | 92.3 | 109 | 2 | H30607 |
| 21 | 514 | 92.1 | 107 | 2 | H30965 |
| 22 | 514 | 92.1 | 108 | 2 | H30608 |
| 23 | 513 | 91.9 | 124 | 2 | S20633 |
| 24 | 511 | 91.6 | 121 | 1 | S40327 |
| 25 | 508 | 91.0 | 109 | 1 | K3HULI |
| 26 | 507 | 90.9 | 110 | 2 | S20635 |
| 27 | 504.5 | 90.4 | 108 | 2 | E30609 |
| 28 | 503.5 | 90.2 | 110 | 2 | E30607 |
| 29 | 503 | 90.1 | 108 | 1 | K3HUB6 |

30 502 90.0 109 2 F44151
31 501.5 89.9 108 2 H44151
32 500 89.6 109 1 K3HUGO
33 500 89.6 130 2 S20637
34 499 89.4 129 2 A32274
35 497.5 89.2 110 2 S44120
36 495 88.7 109 2 S47181
37 488.5 87.5 104 2 PH0964
38 488 87.5 215 2 JE0242
39 486.5 87.2 129 2 S40325
40 485 86.9 96 2 A30601
41 485 86.9 116 2 B27594
42 484 86.7 215 2 A21746
43 479 85.8 118 2 T03036
44 477 85.5 108 2 S33988
45 475 85.1 116 2 C27594

ALIGNMENTS

RESULT 1

C30608
Ig kappa chain V-III region (Pie) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C/Accession: C30608
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotypic characterization of the L chains of human IgM autoant.
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: C30608
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-108 <GON>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.9%; Score 535; DB 2; Length 108;
Best Local Similarity 96.3%; Pred. No. 5.3e-38;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQQKPGQAPRLITYASSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQQKPGQAPRLITYASSRATGIP 60
Qy 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSFCSFGQGTKLEIK 108
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSFCSFGQGTKLEIK 108

RESULT 2

H30601
Ig kappa chain V-III region (Gar and Flo) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C/Accession: H30601; E30601
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotypic characterization of the L chains of human IgM autoant.
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: H30601
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-109 <GON1>
A/Accession: E30601
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-109 <GON2>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.9%; Score 535; DB 2; Length 109;
 Best Local Similarity 96.3%; Pred. No. 5.3e-38;
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPSCFGQGTKEIK 108
 DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPYTFGGQGTKEIK 108

RESULT 3
 F30601
 Ig kappa chain V-III region (New) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C:Accession: F30601
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
 J. Immunol. 142, 3158-3163, 1989
 A:Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
 A:Reference number: A30601; MUID:89215279; PMID:2496160
 A:Accession: F30601
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-109 <GON>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.7%; Score 534; DB 2; Length 109;
 Best Local Similarity 93.5%; Pred. No. 6.5e-38;
 Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPSCFGQGTKEIK 108
 DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPCTFGQGTKEIK 108

RESULT 4
 B30601
 Ig kappa chain V-III region (Glo) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C:Accession: B30601
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
 J. Immunol. 142, 3158-3163, 1989
 A:Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
 A:Reference number: A30601; MUID:89215279; PMID:2496160
 A:Accession: B30601
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-109 <GON>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.5%; Score 533; DB 2; Length 109;
 Best Local Similarity 95.4%; Pred. No. 7.8e-38;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPSCFGQGTKEIK 108
 DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPCTFGQGTKEIK 108

DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPSLTFGGQGTKEIK 108

RESULT 5
 PH0963
 Ig kappa chain V region (G6+ CLL-SMI) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
 C:Accession: PH0963
 R:Martin, T.; Duffey, S.F.; Carson, D.A.; Kippes, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A:Title: Evidence for somatic selection of natural autoantibodies.
 A:Reference number: PH0952; MUID:92202880; PMID:1552291
 A:Accession: PH0963
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-109 <VAR>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-23/Region: framework 1
 F:16-91/Domain: immunoglobulin homology <IMM>
 F:24-34/Region: complementarity-determining 1
 F:35-50/Region: framework 2
 F:51-56/Region: complementarity-determining 2
 F:57-89/Region: framework 3
 F:90-97/Region: complementarity-determining 3

Query Match 95.2%; Score 531; DB 2; Length 109;
 Best Local Similarity 95.4%; Pred. No. 1.1e-37;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPSCFGQGTKEIK 108
 DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPAFGQGTKEIK 108

RESULT 6
 D30601
 Ig kappa chain V-III region (Cur) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C:Accession: D30601
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
 J. Immunol. 142, 3158-3163, 1989
 A:Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
 A:Reference number: A30601; MUID:89215279; PMID:2496160
 A:Accession: D30601
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-109 <GON>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.2%; Score 531; DB 2; Length 109;
 Best Local Similarity 95.4%; Pred. No. 1.1e-37;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPSCFGQGTKEIK 108
 DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPRTFGQGTKEIK 108

RESULT 7
 C30601

IG kappa chain V-III region (Pay) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C/Accession: C30601
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies.
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: C30601
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-109 <GON>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 109;
Best Local Similarity 95.4%; Pred. No. 1.4e-37;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 108
DB 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 108

RESULT 8
S46369
IG light chain variable region (VU) - human
C/Species: Homo sapiens (man)
C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: S46369
R/Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rearrangement.
A/Reference number: S46369; MUID:94313975; PMID:8039491
A/Accession: S46369
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-129 <BEN>
A/Cross-references: EMBL:Z27170
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F;36-111/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 129;
Best Local Similarity 95.4%; Pred. No. 1.6e-37;
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQQKPGQAPRLIIYATSSRATGIP 60
DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQQKPGQAPRLIIYATSSRATGIP 80

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 108
DB 81 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 128

RESULT 9
S38643
IG kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S38643
R/Bensimon, C.; Chastagner, P.; Zouali, M.
submitted to the EMBL Data Library, November 1993
A/Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A/Reference number: S38643
A/Accession: S38643
A/Status: preliminary

A/Molecule type: mRNA
A/Residues: 1-134 <BEN>
A/Cross-references: EMBL:Z27170; NID:9415955; PIDN:CAA81694.1; PID:9415956
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;41-116/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 134;
Best Local Similarity 95.4%; Pred. No. 1.7e-37;
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQQKPGQAPRLIIYATSSRATGIP 60
DB 26 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQQKPGQAPRLIIYATSSRATGIP 85

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 108
DB 86 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 133

RESULT 10
G30601
IG kappa chain V-III region (Got) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C/Accession: G30601
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies.
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: G30601
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-109 <GON>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 529; DB 2; Length 109;
Best Local Similarity 95.4%; Pred. No. 1.7e-37;
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 108
DB 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 108

RESULT 11
S49532
anti-Sm antibody VL chain (V kappa 3/J kappa 2) - human
C/Species: Homo sapiens (man)
C/Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C/Accession: S49532
R/Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A/Description: Molecular characterization of natural human anti-Sm autoantibodies.
A/Reference number: S49532
A/Accession: S49532
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-129 <MAH>
A/Cross-references: EMBL:Z46345; NID:9560843; PIDN:CAA8464.1; PID:9560844
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-111/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 529; DB 2; Length 129;
Best Local Similarity 95.4%; Pred. No. 2e-37;
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWSYQVQVSSPCSFQGTGLEIK 60
  |||||
Db 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWSYQVQVQAPRLLIYATSSRATGIP 80
  |||||

QY 61 DRFSGSGGTDFLTITISRLPEDFAVYVCOQYQVSSPCSFQGTGLEIK 108
  |||||
Db 81 DRFSGSGGTDFLTITISRLPEDFAVYVCOQYQVSSPCSFQGTGLEIK 128
  |||||

RESULT 12
K3HUHA
Ig kappa chain precursor V-III region (Hah) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C:Accession: PL0022
R:Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A:Title: Autoantibody-associated kappa light chain variable region gene expressed in ch
A:Reference number: PL0021; MUID:88171307; PMID:3127527
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
C:Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed i
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JK1)
F:43-109/Disulfide bonds: #status predicted

Query Match 94.6%; Score 528; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 2.4e-37;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWSYQVQVQAPRLLIYATSSRATGIP 60
  |||||
Db 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWSYQVQVQAPRLLIYATSSRATGIP 80
  |||||

QY 61 DRFSGSGGTDFLTITISRLPEDFAVYVCOQYQVSSPCSFQGTGLEIK 108
  |||||
Db 81 DRFSGSGGTDFLTITISRLPEDFAVYVCOQYQVSSPCSFQGTGLEIK 128
  |||||

RESULT 13
S20636
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20636
R:Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Reference number: S20631
A:Accession: S20636
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <LEE>
A:Cross-references: EMBL:Z11894; NID:G33200; PDB:CAA77948.1; PID:G33201
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match 94.4%; Score 527; DB 2; Length 128;
```

```
Best Local Similarity 94.4%; Pred. No. 2.9e-37;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWSYQVQVQAPRLLIYATSSRATGIP 60
  |||||
Db 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWSYQVQVQAPRLLIYATSSRATGIP 80
  |||||

QY 61 DRFSGSGGTDFLTITISRLPEDFAVYVCOQYQVSSPCSFQGTGLEIK 108
  |||||
Db 81 DRFSGSGGTDFLTITISRLPEDFAVYVCOQYQVSSPCSFQGTGLEIK 128
  |||||

RESULT 14
K3HUHI
Ig kappa chain precursor V-III region (Hic) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C:Accession: PL0021
R:Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A:Title: Autoantibody-associated kappa light chain variable region gene expressed in ch
A:Reference number: PL0021; MUID:88171307; PMID:3127527
A:Accession: PL0021
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
C:Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed i
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JK1)
F:43-109/Disulfide bonds: #status predicted

Query Match 94.3%; Score 526; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 3.5e-37;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWSYQVQVQAPRLLIYATSSRATGIP 60
  |||||
Db 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWSYQVQVQAPRLLIYATSSRATGIP 80
  |||||

QY 61 DRFSGSGGTDFLTITISRLPEDFAVYVCOQYQVSSPCSFQGTGLEIK 108
  |||||
Db 81 DRFSGSGGTDFLTITISRLPEDFAVYVCOQYQVSSPCSFQGTGLEIK 128
  |||||

RESULT 15
K3HUTI
Ig kappa chain V-III region (Ti) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 21-Jan-2000
C:Accession: A01895
R:Stuter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
A:Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sul
A:Reference number: A91651; MUID:72188439; PMID:5027703
A:Accession: A01895
A:Molecule type: protein
A:Residues: 1-109 <SUT>
A:Note: the sequence of the C region, which has the Inv (3) marker, is also given
C:Comment: This is a Bence Jones protein.
C:Genetics:
```

A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-91/Domain: immunoglobulin homology <IMM>
F:23-89/Disulfide Bonds: #status predicted

Query Match 93.9%; Score 524; DB 1; Length 109;
Best Local Similarity 92.6%; Pred. No. 4.4e-37;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVNSFLAWYQOKPGQAPRLIIYVASSRATGIP 60

QY 61 DRFSGSGGSDFTLTISRLEPEDFAVYCCQYGSSPCSFGQGTKLEIK 108
Db 61 DRFSGSGGSDFTLTISRLEPEDFAVYCCQYGSSPSTFGQGTKVELK 108

Search completed: April 21, 2004, 17:04:25
Job time : 13.515 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:00:06 ; Search time 17.7039 Seconds
(without alignments)
364.511 Million cell updates/sec

Title: US-10-041-860-48
Perfect score: 672
Sequence: 1 QVQLVQGAELKPGAEVKV.....YDIYGMVWGGQTTVTSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 541.5 | 80.6 | 120 | 4 | US-09-025-769B-36 |
| 2 | 541.5 | 80.6 | 120 | 4 | US-09-025-769B-59 |
| 3 | 528 | 78.6 | 117 | 4 | US-09-025-769B-22 |
| 4 | 513 | 76.3 | 125 | 3 | US-09-199-149-3 |
| 5 | 510.5 | 76.0 | 128 | 1 | US-08-202-047-22 |
| 6 | 510.5 | 76.0 | 128 | 3 | US-08-964-690-22 |
| 7 | 510 | 75.9 | 129 | 2 | US-08-561-521-45 |
| 8 | 510 | 75.9 | 129 | 4 | US-08-525-539A-77 |
| 9 | 510 | 75.9 | 129 | 5 | PCT-US95-01219-45 |
| 10 | 502 | 74.7 | 123 | 1 | US-08-477-877B-94 |
| 11 | 502 | 74.7 | 123 | 2 | US-08-472-281A-94 |
| 12 | 502 | 74.7 | 123 | 2 | US-08-477-989B-94 |
| 13 | 501 | 74.6 | 119 | 2 | US-08-561-521-10 |
| 14 | 501 | 74.6 | 119 | 5 | PCT-US95-01219-10 |
| 15 | 498 | 74.1 | 119 | 4 | US-09-438-954-41 |
| 16 | 496 | 73.8 | 117 | 3 | US-08-545-809A-96 |
| 17 | 493.5 | 73.4 | 139 | 1 | US-08-253-877C-19 |
| 18 | 493.5 | 73.4 | 139 | 2 | US-08-452-164A-19 |
| 19 | 493.5 | 73.4 | 139 | 3 | US-08-603-024-18 |
| 20 | 493.5 | 73.4 | 139 | 4 | US-08-450-809-14 |
| 21 | 487 | 72.5 | 121 | 1 | US-08-202-047-23 |
| 22 | 487 | 72.5 | 121 | 3 | US-08-964-690-23 |
| 23 | 482 | 71.7 | 119 | 2 | US-08-561-521-12 |
| 24 | 482 | 71.7 | 119 | 5 | PCT-US95-01219-12 |
| 25 | 481 | 71.6 | 123 | 1 | US-08-482-882-86 |
| 26 | 481 | 71.6 | 123 | 2 | US-08-483-389-86 |
| 27 | 481 | 71.6 | 123 | 2 | US-08-487-113D-86 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 481 | 71.6 | 123 | 2 | US-08-473-503-86 | Sequence 86, Appl |
| 29 | 481 | 71.6 | 123 | 2 | US-08-483-932-86 | Sequence 86, Appl |
| 30 | 481 | 71.6 | 123 | 2 | US-08-720-420A-86 | Sequence 86, Appl |
| 31 | 481 | 71.6 | 123 | 3 | US-08-714-017-86 | Sequence 86, Appl |
| 32 | 481 | 71.6 | 123 | 3 | US-08-475-680-86 | Sequence 86, Appl |
| 33 | 479 | 71.3 | 119 | 1 | US-08-300-386A-65 | Sequence 65, Appl |
| 34 | 479 | 71.3 | 119 | 3 | US-08-931-645-65 | Sequence 65, Appl |
| 35 | 479 | 71.3 | 119 | 5 | PCT-US95-11235-65 | Sequence 65, Appl |
| 36 | 476 | 70.8 | 123 | 2 | US-08-652-816A-1 | Sequence 1, Appl |
| 37 | 476 | 70.8 | 123 | 2 | US-08-652-816A-6 | Sequence 6, Appl |
| 38 | 476 | 70.8 | 123 | 2 | US-08-652-816A-8 | Sequence 8, Appl |
| 39 | 475.5 | 70.8 | 118 | 1 | US-08-491-845-14 | Sequence 14, Appl |
| 40 | 475.5 | 70.8 | 124 | 4 | US-09-301-593-16 | Sequence 16, Appl |
| 41 | 475.5 | 70.8 | 124 | 4 | US-09-301-593-41 | Sequence 41, Appl |
| 42 | 475.5 | 70.8 | 137 | 3 | US-08-513-968-38 | Sequence 38, Appl |
| 43 | 475 | 70.7 | 118 | 1 | US-08-300-386A-64 | Sequence 64, Appl |
| 44 | 475 | 70.7 | 118 | 3 | US-08-931-645-64 | Sequence 64, Appl |
| 45 | 475 | 70.7 | 118 | 5 | PCT-US95-11235-64 | Sequence 64, Appl |

ALIGNMENTS

RESULT 1
US-09-025-769B-36
; Sequence 36, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION NUMBER: EP 95 11 3021.0
; APPLICATION NUMBER: 18-AUG-1995
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-36

Query Match 80.6%; Score 541.5; DB 4; Length 120;
Best Local Similarity 84.0%; Pred. No. 1.4e-44;
Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

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QY 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWNGINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFTSYDINWVRQAPGQGLEWNGINPNSGGTNY 60

QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
DB 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCARWGG-----DGFYMDYWGQGT 115

QY 121 VTVSS 125
DB 116 VTVSS 120

RESULT 2
US-09-025-769B-59
; Sequence 59, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-59

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Query Match 80.6%; Score 541.5; DB 4; Length 120;
Best Local Similarity 84.0%; Pred. No. 1.4e-44;
Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWNGINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFTSYDINWVRQAPGQGLEWNGINPNSGGTNY 60

QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
DB 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCARWGG-----DGFYMDYWGQGT 115

QY 121 VTVSS 125

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DB 116 VTVSS 120

RESULT 3
US-09-025-769B-22
; Sequence 22, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-22

Query Match 78.6%; Score 528; DB 4; Length 117;
Best Local Similarity 82.5%; Pred. No. 2.6e-43;
Matches 104; Conservative 5; Mismatches 7; Indels 10; Gaps 2;

QY 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWNGINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPKGASVKVCKASGYTFTSYDINWVRQAPGQGLEWNGINPNSGNTNY 60

QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
DB 61 AQKFGQGRVTMTSDTSISTAYMELSLRSDDTAVYYCARDG-----GFDYWGQGT 111

QY 120 VTVSS 125
DB 112 LVTSS 117

RESULT 4
US-09-199-149-3
; Sequence 3, Application US/09199149
; Patent No. 6160099
; GENERAL INFORMATION:

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; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Taylor, Alexander H.
; APPLICANT: Trulli Jr., Stephen O.
; APPLICANT: Johanson, Kyung O.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT APPLICATION NUMBER: US/09/199,149
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Kabat VH subgroup I
US-09-199-149-3

Query Match:          76.3%; Score 513; DB 3; Length 125;
Best Local Similarity 80.6%; Pred. No. 7.5e-42;
Matches 104; Conservative 8; Mismatches 9; Indels 8; Gaps 5;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATCGQLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISNVRQAPGQGLEWMGWINP-OGDINY 59
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSDDTAIYICVR-GFGYS---YNYDIYGMVDV 116
DB 60 AQKFGQRTVITADTSTAYMELSLRSDDTAIYICARPGYGGGCGY-WYWG--VMG 116
QY 117 QGTTVTVSS 125
DB 117 QGTLVTVSS 125

RESULT 5
US-08-202-047-22
; Sequence 22, Application US/08202047
; Patent No. 5800815
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= HUMAN_I
US-08-202-047-22

Query Match:          76.0%; Score 510.5; DB 1; Length 128;
Best Local Similarity 77.9%; Pred. No. 1.3e-41;
Matches 102; Conservative 7; Mismatches 13; Indels 9; Gaps 3;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATCGQLEWMGWINP-NSGNTD 59
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISNVRQAPGQGLEWMGWINPYGNGDTN 60
QY 60 YAKFGQRTVMTDTSISTAYMELSLRSDDTAIYICVRGFGYS-----YNYDIYGMVDV 114
DB 61 YAKFGQRTVITADTSTAYMELSLRSDDTAIYICARAPGYGGGCGYRGDYF---DY 117
QY 115 WGQGTIVTVSS 125
DB 118 WGQGTIVTVSS 125

RESULT 6
US-08-964-690-22
; Sequence 22, Application US/08964690
; Patent No. 6033667
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,690
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
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; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= HUMAN_I
US-08-964-690-22

Query Match      76.0%; Score 510.5; DB 3; Length 128;
Best Local Similarity 77.9%; Pred. No. 1.3e-41;
Matches 102; Conservative 7; Mismatches 13; Indels 9; Gaps 3;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINP-NSGNTD 59
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYNGD 60
QY 60 YAKQFQGRVTMTDTSISTAYMELSLRSEDTAIYYCVRGFGYS-----YNDYYGMDV 114
Db 61 YAKQFQGRVTITADTSTAYMELSLRSEDTAIYYCARAPGYGGGCGYRGDYF--DY 118
QY 115 WGQGTITVTSS 125
Db 119 WGQGLTLVTSS 129

RESULT 7
US-08-561-521-45
; Sequence 45 Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Legier, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-45

Query Match      75.9%; Score 510; DB 2; Length 129;
Best Local Similarity 77.9%; Pred. No. 1.5e-41;
Matches 102; Conservative 7; Mismatches 14; Indels 8; Gaps 3;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINP-NSGNTD 59
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYNGD 60
QY 60 YAKQFQGRVTMTDTSISTAYMELSLRSEDTAIYYCVRGFGYS-----YNDYYGMDV 114
Db 61 YAKQFQGRVTITADTSTAYMELSLRSEDTAIYYCARAPGYGGGCGYRGDYF--DY 118
QY 115 WGQGTITVTSS 125
Db 119 WGQGLTLVTSS 129

RESULT 8
US-08-525-539A-77
; Sequence 77 Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-525-539A-77

Query Match      75.9%; Score 510; DB 4; Length 129;
Best Local Similarity 77.9%; Pred. No. 1.5e-41;
Matches 102; Conservative 7; Mismatches 14; Indels 8; Gaps 3;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINP-NSGNTD 59
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYNGD 60
QY 60 YAKQFQGRVTMTDTSISTAYMELSLRSEDTAIYYCVRGFGYS-----YNDYYGMDV 114
Db 61 YAKQFQGRVTITADTSTAYMELSLRSEDTAIYYCARAPGYGGGCGYRGDYF--DY 118
QY 115 WGQGTITVTSS 125
Db 119 WGQGLTLVTSS 129
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RESULT 9
PCT-US95-01219-45
; Sequence 45, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-01219-45

Query Match 75.9%; Score 510; DB 5; Length 129;
Best Local Similarity 77.9%; Pred. No. 1.5e-41;
Matches 102; Conservative 7; Mismatches 14; Indels 8; Gaps 3;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATQGLEWMGWINPNSGNTD 59
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNDTN 60
QY 60 YAQKFGQGRVTMTDRTSISTAYMELSSLSRSEDTAIYVCVRGFGYS-----YNDYYVGMV 114
Db 61 YAQKFGQGRVTITADTSTSTAYMELSSLSRSEDTAIVYCARPFGYSGGCGYRGDXF--DY 118
QY 115 WQGGTIVTVSS 125
Db 119 WQGGTIVTVSS 129

RESULT 10
US-08-477-877B-94
; Sequence 94, Application US/08477877B
; Patent No. 5730979
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activation
; NUMBER OF SEQUENCES: 96
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,877B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable region.
; US-08-477-877B-94

Query Match 74.7%; Score 502; DB 1; Length 123;
Best Local Similarity 78.1%; Pred. No. 8.2e-41;
Matches 100; Conservative 6; Mismatches 14; Indels 8; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMEWVRQAPGQGLEWMGRINPNSGGTNY 60
QY 61 AQKFGQGRVTMTDRTSISTAYMELSSLSRSEDTAIYVCVRGFGYSYNDYY--GMDVWGO 117
Db 61 AQKFGQGRVTMTDRTSISTAYMELSLRLSDTAIVYCARG-----RTEYIVVAEGFDYWGQ 115
QY 118 GTTVTVSS 125
Db 116 GTTVTVSS 123

RESULT 11
US-08-472-281A-94
; Sequence 94, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
```

STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,281A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
FEATURE:
NAME/KEY: Human Amu 5-3 heavy chain variable region.
US-08-472-281A-94

Query Match 74.7%; Score 502; DB 2; Length 123;
Best Local Similarity 78.1%; Pred. No. 8.2e-41;
Matches 100; Conservative 6; Mismatches 14; Indels 8; Gaps 2;
QY 1 QVQLVSGAEVKPKGASVKVSKASGYTFTSDINWVRQATQGLEWMGWNPNSGNTDY 60
Db 1 QVQLVSGAEVKPKGASVKVSKASGYTFTGYMHWVRQAPQGLEWMGRINPNSGGINY 60
QY 61 AQKFGQGVMTTRDTSISTAYMELSLRSDTAIYVCVGFSGSYNDYDY---GMDVWGQ 117
Db 61 AQKFGQGVMTTRDTSISTAYMELSLRSDTAIYVCVGFSGSYNDYDY---GMDVWGQ 115
QY 118 GTTVTVSS 125
Db 116 GTLVTVSS 123

RESULT 12
US-08-477-989B-94
Sequence 94, Application US/08477989B
Patent No. 5951983
GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
APPLICANT: Kaplan, Ruth
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Postema, Christina B.
APPLICANT: White-Scharf, Mary
TITLE OF INVENTION: LO-CD2a Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: T-Cell Activation and
TITLE OF INVENTION: Proliferation
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi, Stewart & Olstein

STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,989B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
FEATURE:
NAME/KEY: Human Amu 5-3 heavy chain variable
US-08-477-989B-94

Query Match 74.7%; Score 502; DB 2; Length 123;
Best Local Similarity 78.1%; Pred. No. 8.2e-41;
Matches 100; Conservative 6; Mismatches 14; Indels 8; Gaps 2;
QY 1 QVQLVSGAEVKPKGASVKVSKASGYTFTSDINWVRQATQGLEWMGWNPNSGNTDY 60
Db 1 QVQLVSGAEVKPKGASVKVSKASGYTFTGYMHWVRQAPQGLEWMGRINPNSGGINY 60
QY 61 AQKFGQGVMTTRDTSISTAYMELSLRSDTAIYVCVGFSGSYNDYDY---GMDVWGQ 117
Db 61 AQKFGQGVMTTRDTSISTAYMELSLRSDTAIYVCVGFSGSYNDYDY---GMDVWGQ 115
QY 118 GTTVTVSS 125
Db 116 GTLVTVSS 123

RESULT 13
US-08-561-521-10
Sequence 10, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561.521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186.269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-10

Query Match 74.6%; Score 501; DB 2; Length 119;
Best Local Similarity 79.2%; Pred. No. 9.9e-41;
Matches 99; Conservative 7; Mismatches 13; Indels 6; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLRWGWINAGNGNTKY 60
QY 61 AQKFGQVRVTTRDTSISTAYMELSSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGIT 120
DB 61 SQKFGQVRVTTRDTSASTAYMELSSLRSEDTAVIYCARG-GY-----YSGSGSNYGQGITL 114
QY 121 VTVSS 125
DB 115 VTVSS 119

RESULT 15
US-09-438-954-41
Sequence 41, Application US/09438954
Patent No. 6458934
GENERAL INFORMATION:
APPLICANT: HONG, Hyo Jeong
APPLICANT: PARK, Sung Sup
APPLICANT: KANG, Young Jun
APPLICANT: KANG, Chang-Yuil
APPLICANT: YOON, Sung Kwan
TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING SAME
FILE REFERENCE: 1303-124P
CURRENT APPLICATION NUMBER: US/09/438,954
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 41
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Variable
OTHER INFORMATION: region of heavy chain of human antibody (M17750)
US-09-438-954-41

Query Match 74.1%; Score 498; DB 4; Length 119;
Best Local Similarity 78.4%; Pred. No. 1.9e-40;
Matches 98; Conservative 8; Mismatches 13; Indels 6; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLRWGWINAGNGNTKY 60
QY 61 AQKFGQVRVTTRDTSISTAYMELSSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGIT 120

STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561.521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186.269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-10

Query Match 74.6%; Score 501; DB 2; Length 119;
Best Local Similarity 79.2%; Pred. No. 9.9e-41;
Matches 99; Conservative 7; Mismatches 13; Indels 6; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLRWGWINAGNGNTKY 60
QY 61 AQKFGQVRVTTRDTSISTAYMELSSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGIT 120
DB 61 SQKFGQVRVTTRDTSASTAYMELSSLRSEDTAVIYCARG-GY-----YSGSGSNYGQGITL 114
QY 121 VTVSS 125
DB 115 VTVSS 119

RESULT 14
PCT-US95-01219-10
Sequence 10, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 16:55:26 ; Search time 54.721 Seconds
(without alignments)
645.427 Million cell updates/sec

Title: US-10-041-860-48
Perfect score: 672
Sequence: 1 QVQLVQSGAEVKKFGASVKV.....YDYIYGMVWGQGTIVTVSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|-------------|
| 1 | 561.5 | 83.6 | 122 | ABR55829 | Heavy cha |
| 2 | 558.5 | 83.1 | 145 | ABP57367 | Anti-TRAI |
| 3 | 553.5 | 82.4 | 126 | ADA89120 | MS-Pro-26 |
| 4 | 551 | 82.0 | 127 | ADA89122 | MS-Pro-29 |
| 5 | 547.5 | 81.5 | 128 | ADA89202 | Human ant |
| 6 | 544 | 81.0 | 476 | AAW88464 | Monoclonal |
| 7 | 542.5 | 80.7 | 126 | ADA89116 | Human Ab |
| 8 | 541.5 | 80.6 | 120 | AAW27551 | Human ant |
| 9 | 541 | 80.5 | 146 | AAW22841 | Human ant |
| 10 | 538 | 80.1 | 136 | ADD28330 | Human ant |
| 11 | 537 | 79.9 | 203 | AAV34301 | IgM antib |
| 12 | 536.5 | 79.8 | 126 | ADA89123 | MS-Pro-54 |
| 13 | 536.5 | 79.8 | 247 | ABP45718 | Human Bly |
| 14 | 536 | 79.8 | 125 | ABR55813 | Heavy cha |
| 15 | 534.5 | 79.5 | 118 | ADA89115 | MS-Pro-2- |
| 16 | 534.5 | 79.5 | 249 | ABP44908 | Human Bly |
| 17 | 533 | 79.3 | 245 | AAAB67619 | Human leu |
| 18 | 532.5 | 79.2 | 230 | ABR01514 | Human ant |
| 19 | 529.5 | 78.8 | 120 | ABJ18719 | Antibody |
| 20 | 529.5 | 78.8 | 120 | ABJ18673 | Antibody |
| 21 | 527.5 | 78.5 | 146 | AAAB53510 | Human col |
| 22 | 526.5 | 78.3 | 228 | ABR01526 | Human ant |
| 23 | 526 | 78.3 | 199 | AAV34302 | IgM antib |
| 24 | 526 | 78.3 | 470 | AAU74296 | Anti-huma |
| 25 | 524.5 | 78.1 | 245 | ABP45885 | Human Bly |

| | | | | | | |
|----|-------|------|-----|---|-----------|-----------|
| 26 | 524 | 78.0 | 255 | 5 | ABP45396 | Human Bly |
| 27 | 523.5 | 77.9 | 247 | 5 | ABP44916 | Human Bly |
| 28 | 523.5 | 77.9 | 247 | 5 | ABP44937 | Human Bly |
| 29 | 521.5 | 77.6 | 126 | 6 | ADA89124 | MS-Pro-55 |
| 30 | 520 | 77.4 | 256 | 5 | ABP45290 | Human Bly |
| 31 | 519.5 | 77.3 | 251 | 5 | ABP45910 | Human Bly |
| 32 | 518.5 | 77.2 | 120 | 6 | ABR55815 | Heavy cha |
| 33 | 518.5 | 77.2 | 238 | 5 | ABP45896 | Human Bly |
| 34 | 518 | 77.1 | 120 | 4 | AAAB62747 | Human HIV |
| 35 | 517.5 | 77.0 | 116 | 5 | ABR57555 | HLA-DR-5p |
| 36 | 517.5 | 77.0 | 249 | 5 | ABP45624 | Human Bly |
| 37 | 515.5 | 76.7 | 249 | 5 | ABP45279 | Human Bly |
| 38 | 515.5 | 76.7 | 249 | 5 | ABP45288 | Human Bly |
| 39 | 515.5 | 76.7 | 252 | 5 | ABP45864 | Human Bly |
| 40 | 515 | 76.6 | 251 | 6 | ABP45795 | Human Bly |
| 41 | 514 | 76.5 | 221 | 6 | ABR01537 | Human ant |
| 42 | 513.5 | 76.4 | 241 | 5 | ABP46020 | Human Bly |
| 43 | 513 | 76.3 | 125 | 3 | AAV71447 | Human hea |
| 44 | 512 | 76.2 | 248 | 5 | ABP45710 | Human Bly |
| 45 | 511.5 | 76.1 | 249 | 5 | ABP44915 | Human Bly |

ALIGNMENTS

RESULT 1
ABR55829
ID: ABR55829 standard; protein; 122 AA.
XX ABR55829;
AC
XX
XX
DT 02-SEP-2003 (first entry)
XX
DE Heavy chain variable region of anti-Ang-2 antibody IP-2C11 HC.
XX
KW Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
KW angiogenesis; antibody.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Region 26..36
FT /note= "complementarity determining region (CDR) 1"
FT Region 50..66
FT /note= "complementarity determining region (CDR) 2"
FT Region 96..112
FT /note= "complementarity determining region (CDR) 3"
XX
XX WO2003030833-A2.
XX
XX 17-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032613.
XX
XX 11-OCT-2001; 2001US-0328604P.
XX 10-OCT-2002; 2002US-00269805.
XX (AMGE-) AMGEN INC.
XX Oliner JD;
XX WPI; 2003-504963/47.
XX
XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
XX for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
XX hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
XX
XX Claim 1; Page 93; 161pp; English.
XX
XX The invention relates to a specific binding agent, which comprises at
XX least one peptide selected from any of 62 peptides (ABR55789-830) or its
XX fragment. The binding agents are antibodies that recognize and bind to

CC a fibroblast growth factor receptor (FGFR), and which blocks constitutive
CC activation of an RPTK. Also described: (1) pharmaceutical compositions
CC comprising (i) as an active ingredient and a pharmaceutical carrier,
CC excipient, or auxiliary agent; (2) a kit comprising (i), at least one
CC reagent for detecting the presence of (i) when bound to the RPTK, and
CC instructions for use; (3) a method for treatment of bone and cartilage
CC related disorders by administering a composition of (1) to the subject;
CC (4) a method for treating or inhibiting a cell proliferative disease or
CC disorder by administering the composition of (1); (5) a method for
CC screening a molecule comprising the antigen-binding portion of an
CC antibody which blocks ligand-dependent activation of RPTK; (6) an
CC isolated nucleic acid molecule encoding a VL-CDR3 DNA region and a VH-
CC CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VL region
CC and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or
CC (7); and (9) host cells transformed with the vector. (1) have
CC osteopathic, cytoskeletal and ophthalmological activities, and can be used
CC as a RPTK inhibitor. Compositions comprising (i) are useful for treating
CC bone and cartilage disorders, including skeletal disorders such as
CC skeletal dysplasia (achondroplasia, thanatophoric dysplasia,
CC achondroplasia, severe achondroplasia with developmental delay and
CC acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g.
CC Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis
CC nigricans). The composition may also be used for treating or inhibiting
CC malignant cell proliferative disease or disorder associated with abnormal
CC RPTK activity, including a haematopoietic malignancy (e.g. multiple
CC myeloma), solid tumours (e.g. mammary, colon, cervical, bladder,
CC colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary
CC tumours, tumour progression (particularly progression of transitional
CC cell carcinoma or mammary carcinoma), or tumour metastasis, where the
CC cell proliferative disorder may be associated with the action of a
CC constitutively activated RPTK, or with ligand-dependent activation of
CC RPTK. The compositions may further be used for treating
CC hyperproliferative diseases and disorders associated with ligand-
CC dependent FGFR signaling, such as vision disorders (e.g. neovascular
CC glaucoma, macular degeneration and proliferative retinopathy including
CC diabetic retinopathy), and non-neoplastic angiogenic pathologic
CC conditions (e.g. haemangiomas, angiofibromas and psoriasis). The present
CC invention is given in the exemplification of the present invention.
XX Sequence 126 AA;

Query Match 82.4%; Score 553.5; DB 6; Length 126;
Best Local Similarity 82.9%; Pred No. 1.8e-43;
Matches 107; Conservative 7; Mismatches 8; Indels 7; Gaps 2;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGWINPNNGMTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGWINPNNGMTNY 60
QY 61 AKQFGRTVMTDTSISTAYMELSLRSEDIAIYCVKRGFVSY---NYDYVYGMVDVWG 116
Db 61 AKQFGRTVMTDTSISTAYMELSLRSEDIAIYCVKRGFVSY---NYDYVYGMVDVWG 117
QY 117 QGTTVTSS 125
Db 118 QGTLVTSS 126

RESULT 4
ID ADA89122 standard; protein; 127 AA.
AC ADA89122;
XX ADA89122;
DT 20-NOV-2003 (first entry)
XX MS-Pro-29-VH amino acid sequence SEQ ID NO:110.
DE
XX antigen binding; antibody; specific binding affinity;
KW receptor protein tyrosine kinase; RPTK;
KW receptor protein tyrosine kinase inhibitor;
KW fibroblast growth factor receptor; FGFR; osteopathic; cytoskeletal;
KW ophthalmological; bone disorder; cartilage disorder; skeletal disorder;

KW skeletal dysplasia; achondroplasia; thanatophoric dysplasia;
KW hypochondroplasia; craniosynostosis disorder;
KW malignant cell proliferative disease; cancer; tumour; vision disorder;
XX non-neoplastic angiogenic pathologic condition.
OS Synthetic.
OS Homo sapiens.
XX WO2002102973-A2.
XX 27-DEC-2002.
XX 20-JUN-2002; 2002WO-IL000495.
XX 20-JUN-2001; 2001US-0299187P.
XX (PROC-) PROCHON BIOTECH LTD.
XX Yayan A, Rom E;
XX WPI; 2003-175236/17.
XX New antibodies which have specific binding affinity for a receptor
XX protein tyrosine kinase (RPTK) and block constitutive activation of RPTK,
XX useful for treating bone and cartilage disorders, or malignant cell
XX proliferative diseases.
XX Claim 52; Page 19; 122pp; English.
XX The present invention describes a molecule (I) comprising the antigen
XX binding portion of an isolated antibody which has specific binding
XX affinity for a receptor protein tyrosine kinase (RPTK), particularly for
XX a fibroblast growth factor receptor (FGFR), and which blocks constitutive
XX activation of an RPTK. Also described: (1) pharmaceutical compositions
XX comprising (i) as an active ingredient and a pharmaceutical carrier,
XX excipient, or auxiliary agent; (2) a kit comprising (i), at least one
XX reagent for detecting the presence of (i) when bound to the RPTK, and
XX instructions for use; (3) a method for treatment of bone and cartilage
XX related disorders by administering a composition of (1) to the subject;
XX (4) a method for treating or inhibiting a cell proliferative disease or
XX disorder by administering the composition of (1); (5) a method for
XX screening a molecule comprising the antigen-binding portion of an
XX antibody which blocks ligand-dependent activation of RPTK; (6) an
XX isolated nucleic acid molecule encoding a VL-CDR3 DNA region and a VH-
XX CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VL region
XX and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or
XX (7); and (9) host cells transformed with the vector. (I) have
XX osteopathic, cytoskeletal and ophthalmological activities, and can be used
XX as a RPTK inhibitor. Compositions comprising (i) are useful for treating
XX bone and cartilage disorders, including skeletal disorders such as
XX skeletal dysplasia (achondroplasia, thanatophoric dysplasia,
XX achondroplasia, severe achondroplasia with developmental delay and
XX acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g.
XX Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis
XX nigricans). The composition may also be used for treating or inhibiting
XX malignant cell proliferative disease or disorder associated with abnormal
XX RPTK activity, including a haematopoietic malignancy (e.g. multiple
XX myeloma), solid tumours (e.g. mammary, colon, cervical, bladder,
XX colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary
XX tumours, tumour progression (particularly progression of transitional
XX cell carcinoma or mammary carcinoma), or tumour metastasis, where the
XX cell proliferative disorder may be associated with the action of a
XX constitutively activated RPTK, or with ligand-dependent activation of
XX RPTK. The compositions may further be used for treating
XX hyperproliferative diseases and disorders associated with ligand-
XX dependent FGFR signaling, such as vision disorders (e.g. neovascular
XX glaucoma, macular degeneration and proliferative retinopathy including
XX diabetic retinopathy), and non-neoplastic angiogenic pathologic
XX conditions (e.g. haemangiomas, angiofibromas and psoriasis). The present
XX invention is given in the exemplification of the present invention.
XX Sequence 127 AA;

Query Match 82.0%; Score 551; DB 6; Length 127;
Best Local Similarity 84.3%; Pred. No. 3.1e-43;
Matches 107; Conservative 6; Mismatches 12; Indels 2; Gaps 1;
QY 1 QVQLVQSGAEVKKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTDY 60
QY 61 AQKFGQGVMTTRDTSTISAYMELSLRSEDTAIYCVRGFGYSNY--DYIYGMWVWQ 118
DB 61 AQKFGQGVMTTRDTSTISAYMELSLRSEDTAIYCVRGFGYSNY--DYIYGMWVWQ 118
QY 119 TITVTSS 125
DB 121 TITVTSS 127
RESULT 5
ADA89202
ID ADA89202 standard; protein; 128 AA.
XX ADA89202;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human antibody 2F1 heavy chain amino acid sequence SEQ ID NO:46.
XX
KW immunoglobulin; Ig; heavy chain variable domain;
KW light chain variable domain; major histocompatibility complex; MHC;
KW gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
KW cancer.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070752-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005128.
XX
PR 20-FEB-2002; 2002US-0358994P.
XX
PA (DYAX-) DYAX CORP.
PA (TECR) TECHNION RES & DEV FOUND LTD.
XX
PI Hoogenboom HRJM, Reiter Y;
XX
DR WPI; 2003-663847/62.
DR N-PSDB; ADA89201.
XX
PT New protein comprising an immunoglobulin heavy chain variable (VH) domain
PT and an immunoglobulin light chain variable (VL) domain, useful for
PT preparing a composition for treating or preventing a cancerous disorder.
XX
PS Disclosure; Fig 10B; 224pp; English.
XX
CC The present invention describes a protein comprising an immunoglobulin
CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC domain. The protein binds a complex comprising a major histocompatibility
CC complex (MHC) and a peptide, does not substantially bind the MHC in the
CC absence of the bound peptide, and does not substantially bind the peptide
CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
CC comprising one or more nucleic acids for expressing the Ig that binds a
CC complex having an MHC and a peptide, does not substantially bind the MHC
CC in the absence of the bound peptide, and does not substantially bind the
CC peptide in the absence of the MHC; (3) an isolated nucleic acid
CC comprising a first segment that encodes the Ig variable domain; (4) a
CC host cell comprising heterologous nucleic acid sequences that encodes the
CC novel protein; (5) a transgenic animal whose genome includes heterologous
CC nucleic acid sequences that encode the protein; (6) identifying the

CC protein that specifically binds the MHC-peptide complex; (7) expressing
CC an antigen-binding protein; (8) ablating or killing a target cell that
CC displays a peptide on a surface MHC molecule; (9) treating or preventing
CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
CC complex in a sample. A protein of the invention has cytostatic activity,
CC and can be used in gene therapy. The protein is useful for preparing a
CC composition for treating or preventing a cancerous disorder. The present
CC sequence represents the heavy chain of an antibody which binds to an MHC-
CC peptide complex where the peptide component in as peptide fragment of
CC gp100.
XX
SQ Sequence 128 AA;

Query Match 81.5%; Score 547.5; DB 6; Length 128;
Best Local Similarity 83.6%; Pred. No. 6.6e-43;
Matches 107; Conservative 5; Mismatches 13; Indels 3; Gaps 1;
QY 1 QVQLVQSGAEVKKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTDY 60
DB 1 EVQLVQSGAEVKKPKGASVKVSKASGYTFTSYIHWRQAPGQGLEWMMGAINPSSGSTPY 60
QY 61 AQKFGQGVMTTRDTSTISAYMELSLRSEDTAIYCVRGFGY--SYNDYIYGMWVWQ 117
DB 61 AQKFGQGVMTTRDTSTISAYMELSLRSEDTAIYCVRGFGY--SYNDYIYGMWVWQ 120
QY 118 GTTIVTSS 125
DB 121 GTTIVTSS 128

RESULT 6

AAW88464

ID AAW88464 standard; protein; 476 AA.

XX AAW88464;

DT 10-MAY-1999 (first entry)

XX Monoclonal antibody 4B5 heavy chain variable region.

XX Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm;
XX diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma;
XX lung carcinoma; metastasis; anti-idiotypic antibody; GD2 antigen; human.

XX Homo sapiens.

XX WO9902545-A2.

XX 21-JAN-1999.

XX 08-JUL-1998; 98WO-IB001046.

XX 08-JUL-1997; 97US-0051945P.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Dan MD;

XX WPI; 1999-120769/10.

XX N-PSDB; AAX06951.

XX New antibody 4B5 polynucleotides and polypeptides - used to develop
XX products for the diagnosis and treatment of cancers and for prophylactic
XX therapy to reduce risk of recurrence.

XX Claim 1; Page 79-80; 83pp; English.

XX This polypeptide comprises the heavy chain variable region of the
XX recombinant human monoclonal antibody (MAB) 4B5. 4B5 recognises
XX antibodies specific for GD2 antigen antibodies. Antibodies specific for
XX GD2 recognise various cancers including glioblastoma, neuroblastoma,
XX malignant and/or metastatic melanoma, breast adenocarcinoma, lung
XX adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and

CC prostate adenocarcinoma. The invention encompasses 4B5 derivatives with
CC immunologic specificity for antibodies specific for CD2. These
CC derivatives, or antigen binding fragments, comprise regions of the 4B5
CC Fv junction and regions spanning the 4B5 CDRs. Other derivatives include
CC Fab, F(ab')₂, Fab', scFv and isolated heavy and light chains (see also
CC AAW88465). Polynucleotide fragments (see AAW06951-54) encoding 4B5
CC antibody V regions are also provided, and therapeutic plasmids and
CC vectors, including vaccinia virus vectors, comprising these
CC polynucleotides. 4B5 has been shown to mimic Gb2, and is particularly
CC useful in generating a host immune response to cancer. Products of the
CC invention can be used in the detection and treatment of e.g. astrocytoma,
CC oligodendroglioma, spindleoma, medulloblastoma, primitive neural
CC ectodermal tumour (PNET), pancreatic ductal adenocarcinoma, small and
CC large cell lung adenocarcinomas, squamous cell carcinoma,
CC bronchoalveolar carcinoma, epithelial adenocarcinoma, and liver metastases,
CC hepatoma, cholangiocarcinoma, breast tumours such as ductal and lobular
CC adenocarcinoma, squamous and adenocarcinomas of the uterine cervix,
CC uterine and ovarian epithelial carcinoma, prostatic adenocarcinoma,
CC transitional squamous cell carcinoma of the bladder, B and T cell
CC lymphoma (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
CC malignant melanoma, soft tissue sarcoma and leiomyosarcoma
XX
XX Sequence 476 AA;

Query Match 81.0%; Score 544; DB 2; Length 476;
Best Local Similarity 78.9%; Pred. No. 5.8e-42;
Matches 105; Conservative 7; Mismatches 7; Indels 14; Gaps 2;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSVDINWVQATGQGLEWMGNPNNSGNTDY 60
DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSFDLWVQAPQGQLEWMGNPNNSGKTCY 79
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYVCVRFYGVSYNYD-----YYGGM 112
DB 80 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYVCAR-----NADNVEMAAIYHYGGM 133
QY 113 DWVGQGTVTWVSS 125
DB 134 DWVGQGTVTWVSS 146

RESULT 7
ADA89116
ID ADA89116 standard; protein; 126 AA.
XX
XX ADA89116;
AC
DT 20-NOV-2003 (first entry)
XX
DE MS-Pro-11-VH amino acid sequence SEQ ID NO:104.
XX
XX antigen binding; antibody; specific binding affinity;
KW receptor protein tyrosine kinase; RPTK;
KW receptor protein tyrosine kinase inhibitor;
KW fibroblast growth factor receptor; FGFR; osteopathic; cytostatic;
KW ophthalmological; bone disorder; cartilage disorder; skeletal disorder;
KW skeletal dysplasia; achondroplasia; thanatophoric dysplasia;
KW hypochondroplasia; craniosynostosis disorder;
KW malignant cell proliferative disease; cancer; tumour; vision disorder;
KW non-neoplastic angiogenic pathologic condition.

XX Synthetic.
OS Homo sapiens.
XX
XX W02002102973-A2.
PN
XX
XX 27-DEC-2002.
XX
XX 20-JUN-2002; 2002MO-IL0000495.
PF
XX
XX 20-JUN-2001; 2001US-0299187P.
PR
XX
XX (PROC-) PROCHON BIOTECH LTD.

XX
PI Yayon A, Rom E;
XX WPI; 2003-175236/17.
DR
XX
XX New antibodies which have specific binding affinity for a receptor
PT protein tyrosine kinase (RPTK) and block constitutive activation of RPTK,
PT useful for treating bone and cartilage disorders, or malignant cell
PT proliferative diseases.
XX
XX Claim 52; Page 18; 122pp; English.

XX The present invention describes a molecule (I) comprising the antigen
CC binding portion of an isolated antibody which has specific binding
CC affinity for a receptor protein tyrosine kinase (RPTK), particularly for
CC a fibroblast growth factor receptor (FGFR), and which blocks constitutive
CC activation of an RPTK. Also described: (1) pharmaceutical compositions
CC comprising (I) as an active ingredient and a pharmaceutical carrier,
CC excipient, or auxiliary agent; (2) a kit comprising (I), at least one
CC reagent for detecting the presence of (I) when bound to the RPTK, and
CC instructions for use; (3) a method for treatment of bone and cartilage
CC related disorders by administering a composition of (I) to the subject;
CC (4) a method for treating or inhibiting a cell proliferative disease or
CC disorder by administering the composition of (I); (5) a method for
CC screening a molecule comprising the antigen-binding portion of an
CC antibody which blocks ligand-dependent activation of RPTK; (6) an
CC isolated nucleic acid molecule encoding a VL-CDR3 DNA region and a VH-
CC CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VI region
CC and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or
CC (7); and (9) host cells transformed with the vector. (I) have
CC osteopathic, cytostatic and ophthalmological activities, and can be used
CC as a RPTK inhibitor. Compositions comprising (I) are useful for treating
CC bone and cartilage disorders, including skeletal disorders such as
CC skeletal dysplasia (achondroplasia, thanatophoric dysplasia, and
CC hypochondroplasia, severe achondroplasia with developmental delay and
CC acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g.
CC Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis
CC nigricans). The composition may also be used for treating or inhibiting
CC malignant cell proliferative disease or disorder associated with abnormal
CC RPTK activity, including a haematopoietic malignancy (e.g. multiple
CC myeloma), solid tumours (e.g. mammary, colon, cervical, bladder, prostate,
CC colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary
CC tumours, tumour progression (particularly progression of transitional
CC cell carcinoma or mammary carcinoma), or tumour metastasis, where the
CC cell proliferative disorder may be associated with the action of a
CC constitutively activated RPTK, or with ligand-dependent activation of
CC RPTK. The compositions may further be used for treating
CC hyperproliferative diseases and disorders associated with ligand-
CC dependent FGFR signaling, such as vision disorders (e.g. neovascular
CC glaucoma, macular degeneration and proliferative retinopathy including
CC diabetic retinopathy), and non-neoplastic angiogenic pathologic
CC conditions (e.g. haemangiomas, angiofibromas and psoriasis). The present
CC sequence is given in the exemplification of the present invention.

Sequence 126 AA;

Query Match 80.7%; Score 542.5; DB 6; Length 126;
Best Local Similarity 83.5%; Pred. No. 1.9e-42;
Matches 106; Conservative 7; Mismatches 11; Indels 3; Gaps 2;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSVDINWVQATGQGLEWMGNPNNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYNHWVRQAPQGQLEWMGNPNNSGNTNY 60
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYVCVRFYGVSYNYDYYG--MDVWGQG 118
DB 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYVCARYYGSSL-VHYVFGFDYWGQG 119
QY 119 TTVTVSS 125
DB 120 TTVTVSS 126

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RESULT 8
AAW27551
ID AAW27551 standard; protein; 120 AA.
XX AC AAW27551;
XX DT 23-JAN-1998 (first entry)
XX DE Human Ab heavy chain variable region VH1B consensus.
XX KW Human; antibody; preparation; library; VH1B; variable region;
XX KW heavy chain; consensus.
XX OS Homo sapiens.
XX PN W09708320-A1.
XX PD 06-MAR-1997.
XX PF 19-AUG-1996; 96WO-EP003647.
XX PR 18-AUG-1995; 95EP-00113021.
XX PA (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
XX FI Knappik A, Pack P, Ilag V, Ge L, Moroney S, Plueckthun A;
XX DR WPI; 1997-179277/16.
XX DR N-PSDB; AAT87949.
XX PT Preparation of human derived antibody gene library - using synthetic
XX PT consensus sequences, and signal consensus antibody gene as universal
XX PT framework for highly diverse antibody libraries.
XX PS Example 1; Fig 5B; 436pp; English.
XX CC The present sequence is the human antibody heavy chain variable region
XX CC synthetic sequence VH1B, used in the preparation of a human derived
XX CC antibody gene library
XX SQ Sequence 120 AA;

Query Match 80.6%; Score 541.5; DB 2; Length 120;
Best Local Similarity 84.0%; Pred. No. 2.2e-42;
Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQAPQGLEWMGWINPNSGGTNY 60
Qy 61 AQKFGQRTVTRDTSTISATMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQTT 120
Db 61 AQKFGQRTVTRDTSTISATMELSLRSEDTAIYYCARWGG-----DGFYAMDYWGQGT 115
Qy 121 VTSS 125
Db 116 VTSS 120

RESULT 9
AAW22841
ID AAW22841 standard; protein; 146 AA.
XX AC AAW22841;
XX DT 12-SEP-1997 (first entry)
XX DE Human anti-tumour antigen antibody heavy chain variable region.
XX KW Human; tumour antigen; cancer; monoclonal; antibody; heavy chain;
XX KW variable region; medicine; pharmacology; biochemistry; CDR;
XX KW complementarity determining region.
XX

RESULT 10
ADD28330
ID ADD28330 standard; protein; 136 AA.
XX AC ADD28330;
XX DT 15-JAN-2004 (first entry)
XX DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:108.
XX KW human heterodimeric antibody; human; antibody; binding affinity;
XX KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
XX KW edema factor; lethal factor; viricide; antibacterial; immunotherapy;
XX KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
XX KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
XX

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OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= sig_peptide
FT 20..146
FT /label= mat_peptide
FT Region 50..54
FT /label= CDR_1
FT Region 69..85
FT /label= CDR_2
FT Region 118..139
FT /label= CDR_3
XX JF09100300-A.
XX 15-APR-1997.
XX 03-OCT-1995; 95JP-00278266.
XX 03-OCT-1995; 95JP-00278266.
XX (HAGI/) HAGIWARA Y.
XX WPI; 1997-276726/25.
XX DR N-PSDB; AAT75422.
XX PT Anticancer human monoclonal antibody variable region sequences - and
XX PT related DNA and RNA.
XX PS Claim 3; Page 10; 14pp; Japanese.
XX CC The present sequence is a human anti-tumour antigen monoclonal antibody
XX CC (MAB) heavy chain variable region, useful in medicine, pharmacology and
XX CC biochemistry. The isotype of a MAB secreted by the human/human hybridoma
XX CC HT was determined to be mu and kappa. Human MAB was purified, and the
XX CC antigen recognised by human MAB CLN"-IgM identified by western blotting
XX SQ Sequence 146 AA;

Query Match 80.5%; Score 541; DB 2; Length 146;
Best Local Similarity 83.5%; Pred. No. 3e-42;
Matches 106; Conservative 6; Mismatches 9; Indels 6; Gaps 3;

Qy 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATQGLEWMGWINPNSGNTDY 60
Db 20 QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHWVRQAPQGLEWMGWINPNSGGTNY 79
Qy 61 AQKFGQRTVTRDTSTISATMELSLRSEDTAIYYCVRG-FGY----SYND-YYYGMDV 114
Db 80 AQKFGQRTVTRDTSTISATMELSLRSDTAIYYCARGPVKGYCSSTSCYFDIYYGMDV 139
Qy 115 WQGGTTV 121
Db 140 WQGGTTV 146

RESULT 10
ADD28330
ID ADD28330 standard; protein; 136 AA.
XX AC ADD28330;
XX DT 15-JAN-2004 (first entry)
XX DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:108.
XX KW human heterodimeric antibody; human; antibody; binding affinity;
XX KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
XX KW edema factor; lethal factor; viricide; antibacterial; immunotherapy;
XX KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
XX KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
XX

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OS Synthetic.
OS Homo sapiens.
XX WO2003076568-A2.
XX 18-SEP-2003.
XX 11-FEB-2003; 2003WO-US004206.
XX 11-FEB-2002; 2002US-0356086P.
PR 29-APR-2002; 2002US-0376408P.
PR 27-SEP-2002; 2002US-0414053P.
PR 25-NOV-2002; 2002US-0428807P.
XX (ALEX-) ALEXION PHARM INC.
XX Bowdish KS, Wild WA;
XX WPI; 2003-722327/68.
XX New human heterodimeric antibodies or their antibody fragments, useful as
PT anti-toxins or anti-infectives with respect to infective agents, e.g.
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
PT Nile virus.
XX Claim 11; SEQ ID NO 108; 67pp; English.
XX The present invention describes a human heterodimeric antibody (I)
CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
CC protective antigen of Bacillus anthracis or a molecule involved in
CC anthrax infection that blocks binding of the antigen or molecule to cell
CC receptors, edema factor and lethal factor. (I) has virucide and
CC antibacterial activities, and can be used in immunotherapy. The
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
CC present sequence represents a human heterodimeric antibody heavy chain
CC variable region amino acid sequence, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 136 AA;
Query Match 80.1%; Score 538; DB 7; Length 136;
Best Local Similarity 80.0%; Pred. No. 5.3e-42;
Matches 104; Conservative 7; Mismatches 13; Indels 6; Gaps 2;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGWINPNSGNTDY 60
DB 3 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQAPGQGLEWMGWINPNTGNTY 62
QY 61 AQKFGQVTRTDRDTSISTAYMELSLRSEDTAIYCVRGF----GYSYNDYYGMDVW 115
DB 63 AQNFGQVTRTDRDTSIRIAYTELRLRLSDDTAVYICARDFYSDSSGYYGY-YSYGMVW 121
QY 116 GQGTITVTSS 125
DB 122 GQGTITVTSS 131
RESULT 11
AA34301
ID AAY34301 standard; protein; 203 AA.
XX
XX AAY34301;
AC
DT 19-NOV-1999 (first entry)
XX
DE IgM antibody CEM 10.12 F3 heavy chain sequence.
XX
XX Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Homo sapiens.
XX WO9945031-A2.
XX 10-SEP-1999.
XX 03-MAR-1999; 99WO-US004583.
XX 03-MAR-1998; 98US-00034607.
PR 03-FEB-1999; 99US-00244253.
XX (ABGE-) ABGENIX INC.
XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX WPI; 1999-540816/45.
DR N-PSDB; AA220402.
XX New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
PT Claim 60; Fig 26; 245pp; English.
XX This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX Sequence 203 AA;
Query Match 79.9%; Score 537; DB 2; Length 203;
Best Local Similarity 89.7%; Pred. No. 1e-41;
Matches 102; Conservative 5; Mismatches 6; Indels 2; Gaps 2;
QY 12 KPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGWINPNSGNTDYAQKFGQVTRVT 71
DB 1 KPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGWINPNSGNTGYAQKFGQVTRVN 60
QY 72 RDTSTSTAYMELSLRSEDTAIYCVRGFGYSYNDY-YYGMDVWGQGTITVTSS 125
DB 61 RNTSISTAYMELSLRSEDTAIYCVARG-GHGGSYFYISYGMVWGQGTITVTSS 114
RESULT 12
ADA89123
ID ADA89123 standard; protein; 126 AA.
XX
XX ADA89123;
AC
DT 20-NOV-2003 (first entry)
XX
DE MS-Pro-54-VH amino acid sequence SEQ ID NO:111.
XX
XX antigen binding; antibody; specific binding affinity;
KW receptor protein tyrosine kinase; RPTK;
KW receptor protein tyrosine kinase inhibitor;
KW fibroblast growth factor receptor; FGFR; osteopathic; cytostatic;
KW ophthalmological; bone disorder; cartilage disorder; skeletal disorder;
KW skeletal dysplasia; achondroplasia; thanatophoric dysplasia;
KW hypochondroplasia; craniosynostosis disorder;
KW malignant cell proliferative disease; cancer;
XX non-neoplastic angiogenic pathologic condition.
XX Synthetic.

Query Match 79.8%; Score 536.5; DB 5; Length 247;
 Best Local Similarity 81.6%; Pred. No. 1.4e-41;
 Matches 102; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

CC disease, bone-related disease, or psoriasis) in a mammal. The present
 CC sequence represents a heavy chain variable region of an anti-Ang-2
 CC antibody
 XX
 SQ Sequence 125 AA;

Query Match 79.8%; Score 536; DB 6; Length 125;
 Best Local Similarity 81.6%; Pred. No. 7.4e-42;
 Matches 102; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWGHNPNISGNTDY 60
 Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWGHNPNISGNTDY 60
 QY 61 AQKFGQVTRTDTSTAYMELSLRSEDATYYCVRGFGSYNYDYVYGMVWGQGT 120
 Db 61 AQKFGQVTRTDTSTAYMELSLRSEDATYYCVRGFGSYNYDYVYGMVWGQGT 120
 QY 121 VTVSS 125
 Db 121 VTVSS 125

RESULT 15
 ADA89115
 ID ADA89115 standard; protein; 118 AA.
 XX
 AC ADA89115;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE MS-Pro-2-VH amino acid sequence SEQ ID NO:103.
 XX
 KW antigen binding; antibody; specific binding affinity;
 KW receptor protein tyrosine kinase; RPTK;
 KW fibroblast growth factor receptor; FGFR; osteopathic; cytostatic;
 KW ophthalmological; bone disorder; cartilage disorder; skeletal disorder;
 KW skeletal dysplasia; achondroplasia; thanatophoric dysplasia;
 KW hypochondroplasia; craniosynostosis disorder;
 KW malignant cell proliferative disease; cancer; tumour; vision disorder;
 KW non-neoplastic angiogenic pathologic condition.
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2002102973-A2.
 XX
 PD 27-DEC-2002.
 XX
 PF 20-JUN-2002; 2002WO-IL000495.
 XX
 PR 20-JUN-2001; 2001US-0299187P.
 XX
 PA (PROC-) PROCHON BIOTECH LTD.
 XX
 PI Yayon A, Rom E;
 XX
 DR WPI; 2003-175236/17.
 XX
 PT New antibodies which have specific binding affinity for a receptor
 PT protein tyrosine kinase (RPTK) and block constitutive activation of RPTK,
 PT useful for treating bone and cartilage disorders, or malignant cell
 PT proliferative diseases.
 XX
 PS Claim 42; Page 18; 122pp; English.
 XX
 CC The present invention describes a molecule (I) comprising the antigen
 CC binding portion of an isolated antibody which has specific binding
 CC affinity for a receptor protein tyrosine kinase (RPTK), particularly for
 CC a fibroblast growth factor receptor (FGFR), and which blocks constitutive
 CC activation of an RPTK, also described; (i) pharmaceutical compositions
 CC comprising (I) as an active ingredient and a pharmaceutical carrier,

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWGHNPNISGNTDY 60
 Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWGHNPNISGNTDY 60
 QY 61 AQKFGQVTRTDTSTAYMELSLRSEDATYYCVRGFGSYNYDYVYGMVWGQGT 120
 Db 61 AQKFGQVTRTDTSTAYMELSLRSEDATYYCVRGFGSYNYDYVYGMVWGQGT 120
 QY 121 VTVSS 125
 Db 120 VTVSS 124

RESULT 14
 ABR55813
 ID ABR55813 standard; protein; 125 AA.
 XX
 AC ABR55813;
 XX
 DT 02-SEP-2003 (first entry)
 XX
 DE Heavy chain variable region of anti-Ang-2 antibody FJ-G11 HC.
 XX
 KW Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic;
 KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
 KW angiogenesis; antibody.
 XX
 OS Homo sapiens.
 XX
 FH Location/Qualifiers
 FT Region 26..36
 FT Region /note= "complementarity determining region (CDR) 1"
 FT Region 50..66
 FT Region /note= "complementarity determining region (CDR) 2"
 FT Region 96..115
 FT Region /note= "complementarity determining region (CDR) 3"
 PN WO2003030833-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032613.
 XX
 PR 11-OCT-2001; 2001US-0328604P.
 PR 10-OCT-2002; 2002US-00269805.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Oliner JD;
 XX
 DR WPI; 2003-504963/47.
 XX
 PT New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful
 PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
 PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
 XX
 PS Claim 1; Page 92; 161pp; English.
 XX
 CC The invention relates to a specific binding agent, which comprises at
 CC least one peptide selected from any of 62 peptides (ABR5769-850) or its
 CC fragment. The binding agents are antibodies that recognize and bind to
 CC angiopoietin-2 (Ang-2). The specific binding agent, particularly the
 CC antibody, is useful for inhibiting undesired angiogenesis, treating
 CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
 CC 2 activity, modulating vascular permeability or plasma leakage, or
 CC treating a disease (e.g. ocular neovascular disease, obesity, or
 CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
 CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic

CC excipient, or auxiliary agent; (2) a kit comprising (1), at least one
CC reagent for detecting the presence of (1) when bound to the RPTK, and
CC instructions for use; (3) a method for treatment of bone and cartilage
CC related disorders by administering a composition of (1) to the subject;
CC (4) a method for treating or inhibiting a cell proliferative disease or
CC disorder by administering the composition of (1); (5) a method for
CC screening a molecule comprising the antigen-binding portion of an
CC antibody which blocks ligand-dependent activation of RPTK; (6) an
CC isolated nucleic acid molecule encoding a VL-CDR3 DNA region and a VH-
CC CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VI region
CC and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or
CC (7); and (9) host cells transformed with the vector. (1) have
CC osteopathic, cytostatic and ophthalmological activities, and can be used
CC as a RPTK inhibitor. Compositions comprising (1) are useful for treating
CC bone and cartilage disorders, including skeletal disorders such as
CC skeletal dysplasia (achondroplasia, chondroplasia, chondrodysplasia, delay and
CC hypochondroplasia, severe achondroplasia with developmental delay and
CC acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g.
CC Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis
CC nigricans). The composition may also be used for treating or inhibiting
CC malignant cell proliferative disease or disorder associated with abnormal
CC RPTK activity, including a haematopoietic malignancy (e.g. multiple
CC myeloma), solid tumours (e.g. mammary, colon, cervical, bladder, primary
CC colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary
CC tumours, tumour progression (particularly progression of transitional
CC cell carcinoma or mammary carcinoma), or tumour metastasis, where the
CC cell proliferative disorder may be associated with the action of a
CC constitutively activated RPTK, or with ligand-dependent activation of
CC RPTK. The compositions may further be used for treating
CC hyperproliferative diseases and disorders associated with ligand-
CC dependent FGFR signaling, such as vision disorders (e.g. neovascular
CC glaucoma, macular degeneration and proliferative retinopathy including
CC diabetic retinopathy), and non-neoplastic angiogenic pathologic
CC conditions (e.g. haemangiomas, angiofibromas and psoriasis). The present
CC sequence is given in the exemplification of the present invention.

XX
SQ Sequence 118 AA;

Query Match 79.5%; Score 534.5; DB 6; Length 118;
Beat Local Similarity 82.5%; Pred. No. 9.6e-42;
Matches 104; Conservative 6; Mismatches 7; Indels 9; Gaps 2;
QY 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60
QY 61 AOKPQGRVTMTDTSISTAYMELSLRSEDTAIYVCVRGF-GYSINYDYIYGMVWGQGT 119
Db 61 AOKPQGRVTMTDTSISTAYMELSLRSEDTAIYVCVRGF-GYSINYDYIYGMVWGQGT 112
QY 120 TVTVSS 125
Db 113 LVTSS 118

Search completed: April 21, 2004, 17:01:52
Job time : 60.721 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:03:52 ; Search time 41.309 Seconds
(without alignments)
836.607 Million cell updates/sec

Title: US-10-041-860-48
Perfect score: 672
Sequence: 1 QVOLVSGAEVKPGASVKV.....YDYVGMVWGQTTVTSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query % | Score | Match | Length | ID | Description |
|------------|---------|-------|-------|--------|-------------------|-------------------|
| 1 | 672 | 100.0 | 125 | 14 | US-10-041-860-48 | Sequence 48, Appl |
| 2 | 672 | 100.0 | 125 | 14 | US-10-041-860-200 | Sequence 200, App |
| 3 | 672 | 100.0 | 125 | 14 | US-10-041-860-237 | Sequence 237, App |
| 4 | 672 | 100.0 | 125 | 14 | US-10-041-860-372 | Sequence 372, App |
| 5 | 638 | 94.9 | 125 | 14 | US-10-041-860-38 | Sequence 38, Appl |
| 6 | 638 | 94.9 | 125 | 14 | US-10-041-860-203 | Sequence 203, App |
| 7 | 638 | 94.9 | 125 | 14 | US-10-041-860-240 | Sequence 240, App |
| 8 | 638 | 94.9 | 125 | 14 | US-10-041-860-343 | Sequence 343, App |
| 9 | 593.5 | 88.3 | 126 | 14 | US-10-041-860-19 | Sequence 19, Appl |
| 10 | 593.5 | 88.3 | 126 | 14 | US-10-041-860-201 | Sequence 201, App |
| 11 | 593.5 | 88.3 | 126 | 14 | US-10-041-860-288 | Sequence 288, App |
| 12 | 579.5 | 86.2 | 125 | 14 | US-10-041-860-238 | Sequence 238, App |
| 13 | 575.5 | 85.6 | 126 | 14 | US-10-041-860-40 | Sequence 40, Appl |
| 14 | 575.5 | 85.6 | 126 | 14 | US-10-041-860-204 | Sequence 204, App |
| 15 | 575.5 | 85.6 | 126 | 14 | US-10-041-860-241 | Sequence 241, App |

ALIGNMENTS

RESULT 1

US-10-041-860-48
; Sequence 48, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadl
; APPLICANT: Weber, Richard
; APPLICANT: Bezaheh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX 051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-48

Query Match 100.0%; Score 672; DB 14; Length 125;

Best Local Similarity 100.0%; Pred. No. 1e-56;

Mismatches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
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| Qy | 1 | QVOLVSGAEVKPGASVKVSKASGYFTSVDINWRQATCGGLEWGWINPNSGNTDY | 60 |
| Db | 1 | QVOLVSGAEVKPGASVKVSKASGYFTSVDINWRQATCGGLEWGWINPNSGNTDY | 60 |
| Qy | 61 | AQKFGQVMTTRDTSISTAYMELSLRSDTAIYCVRGFGYSYNYDYVGMVWGQTT | 120 |
| Db | 61 | AQKFGQVMTTRDTSISTAYMELSLRSDTAIYCVRGFGYSYNYDYVGMVWGQTT | 120 |

Sequence 349, App
Sequence 44, Appl
Sequence 205, App
Sequence 242, App
Sequence 360, App
Sequence 21, Appl
Sequence 199, App
Sequence 236, App
Sequence 294, App
Sequence 125, App
Sequence 61, Appl
Sequence 37, Appl
Sequence 202, App
Sequence 239, App
Sequence 124, App
Sequence 46, Appl
Sequence 3, Appl
Sequence 188, App
Sequence 1729, Ap
Sequence 45, Appl
Sequence 919, App
Sequence 919, App
Sequence 2, Appl
Sequence 31, Appl
Sequence 23, App
Sequence 325, App
Sequence 110, App
Sequence 1050, Ap

16 575.5 85.6 126 14 US-10-041-860-349
17 572 85.1 127 14 US-10-041-860-44
18 572 85.1 127 14 US-10-041-860-205
19 572 85.1 127 14 US-10-041-860-242
20 572 85.1 127 14 US-10-041-860-360
21 567.5 84.4 126 14 US-10-041-860-21
22 567.5 84.4 126 14 US-10-041-860-199
23 567.5 84.4 126 14 US-10-041-860-236
24 567.5 84.4 126 14 US-10-041-860-294
25 562.5 83.7 124 15 US-10-309-762-125
26 561.5 83.6 122 14 US-10-269-805-61
27 561.5 83.6 126 14 US-10-041-860-37
28 561.5 83.6 126 14 US-10-041-860-202
29 561.5 83.6 126 14 US-10-041-860-239
30 551.5 82.1 118 15 US-10-309-762-124
31 547.5 81.5 128 12 US-10-371-942-46
32 544 81.0 476 9 US-09-747-669-3
33 544 81.0 476 14 US-10-290-703-3
34 538 80.1 136 15 US-10-364-743-108
35 536.5 79.8 247 10 US-09-880-748-1729
36 536.5 79.8 247 12 US-10-293-418-1729
37 536 79.8 125 14 US-10-269-805-45
38 534.5 79.5 249 10 US-09-880-748-919
39 534.5 79.5 249 12 US-10-293-418-919
40 529.5 78.8 120 14 US-10-125-687-2
41 528 78.6 127 14 US-10-041-860-31
42 528 78.6 127 14 US-10-041-860-243
43 528 78.6 127 14 US-10-041-860-325
44 527.5 78.5 122 12 US-10-292-088-110
45 527.5 78.5 146 9 US-09-925-299-1050

Qy 121 VTSS 125
Db 121 VTSS 125

RESULT 2
US-10-041-860-200
; Sequence 200, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-200

Query Match 100.0%; Score 672; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 1e-56;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

Qy 61 AQKFGQRTVMTDRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
Db 61 AQKFGQRTVMTDRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120

Qy 121 VTSS 125
Db 121 VTSS 125

RESULT 3
US-10-041-860-237
; Sequence 237, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-237

Query Match 100.0%; Score 672; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 1e-56;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

Qy 61 AQKFGQRTVMTDRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
Db 61 AQKFGQRTVMTDRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120

Qy 121 VTSS 125
Db 121 VTSS 125

Query Match 100.0%; Score 672; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 1e-56;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

Qy 61 AQKFGQRTVMTDRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
Db 61 AQKFGQRTVMTDRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120

Qy 121 VTSS 125
Db 121 VTSS 125

RESULT 4
US-10-041-860-372
; Sequence 372, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-372

Query Match 100.0%; Score 672; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 1e-56;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

Qy 61 AQKFGQRTVMTDRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
Db 61 AQKFGQRTVMTDRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120

Qy 121 VTSS 125
Db 121 VTSS 125

RESULT 5
US-10-041-860-38
; Sequence 38, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard

```

; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-38

Query Match          94.9%; Score 638; DB 14; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.9e-53;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINFNSGNTDY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINFNSGNTGY 60
Qy 61 AQKFGQGVTTTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGIT 120
Db 61 AQKFGQGVTTTRNTSISTAYMELSLRSEDTAIYYCARGSGYSYGYDYYGMDVWGQGIT 120
Qy 121 VTSS 125
Db 121 VTSS 125

RESULT 6
US-10-041-860-203
; Sequence 203, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-203

Query Match          94.9%; Score 638; DB 14; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.9e-53;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINFNSGNTDY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINFNSGNTGY 60
Qy 61 AQKFGQGVTTTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGIT 120
Db 61 AQKFGQGVTTTRNTSISTAYMELSLRSEDTAIYYCARGSGYSYGYDYYGMDVWGQGIT 120
Qy 121 VTSS 125
Db 121 VTSS 125

RESULT 7
US-10-041-860-240
; Sequence 240, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-240

Query Match          94.9%; Score 638; DB 14; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.9e-53;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINFNSGNTDY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINFNSGNTGY 60
Qy 61 AQKFGQGVTTTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGIT 120
Db 61 AQKFGQGVTTTRNTSISTAYMELSLRSEDTAIYYCARGSGYSYGYDYYGMDVWGQGIT 120
Qy 121 VTSS 125
Db 121 VTSS 125

RESULT 8
US-10-041-860-343
; Sequence 343, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-343

Query Match          94.9%; Score 638; DB 14; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.9e-53;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTGY 60
QY 61 AQKFGQRTVMTTRDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 120
Db 61 AQKFGQRTVMTTRNTSISTAYMELSSLRSEDTAIYYCAREGIAVAGTYYYYYGMVWGQGT 120
QY 121 TVTVSS 125
Db 121 TVTVSS 125
RESULT 9
US-10-041-860-19
; Sequence 19, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-19
Query Match 88.3%; Score 593.5; DB 14; Length 126;
Best Local Similarity 89.7%; Pred. No. 3.4e-49;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTGY 60
QY 61 AQKFGQRTVMTTRDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
Db 61 AQKFGQRTVMTTRNTSISTAYMELSSLRSEDTAIYYCAREGIAVAGTYYYYYGMVWGQGT 120
QY 120 TVTVSS 125
Db 121 TVTVSS 126
RESULT 10
US-10-041-860-201
; Sequence 201, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
```

```
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-201
Query Match 88.3%; Score 593.5; DB 14; Length 126;
Best Local Similarity 89.7%; Pred. No. 3.4e-49;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTGY 60
QY 61 AQKFGQRTVMTTRDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
Db 61 AQKFGQRTVMTTRNTSISTAYMELSSLRSEDTAIYYCAREGIAVAGTYYYYYGMVWGQGT 120
QY 120 TVTVSS 125
Db 121 TVTVSS 126
RESULT 11
US-10-041-860-288
; Sequence 288, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-288
Query Match 88.3%; Score 593.5; DB 14; Length 126;
Best Local Similarity 89.7%; Pred. No. 3.4e-49;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTGY 60
QY 61 AQKFGQRTVMTTRDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
Db 61 AQKFGQRTVMTTRNTSISTAYMELSSLRSEDTAIYYCAREGIAVAGTYYYYYGMVWGQGT 120
QY 120 TVTVSS 125
Db 121 TVTVSS 126
RESULT 12
US-10-041-860-238
; Sequence 238, Application US/10041860
```

Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 238
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-238

Query Match 86.2%; Score 579.5; DB 14; Length 125;
 Best Local Similarity 89.4%; Pred. No. 7.3e-48;
 Matches 110; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 4 LVQSGAEVKKPGASVKASKGYFTSYDINWVRQATGQGLEWMGWNPNSGNTDYAQK 63

Db 3 LVQSGAEVKKPGASVKASKGYFTSYDINWVRQATGQGLEWMGWNPNSGNTDYAQK 62

Qy 64 FQGRVTMTDTSISTAYMELSLRSEDATAYCYVR-GFGYSYNDYVYGGMDVWGQGT 122

Db 63 FQGRVTMTDTSISTAYMELSLRSEDATAYCYVRGAGTAVAGTGYVYGGMDVWGQGT 122

Qy 123 VSS 125

Db 123 VSS 125

RESULT 13
 US-10-041-860-40
 ; Sequence 40, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 40
 ; LENGTH: 126
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-40

Query Match 85.6%; Score 575.5; DB 14; Length 126;
 Best Local Similarity 87.3%; Pred. No. 1.8e-47;
 Matches 110; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Qy 1 QVOLVQSGAEVKKPGASVKASKGYFTSYDINWVRQATGQGLEWMGWNPNSGNTDY 60

Db 1 QVOLVQSGAEVKKPGASVKASKGYFTSYDINWVRQATGQGLEWMGWNPNSGNTGY 60

Qy 61 AQKFGQGRVTMTDTSISTAYMELSLRSEDATAYCYVRGFGYSYN-YDYVYGGMDVWGQGT 119
 Db 61 AQKFGQGRVTMTDTSISTAYMELSLRSEDATAYCYVRGFGYSYN-YDYVYGGMDVWGQGT 120
 Qy 120 TVTVSS 125
 Db 121 TVTVSS 126

RESULT 14
 US-10-041-860-204
 ; Sequence 204, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 204
 ; LENGTH: 126
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-204

Query Match 85.6%; Score 575.5; DB 14; Length 126;
 Best Local Similarity 87.3%; Pred. No. 1.8e-47;
 Matches 110; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Qy 1 QVOLVQSGAEVKKPGASVKASKGYFTSYDINWVRQATGQGLEWMGWNPNSGNTDY 60

Db 1 QVOLVQSGAEVKKPGASVKASKGYFTSYDINWVRQATGQGLEWMGWNPNSGNTGY 60

Qy 61 AQKFGQGRVTMTDTSISTAYMELSLRSEDATAYCYVRGFGYSYN-YDYVYGGMDVWGQGT 119

Db 61 AQKFGQGRVTMTDTSISTAYMELSLRSEDATAYCYVRGFGYSYN-YDYVYGGMDVWGQGT 120

Qy 120 TVTVSS 125

Db 121 TVTVSS 126

RESULT 15
 US-10-041-860-241
 ; Sequence 241, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 241
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-241

Query Match      85.6%; Score 575.5; DB 14; Length 126;
Best Local Similarity 87.3%; Pred. No. 1.8e-47;
Matches 110; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

Qy      61 AOKFQGRVTMTNRTSISTAYNELSLRSEDTAIYVCVRGFGYSYN-YDYIYGGNDVWGQGT 119
Db      61 AOKFQGRVTMTNRTSISTAYNELSLRSEDTAIYVCVRGFGYSYN-YDYIYGGNDVWGQGT 120

Qy      120 TTVVSS 125
Db      121 TTVVSS 126

```

Search completed: April 21, 2004, 17:13:22
Job time : 42.309 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2004, 16:59:07 ; Search time 38.0301 Seconds
(without alignments)
1035.433 Million cell updates/sec

Title: US-10-041-860-48
Perfect score: 672
Sequence: 1 QVQLVQSGAEVKPGASVKV.....YDYVYGMVWGQGTITVTVSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriaph:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 497.5 | 74.0 | 159 | 4 Q96QSO | Q96QSO homo sapien |
| 2 | 494 | 73.5 | 119 | 4 Q9UL34 | Q9UL34 homo sapien |
| 3 | 494 | 73.5 | 125 | 4 Q9UL95 | Q9UL95 homo sapien |
| 4 | 481.5 | 71.7 | 124 | 4 Q9UL92 | Q9UL92 homo sapien |
| 5 | 474 | 70.5 | 497 | 4 Q8WY24 | Q8WY24 homo sapien |
| 6 | 470.5 | 70.0 | 500 | 4 Q9BRV0 | Q9BRV0 homo sapien |
| 7 | 468 | 69.6 | 614 | 4 Q96GA6 | Q96GA6 homo sapien |
| 8 | 455 | 67.7 | 119 | 5 Q9GY22 | Q9GY22 achistosoma |
| 9 | 433.5 | 64.5 | 469 | 4 Q7Z7F5 | Q7Z7F5 homo sapien |
| 10 | 431.5 | 64.2 | 278 | 11 Q92IK1 | Q92IK1 mus musculus |
| 11 | 430 | 64.0 | 481 | 11 Q91WT1 | Q91WT1 mus musculus |
| 12 | 429.5 | 63.9 | 116 | 4 Q9UL89 | Q9UL89 homo sapien |
| 13 | 425.5 | 63.3 | 145 | 11 Q92LR4 | Q92LR4 mus musculus |
| 14 | 422 | 62.8 | 147 | 11 Q92S53 | Q92S53 mus musculus |
| 15 | 420 | 62.5 | 157 | 4 Q85978 | Q85978 homo sapien |
| 16 | 419 | 62.4 | 470 | 11 Q7TWK1 | Q7TWK1 mus musculus |

| | | | | | |
|----|-------|------|-----|-----------|---------------------|
| 17 | 418 | 62.2 | 117 | 11 Q9QXE9 | Q9QXE9 mus musculus |
| 18 | 417 | 62.1 | 473 | 11 Q9D9L4 | Q9D9L4 mus musculus |
| 19 | 416.5 | 62.0 | 463 | 11 Q99LC4 | Q99LC4 mus musculus |
| 20 | 415.5 | 61.8 | 145 | 11 Q924Q6 | Q924Q6 mus musculus |
| 21 | 414 | 61.6 | 146 | 11 Q924Q3 | Q924Q3 mus musculus |
| 22 | 413.5 | 61.5 | 145 | 11 Q924R1 | Q924R1 mus musculus |
| 23 | 412.5 | 61.4 | 143 | 11 Q924Q5 | Q924Q5 mus musculus |
| 24 | 412.5 | 61.4 | 145 | 11 Q924R3 | Q924R3 mus musculus |
| 25 | 412.5 | 61.4 | 613 | 11 Q8VCX7 | Q8VCX7 mus musculus |
| 26 | 410.5 | 61.1 | 145 | 11 Q924Q9 | Q924Q9 mus musculus |
| 27 | 409.5 | 60.9 | 143 | 11 Q924R0 | Q924R0 mus musculus |
| 28 | 408.5 | 60.8 | 145 | 11 Q924Q7 | Q924Q7 mus musculus |
| 29 | 408 | 60.7 | 117 | 11 Q9QXF0 | Q9QXF0 mus musculus |
| 30 | 408 | 60.7 | 144 | 11 Q924P5 | Q924P5 mus musculus |
| 31 | 408 | 60.7 | 146 | 11 Q924R8 | Q924R8 mus musculus |
| 32 | 407.5 | 60.6 | 145 | 11 Q924P7 | Q924P7 mus musculus |
| 33 | 407 | 60.6 | 142 | 11 Q924Q2 | Q924Q2 mus musculus |
| 34 | 406.5 | 60.5 | 143 | 11 Q924F9 | Q924F9 mus musculus |
| 35 | 403.5 | 60.0 | 473 | 11 Q99125 | Q99125 mus musculus |
| 36 | 403 | 60.0 | 150 | 4 Q9Y298 | Q9Y298 homo sapien |
| 37 | 401 | 59.7 | 484 | 11 Q991A6 | Q991A6 mus musculus |
| 38 | 400.5 | 59.6 | 482 | 11 Q8K172 | Q8K172 mus musculus |
| 39 | 398 | 59.2 | 142 | 11 Q924Q1 | Q924Q1 mus musculus |
| 40 | 397.5 | 59.2 | 143 | 11 Q924R7 | Q924R7 mus musculus |
| 41 | 397 | 59.1 | 168 | 11 Q8VDC9 | Q8VDC9 mus musculus |
| 42 | 396.5 | 59.0 | 143 | 11 Q91V67 | Q91V67 mus musculus |
| 43 | 396 | 58.9 | 140 | 11 Q924R2 | Q924R2 mus musculus |
| 44 | 395.5 | 58.9 | 141 | 11 Q924Q4 | Q924Q4 mus musculus |
| 45 | 394.5 | 58.7 | 496 | 4 Q96DK0 | Q96DK0 homo sapien |

ALIGNMENTS

RESULT 1

Q96QSO PRELIMINARY; PRT; 159 AA.
AC Q96QSO
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY039025; AAX82649.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 74.0%; Score 497.5; DB 4; Length 159;

Best Local Similarity 74.0%; Pred. No. 1.2e-42;

Matches 97; Conservative 12; Mismatches 15; Indels 7; Gaps 2;

| | | | |
|----|-----|---|-----|
| QY | 1 | QVQLVQSGAEVKPGASVKVSKASGYTFTSYDINVRQATQGLWMGWINPNSGNTDY | 60 |
| Db | 20 | QVQLVQSGAEVKPGASVKVSKASGYTFTSYNMVWVQAPQGPFWGVNPSGGSARY | 79 |
| QY | 61 | AQKQFGRVTMTDTSISTAYMELSLRSEDIAIYYCVR-----GFGSYNDIYYGMDV | 114 |
| Db | 80 | SKQFQRLTMTDTSITVMDLSLRSDTAVYFCAREMEITFGGAVSKGF-YYIGMDV | 138 |
| QY | 115 | WGQGITVTIVSS | 125 |

Db 139 WGGTTVTVSS 149

|||||

RESULT 2

Q9UL94 PRELIMINARY; PRT; 119 AA.

AC Q9UL94; 2000 (TREMELrel. 13, Created)

DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."

RT 121 VTVSS 125

DB 115 VTVSS 119

Query Match 73.5%; Score 494; DB 4; Length 119;

Best Local Similarity 76.0%; Pred. No. 2e-42;

Matches 95; Conservative 10; Mismatches 14; Indels 6; Gaps 1;

QY 1 QVQLVQSGAEVKKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60

DB 1 EVQLVESGAEVKKPKGASVKVSKASGYTFTGYVHWVRQAPGQGLEWGWINPNSWTNY 60

QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGMVWGQTT 120

DB 61 AQKFGQRTVTRDTSISTAYMELSLRSDDTAVYYCARGGGRGLWF-----DPWGGTLL 114

QY 121 VTVSS 125

DB 115 VTVSS 119

RESULT 3

Q9UL95 PRELIMINARY; PRT; 125 AA.

AC Q9UL95; 2000 (TREMELrel. 13, Created)

DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."

RT 121 VTVSS 125

DB 115 VTVSS 119

Query Match 73.5%; Score 494; DB 4; Length 119;

Best Local Similarity 76.0%; Pred. No. 2e-42;

Matches 95; Conservative 10; Mismatches 14; Indels 6; Gaps 1;

QY 1 QVQLVQSGAEVKKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60

DB 1 EVQLVESGAEVKKPKGASVKVSKASGYTFTGYVHWVRQAPGQGLEWGWINPNSWTNY 60

QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGMVWGQTT 120

DB 61 AQKFGQRTVTRDTSISTAYMELSLRSDDTAVYYCARGGGRGLWF-----DPWGGTLL 114

QY 121 VTVSS 125

DB 115 VTVSS 119

CLin. Immunol. Immunopathol. 87:184-192 (1998).

EMBL; AF035019; AAD56255.1; -.

HSSP; P01810; 2FBJ.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 1.

NON_TER 1 125

NON_TER 125 125

SEQUENCE 125 AA; 13516 MW; 0D3CD5C32488EAC CRC64;

Query Match 73.5%; Score 494; DB 4; Length 125;

Best Local Similarity 76.0%; Pred. No. 2.1e-42;

Matches 95; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60

DB 1 EVQLVESGAEVKKPKGASVKVSKASGYTFTGYVHWVRQAPGQGLEWGWINPNSGGTNY 60

QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGMVWGQTT 120

DB 61 AQKFGQRTVTRDTSISTAYMELSLRSDDTAVYYCARGGGRGLWF-----DPWGGTLL 120

QY 121 VTVSS 125

DB 121 VTVSS 125

RESULT 4

Q9UL92 PRELIMINARY; PRT; 124 AA.

AC Q9UL92; 2000 (TREMELrel. 13, Created)

DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."

RT 121 VTVSS 125

DB 115 VTVSS 119

Query Match 71.7%; Score 481.5; DB 4; Length 124;

Best Local Similarity 76.0%; Pred. No. 3.8e-41;

Matches 95; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60

DB 1 EVQLVESGAEVKKPKGASVKVSKASGYTFTSYVHWVRQAPGQGLEWGWINPNSGTSY 60

QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGMVWGQTT 120

DB 61 AQKFGQRTVTRDTSISTAYMELSLRSDDTAVYYCARGL-YVVPAPAFSRFDYWGQTT 119


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QY 121 VTSS 125
Db 120 VTSS 124

RESULT 5
Q8WY24
ID Q8WY24 PRELIMINARY; PRT; 497 AA.
AC Q8WY24
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE SMC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RT "Identification and characterization of SMC66, a Ig-like gene which is
RT down-regulated in colorectal cancer.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF203656; AAL36987.1;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 497 AA; 5365 MW; F24D08DFA5A63E5 CRC64;

Query Match 70.5%; Score 474; DB 4; Length 497;
Best Local Similarity 70.0%; Pred. No. 1.2e-39;
Matches 91; Conservative 13; Mismatches 16; Indels 10; Gaps 2;

QY 1 QVQLVQSGAEVKKPKASVKSCASGYTFTSYDINWVRQATGCGLEWGWNPNSGNTDY 60
Db 20 QEQLQSGAEVKKPKASVKSCASGYTFTSYDINWVRQAPQGQLEWGWNPQTGTF 79

QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYYCVR-----GFGSYNDYYIGMDVW 115
Db 80 AQKFGRLTFRSDTSINTAYVLSLSTEDSAIFYCARGNLGRGFGYNW-----FDPW 134

QY 116 CGTIVTVSS 125
Db 135 GGTIVTVSS 144

RESULT 6
Q8WY24
ID Q8WY24 PRELIMINARY; PRT; 500 AA.
AC Q8WY24
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AAH05951.1;
DR HSSP; P01789; LMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 4.

Query Match 69.6%; Score 468; DB 4; Length 614;
Best Local Similarity 73.6%; Pred. No. 6.4e-39;
Matches 92; Conservative 14; Mismatches 15; Indels 4; Gaps 2;

QY 1 QVQLVQSGAEVKKPKASVKSCASGYTFTSYDINWVRQATGCGLEWGWNPNSGNTDY 60
Db 20 QMQLVQSGAEVKKPKASVKSCASGYTFTSYLHWVRQAPQALEWGWNPFGNTNY 79

QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYYCVRGFGSYNDYYIGMDVWQGGT 120
Db 80 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYYCAR--GYSSSWDDAF--DINQGGTM 135

QY 121 VTSS 125
Db 136 VTSS 140
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RESULT 8
Q9GYZ2 PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.F., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -.
DR HSSP; P01772; 2FB4
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match 67.7%; Score 455; DB 5; Length 119;
Best Local Similarity 69.6%; Pred. No. 1.8e-38;
Matches 87; Conservative 14; Mismatches 18; Indels 6; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMGNPNNSGNTDY 60
Db 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQAPGSGLEWIGVINSRGYNY 60

QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCV---RGFGSYNYDYIGMDVWGQTT 120
Db 61 NQKFKDRVTMTDKSFSTAYMDLSRLSADSAVYYCAR-----YDDHCLDYWGQGT 114

QY 121 VTVSS 125
Db 115 VTVSS 119

RESULT 9
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zerbberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 64.5%; Score 433.5; DB 4; Length 469;
Best Local Similarity 66.4%; Pred. No. 1.5e-35;
Matches 85; Conservative 13; Mismatches 19; Indels 11; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMGNPNNSGNTDY 60
Db 20 QVHLVSGAEVKKPGASVKLSCKTSYTFSSYDILWVRQAPGQGLEWGMWISAHNGDTKY 79

QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCV---RGFGSYNYDYIGMDVWGQ 117
Db 80 ARKFGQRTVTRDTSATTSMYFSLRSDDTALFYCATKSRG-----QVGFDFSWGQ 131

QY 118 GTTVVSS 125
Db 132 GTLVTVSS 139

RESULT 10
Q921K1 PRELIMINARY; PRT; 278 AA.
ID Q921K1
AC Q921K1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAH12207.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 64.2%; Score 431.5; DB 11; Length 278;
Best Local Similarity 66.4%; Pred. No. 1.2e-35;
Matches 83; Conservative 16; Mismatches 21; Indels 5; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMGNPNNSGNTDY 60
Db 20 QVQLVSGAEVKKPGASVKLSCKASGYTFTSYDINWVRQAPGQGLEWGMWISAHNGDTKY 79

QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCV---RGFGSYNYDYIGMDVWGQTT 120
Db 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCV---RGFGSYNYDYIGMDVWGQTT 120
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Db 80 NEKFKATLAVDKSSSTVMQLSSLTSEDSSAVYCTRGYGD---DVYF--DVGAGTT 134
QY 121 VTSS 125
   |||||
Db 135 VTSS 139

RESULT 11
Q91WT1 PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Colon;
RA Strauberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 64.0%; Score 430; DB 11; Length 481;
Best Local Similarity 64.0%; Pred. No. 3.4e-35;
Matches 80; Conservative 18; Mismatches 19; Indels 8; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGWINPNSGNTDY 60
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGWINPNSGNTDY 79

QY 61 AQKQGRVTMTDRTSISTAYMELSLRSEDTAIYCYVRGFGYSYNYDYGMVWGQGT 120
   :|||:
Db 80 NEKFKGKTLTADKSSSTAYMFLSLTSEDSSAVYCTRGGWAFDY-----WGQGT 131

QY 121 VTSS 125
   |||||
Db 132 LTVSS 136

RESULT 12
Q9UL89 PRELIMINARY; PRT; 116 AA.
AC Q9UL89;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9627139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
   Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
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DR EMBL; AF035025; AAD56261.1; -.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12605 MW; C8P9131DE13EA898 CRC64;

Query Match 63.9%; Score 429.5; DB 4; Length 116;
Best Local Similarity 71.9%; Pred. No. 6.7e-36;
Matches 87; Conservative 10; Mismatches 19; Indels 5; Gaps 1;

QY 5 VOSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGWINPNSGNTDYAQKF 64
Db 1 VOSGAEVKKPGSSVKVSCKASGTFSSVAISVWRAPGQGLEWMGRITPILGIANYAQKF 60
   |||||

QY 65 QGRVTMTDRTSISTAYMELSLRSEDTAIYCYVRGFGYSYNYDYGMVWGQGT 124
   :|||:
Db 61 QGRVTITADKSTSTAYMELSLRSEDTAIYCYA-----SSNWGPVYFELWGRGTLTVTS 115

QY 125 S 125
   |
Db 116 S 116

RESULT 13
Q924R4 PRELIMINARY; PRT; 145 AA.
AC Q924R4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Vh186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067785; BAB63270.1; -.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; IG-like.
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DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG_LIKE; 1.  
FT NON_TER 1 145  
FT NON_TER 145 145  
SQ SEQUENCE 145 AA; 16081 MW; ECDLIAI35E05B8AA CRC64;  
  
Query Match 63.3%; Score 425.5; DB 11; Length 145;  
Best Local Similarity 64.8%; Pred. No. 2.2e-35;  
Matches 81; Conservative 17; Mismatches 22; Indels 5; Gaps 1;  
  
Qy 1 QVQLVSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATCGGLEWGMWNPNSGNTDY 60  
Db 1 QVQLVSGAEVKKPGASVKLSCKASGYTFSTYDINWVRQATCGGLEWGMWNPNSGNTDY 60  
Qy 61 AQKFGQGVMTWTRDTSISTAYMELSLRSSEDTAIYVCVRGFGY-SYNDYYGMDVWGQGT 120  
Db 61 NEKFKSKATLTVDKPSSATYMQLSLTSEDSAVIYCARS-----DYDYDYAMDVWGQGT 115  
  
Qy 121 TVTVSS 125  
Db 116 TVTVSS 120  
  
RESULT 14  
Q925S3 PRELIMINARY; PRT; 147 AA.  
AC Q925S3 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE MRP3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX PubMed=11819679;  
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
RA Su C.;  
RT "Mechanism of exogenous nucleic acids and their precursors improving  
RT the repair of intestinal epithelium after irradiation in mice."  
RL World J. Gastroenterol. 6:709-717(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RA "Cloning of mouse genes related to repairing of intestinal epithelium  
RT of the irradiated mice by treatment with the intestinal RNA of mice of  
RT the same strain."  
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
DR EMBL; AF240166; AAK43731.1; --  
DR InterPro; IPR007110; IG_LIKE.  
DR InterPro; IPR003596; IG_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG_LIKE; 1.  
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;  
  
Query Match 62.8%; Score 422; DB 11; Length 147;  
Best Local Similarity 65.1%; Pred. No. 5.2e-35;  
Matches 82; Conservative 15; Mismatches 21; Indels 8; Gaps 2;  
  
Qy 1 QVQLVSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATCGGLEWGMWNPNSGNTDY 60  
Db 3 QVQLHSGPEVKKPGASVKLSCKASGYTFSTYDINWVRQATCGGLEWGMWNPNSGNTDY 62  
Qy 61 AQKFGQGVMTWTRDTSISTAYMELSLRSSEDTAIYVCVRGFGY-SYNDYYGMDVWGQGT 119  
Db 63 NEKFKGRATLSVDKSSSTAYMELTRLTSEDSAVIPCARG-----DYTRYFDLWGQGT 115  
  
InterPro; IPR003596; Ig_v.  
Pfam; PF00047; Ig; 1.  
SMART; SM00406; IGV; 1.  
PROSITE; PSS0835; IG_LIKE; 1.  
NON_TER 1 145  
NON_TER 145 145  
SEQUENCE 145 AA; 16081 MW; ECDLIAI35E05B8AA CRC64;  
  
Query Match 63.3%; Score 425.5; DB 11; Length 145;  
Best Local Similarity 64.8%; Pred. No. 2.2e-35;  
Matches 81; Conservative 17; Mismatches 22; Indels 5; Gaps 1;  
  
Qy 1 QVQLVSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATCGGLEWGMWNPNSGNTDY 60  
Db 1 QVQLVSGAEVKKPGASVKLSCKASGYTFSTYDINWVRQATCGGLEWGMWNPNSGNTDY 60  
Qy 61 AQKFGQGVMTWTRDTSISTAYMELSLRSSEDTAIYVCVRGFGY-SYNDYYGMDVWGQGT 120  
Db 61 NEKFKSKATLTVDKPSSATYMQLSLTSEDSAVIYCARS-----DYDYDYAMDVWGQGT 115  
  
Qy 121 TVTVSS 125  
Db 116 TVTVSS 120  
  
RESULT 15  
O95978 PRELIMINARY; PRT; 157 AA.  
AC O95978 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Vhl protein precursor (fragment).  
GN VHL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Peripheral blood;  
RA Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,  
RA Bohlen H., Diehl V., Wolf J.;  
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a  
RT patient with mixed cellularly Hodgkin's disease is associated with  
RT somatic mutations within the untranslated regions of rearranged and  
RT class switch recombined Ig genes."  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ005570; CAA06599.1; --  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; IG_LIKE.  
DR InterPro; IPR003596; IG_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG_LIKE; 1.  
KW Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT NON_TER 157 157  
SQ SEQUENCE 157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;  
  
Query Match 62.5%; Score 420; DB 4; Length 157;  
Best Local Similarity 67.5%; Pred. No. 9e-35;  
Matches 85; Conservative 13; Mismatches 22; Indels 6; Gaps 2;  
  
Qy 1 QVQLVSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATCGGLEWGMWNPNSGNTDY 60  
Db 20 QVQLVSGAEIKRPGASVKVCHKTSYVFTSYIHWVRQPGQGLEWGMGIGFGVGTMC 79  
Qy 61 AQKFGQGVMTWTRDTSISTAYMELSLRSSEDTAIYVCVRGFGY-SYNDYYGMDVWGQGT 119  
Db 80 AEKFGRLTWTRNTSTITVTMELSLRFDFTAVYFCGRGRWRSNGYNH-----WGQGT 134  
  
Qy 120 TVTVSS 125  
Db 135 PVTVSS 140  
  
Search completed: April 21, 2004, 17:03:46  
Job time : 41.0901 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 16:59:07 ; Search time 14.485 Seconds
(without alignments)
830.097 Million cell updates/sec

Title: US-10-041-860-48
Perfect score: 672
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....YDYVGMVWGQTTVTSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------|--------------------|
| 1 | 557 | 82.9 | 127 | S34014 | Ig heavy chain V r |
| 2 | 537.5 | 80.0 | 136 | S31600 | Ig heavy chain V r |
| 3 | 534 | 79.5 | 129 | S46393 | Ig heavy chain V r |
| 4 | 516.5 | 76.9 | 118 | S36265 | Ig heavy chain V r |
| 5 | 515 | 76.6 | 123 | D33548 | Ig heavy chain V-1 |
| 6 | 514 | 76.5 | 129 | S36260 | Ig heavy chain V r |
| 7 | 511.5 | 76.1 | 135 | S49530 | anti-Sm antibody V |
| 8 | 510.5 | 76.0 | 132 | S31596 | Ig heavy chain V r |
| 9 | 500 | 74.4 | 131 | S26792 | Ig heavy chain V r |
| 10 | 499 | 74.3 | 119 | PH0961 | Ig heavy chain V r |
| 11 | 496.5 | 73.9 | 110 | PH1670 | Ig heavy chain V r |
| 12 | 496 | 73.8 | 98 | S26918 | Ig heavy chain V r |
| 13 | 495.5 | 73.7 | 132 | PH0954 | Ig heavy chain V r |
| 14 | 495.5 | 73.6 | 171 | S23623 | Ig heavy chain V r |
| 15 | 494.5 | 73.6 | 118 | PH1666 | Ig heavy chain V r |
| 16 | 493.5 | 73.4 | 136 | PH0960 | Ig heavy chain pre |
| 17 | 488.5 | 72.7 | 143 | EHUND | Ig heavy chain V r |
| 18 | 488 | 72.6 | 127 | PH0955 | Ig heavy chain V r |
| 19 | 487.5 | 72.5 | 124 | S19665 | Ig heavy chain V r |
| 20 | 486 | 72.3 | 133 | C33548 | Ig heavy chain V-1 |
| 21 | 486 | 72.3 | 627 | S14683 | Ig mu chain precu |
| 22 | 484 | 72.0 | 142 | A32483 | Ig heavy chain V r |
| 23 | 480 | 71.4 | 122 | S36271 | Ig heavy chain V r |
| 24 | 480 | 71.4 | 160 | FL0105 | anti-PR2 erythrocy |
| 25 | 477.5 | 71.1 | 126 | B33548 | Ig heavy chain V-1 |
| 26 | 476.5 | 70.9 | 114 | PH1667 | Ig heavy chain V r |
| 27 | 473.5 | 70.5 | 128 | PH0952 | Ig heavy chain V r |
| 28 | 472.5 | 70.3 | 120 | S31999 | Ig heavy chain V r |
| 29 | 468 | 69.6 | 109 | PH1668 | Ig heavy chain V r |

30 465 69.2 98 2 S26938 Ig heavy chain V r
31 465 69.2 117 2 S31680 Ig heavy chain V r
32 465 69.2 117 2 S18551 Ig heavy chain V r
33 465 69.2 126 2 S14111 Ig heavy chain V r
34 463 68.9 104 2 S69899 Ig heavy chain V r
35 462 68.8 121 2 S20783 Ig heavy chain V r
36 460.5 68.5 122 2 PH0958 Ig heavy chain V r
37 457 68.0 98 2 S26912 Ig heavy chain V r
38 456 67.9 125 2 PH0957 Ig heavy chain V r
39 455.5 67.8 120 2 S26789 Ig heavy chain V r
40 454.5 67.6 132 2 S46394 Ig heavy chain V-1
41 454 67.6 129 2 A33548 Ig heavy chain V r
42 452.5 67.3 110 2 PH1669 Ig heavy chain V r
43 449 66.8 125 2 S68170 Ig heavy chain V r
44 448.5 66.7 116 2 PH0959 Ig heavy chain V r
45 446.5 66.4 135 2 B32274 Ig heavy chain pre

ALIGNMENTS

RESULT 1
S34014
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C/Accession: S34014; S30535
R/Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A/Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A/Reference number: S34001; MUID:93209281; PMID:7681398
A/Accession: S34014
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-127 <NAR>
A/Cross-references: EMBL:Z18321
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
P/15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 557; DB 2; Length 127;
Best Local Similarity 82.7%; Pred. No. 1.5e-42;
Matches 105; Conservative 10; Mismatches 10; Indels 2; Gaps 1;
QY 1 QVQLVQSGAEVKKPGASVKVCASGYSYDINNVRAQTGGLEWMGWINPNSGNTDY 60
Db 1 QVQVWSGAEVKKPGASVKVCASGYTFTSDINNVRAQTGGLEWMGWINPSSGNTGY 60
QY 61 AQKFGKRVMTNRTSISTAYMELSLRSEDYIYCVR--GFGYSYNDYIYGMVWGOG 118
Db 61 AQKFGKRVMTNRTSISTAYMELSLRSEDYIYCVR--GFGYSYNDYIYGMVWGOG 120
QY 119 TTVTVSS 125
Db 121 TTVSVSS 127

RESULT 2
S31600
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31600
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31600
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-136 <CUI>
A/Cross-references: EMBL:Z14165; NID:G30994; PIDN:CAA78534.1; PID:G30995
C/Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 537.5; DB 2; Length 136;
Best Local Similarity 82.4%; Pred. No. 8.6e-41;
Matches 103; Conservative 6; Mismatches 7; Indels 9; Gaps 1;

QY 1 QVQLVSGAEVKKPKGASVKVSKASGYTFTSDINWVRQATGQGLEWMGWNPNSGNTDY 60
DB 20 QVQLVSGAEVKKPKGASVKVSKASGYTFTSDINWVRQATGQGLEWMGWNPNSGNTGY 79

QY 61 AQKFGQGVMTTRDTSISTAYMELSLRSEDIAIYVCVRGFGYSYNDYYGMDVWGQGT 120
DB 80 AQKFGQGVMTTRDTSISTAYMELSLRSEDIAIYVCVRGFGYSYNDYYGMDVWGQGT 120

QY 121 VTVSS 125
DB 131 VTVSS 135

RESULT 3

S46393
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46393
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <FIG>
A;Cross-references: EMBL:Z31690; NID:G509786; PIDN:CAA83485.1; PID:gl335146
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 534; DB 2; Length 129;
Best Local Similarity 79.8%; Pred. No. 1.7e-40;
Matches 103; Conservative 7; Mismatches 15; Indels 4; Gaps 1;

QY 1 QVQLVSGAEVKKPKGASVKVSKASGYTFTSDINWVRQATGQGLEWMGWNPNSGNTDY 60
DB 1 QVQLVSGAEVKKPKGASVKVSKASGYTFTGYVHWVRQAPGQGLEWMGWNPNSGNTY 60

QY 61 AQKFGQGVMTTRDTSISTAYMELSLRSEDIAIYVCVRGFGYSYNDYYG----WDYWG 116
DB 61 AQKFGQGVMTTRDTSISTAYMELSLRSEDIAIYVCVRGFGYSYNDYYG----WDYWG 120

QY 117 QGTVTVSS 125
DB 121 KGTVTVSS 129

RESULT 4

S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36265
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36265
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-118 <GRI>
A;Cross-references: EMBL:Z18846; NID:G33121; PIDN:CAA79298.1; PID:G939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 516.5; DB 2; Length 118;
Best Local Similarity 80.0%; Pred. No. 5.4e-39;
Matches 100; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

QY 1 QVQLVSGAEVKKPKGASVKVSKASGYTFTSDINWVRQATGQGLEWMGWNPNSGNTDY 60
DB 1 QVQLVSGAEVKKPKGASVKVSKASGYTFTGYVHWVRQAPGQGLEWMGWNPNSGNTY 60

QY 61 AQKFGQGVMTTRDTSISTAYMELSLRSEDIAIYVCVRGFGYSYNDYYGMDVWGQGT 120
DB 61 AQKFGQGVMTTRDTSISTAYMELSLRSEDIAIYVCVRGFGYSYNDYYGMDVWGQGT 113

QY 121 VTVSS 125
DB 114 VTVSS 118

RESULT 5

D33548
Ig heavy chain V-1 region (WIL2) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: D33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene exp.
A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: D33548
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A;Molecule type: mRNA
A;Residues: 1-123 <KIP>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 515; DB 2; Length 123;
Best Local Similarity 78.6%; Pred. No. 7.6e-39;
Matches 99; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

QY 1 QVQLVSGAEVKKPKGASVKVSKASGYTFTSDINWVRQATGQGLEWMGWNPNSGNTDY 60
DB 1 QVQLVSGAEVKKPKGASVKVSKASGYTFTGYVHWVRQAPGQGLEWMGWNPNSGNTY 60

QY 61 AQKFGQGVMTTRDTSISTAYMELSLRSEDIAIYVCVRGFGYSYNDYYGMDVWGQGT 119
DB 61 AQKFGQGVMTTRDTSINTAYMELSLRSDTAIYVCARA---SYCGYDCVYFPDYWGQGT 117

QY 120 VTVSS 125
DB 118 LTVSS 123

RESULT 6

S36260
Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36260
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36260
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-129 <GRI>
A;Cross-references: EMBL:Z18851; NID:G33124; PIDN:CAA79303.1; PID:G939903
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

```

Query Match          76.0%; Score 510.5; DB 2; Length 132;
Best Local Similarity 79.2%; Pred. No. 2.1e-38;

```

```

RESULT 10
PH0961
Ig heavy chain V region (G6+ T-L33) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0961
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0961
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-119 <NAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3

```

F;99-107/Region: complementarity-determining 3

Query Match 74.3%; Score 499; DB 2; Length 119;
Best Local Similarity 79.2%; Pred. No. 1.9e-37;
Matches 99; Conservative 6; Mismatches 14; Indels 6; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGSSVKVSCKASGCTFSSYALISWVRQAPGQGLEWMGGIPIFGTANY 60

QY 61 AQKFGQRTVMTDRDTSISLAYMELSLRSEDTAIYCVRGFGYSVNYDYVYGMVWGQGT 120
DB 61 AQKFGQRTVMTDRDTSISLAYMELSLRSEDTAIYCVRGFGYSVNYDYVYGMVWGQGT 114

QY 121 VTSS 125

DB 115 VTSS 119

RESULT 11

PH1670 Ig heavy chain V region (clone 2A12) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C:Accession: PH1670

R: Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A: Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A

A: Reference number: PH1642; MUID: 93301610; PMID: 8315386

A: Accession: PH1670

A: Molecule type: mRNA

A: Residues: 1-110 <HIL>

A: Experimental source: B cell

C: Superfamily: immunoglobulin V region; immunoglobulin homology

C: Keywords: heterotetramer; immunoglobulin

F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 73.9%; Score 496.5; DB 2; Length 110;
Best Local Similarity 82.1%; Pred. No. 3e-37;
Matches 96; Conservative 6; Mismatches 8; Indels 7; Gaps 2;

QY 9 AEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAKKFGQGV 68
DB 1 AEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAKKFGQGV 60

QY 69 TMTDRDTSISLAYMELSLRSEDTAIYCVRGFGYSVNYDYVYGMVWGQGT 125

DB 61 TMTDRDTSISLAYMELSLRSEDTAIYCVRGFGYSVNYDYVYGMVWGQGT 110

RESULT 12

S26918

Ig heavy chain V region (DP-15) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26918

R: Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A: Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A: Reference number: S26885; MUID: 93021117; PMID: 1404388

A: Accession: S26918

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-98 <TOM>

A: Cross-references: EMBL:Z12317; NID:G32857; PID:CAA78187.1; PID:G32858

C: Superfamily: immunoglobulin V region; immunoglobulin homology

C: Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.8%; Score 496; DB 2; Length 98;
Best Local Similarity 94.9%; Pred. No. 2.9e-37;
Matches 93; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

QY 61 AQKFGQRTVMTDRDTSISLAYMELSLRSEDTAIYCVVR 98

DB 61 AQKFGQRTVMTDRDTSISLAYMELSLRSEDTAIYVCAR 98

RESULT 13

PH0954

Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C:Accession: PH0954

R: Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A: Title: Evidence for somatic selection of natural autoantibodies.

A: Reference number: PH0952; MUID: 92202880; PMID: 1552291

A: Accession: PH0954

A: Status: nucleic acid sequence not shown

A: Molecule type: DNA

A: Residues: 1-132 <MAR>

C: Superfamily: immunoglobulin V region; immunoglobulin homology

C: Keywords: heterotetramer; immunoglobulin

F;1-30/Region: framework 1

F;15-98/Domain: immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;36-50/Region: framework 2

F;51-67/Region: complementarity-determining 2

F;68-98/Region: framework 3

F;99-120/Region: complementarity-determining 3

Query Match 73.7%; Score 495.5; DB 2; Length 132;
Best Local Similarity 75.9%; Pred. No. 4.4e-37;
Matches 101; Conservative 6; Mismatches 17; Indels 9; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGSSVKVSCKASGCTFSSYALISWVRQAPGQGLEWMGGIPIFGTANY 60

QY 61 AQKFGQRTVMTDRDTSISLAYMELSLRSEDTAIYCVRGF-----GYSVNYDYVYGM 112

DB 61 AQKFGQRTVMTDRDTSISLAYMELSLRSEDTAIYVCARPHASIDDFWSGYVNY-YVYGM 119

QY 113 DVWGQGT 125

DB 120 DVWGQGT 132

RESULT 14

S23623

Ig heavy chain V region precursor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S23623

R: Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A: Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from

A: Reference number: S23623; MUID: 92156804; PMID: 1740665

A: Accession: S23623

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-171 <OLE>

A: Cross-references: EMBL:X59702; NID:G32010; PID:CAA42223.1; PID:G32011

C: Superfamily: immunoglobulin V region; immunoglobulin homology

C: Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 495.5; DB 2; Length 171;
Best Local Similarity 70.9%; Pred. No. 5.8e-37;
Matches 95; Conservative 9; Mismatches 13; Indels 17; Gaps 2;


```
Qy 1 QVQLVSGAEVKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 20 QVQLVSGAEVKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWINPNSGGTGY 79
Qy 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYYG----- 111
Db 80 GQKFGQGRVTMTSDTSISTAYMELSLRSDTAIYYCA-----IEYFYDGSDLKPSDV 131
Qy 112 MDVWGQGTITVTVSS 125
Db 132 FDIWGQGTMTVTVSS 145

RESULT 15
PH1666
Ig heavy chain V region (clone 6C9) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C/Accession: PH1666
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH1666
A/Molecule type: mRNA
A/Residues: 1-118 <Hil>
A/Experimental source: B cell
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 494.5; DB 2; Length 118;
Best Local Similarity 80.5%; Pred. No. 4.8e-37;
Matches 95; Conservative 6; Mismatches 16; Indels 1; Gaps 1;
Qy 9 AEVKKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAKKFGGRV 68
Db 1 AEVKKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWINAGNTKYAKKFGGRV 60
Qy 69 TMTSDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGTITVTVSS 125
Db 61 TITRDTASTAYMELSLRSEDTAIYYCARVTLDDGKIFYYGMDVWGQGTITVTVSS 118
```

Search completed: April 21, 2004, 17:04:24
Job time : 15.485 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 16:58:51 ; Search time 11.2661 Seconds

(without alignments)
577.731 Million cell updates/sec

Title: US-10-041-860-48

Perfect score: 672

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....YDYVYGMDVWGQCTIVTVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 488.5 | 72.7 | 147 | 1 HV1G HUMAN | P01744 homo sapien |
| 2 | 441 | 65.6 | 117 | 1 HV1G HUMAN | P23083 homo sapien |
| 3 | 440 | 65.5 | 117 | 1 HV1B HUMAN | P01743 homo sapien |
| 4 | 418.5 | 62.3 | 118 | 1 HV51 MOUSE | P06330 mus musculus |
| 5 | 414 | 61.6 | 117 | 1 HV12 MOUSE | P01756 mus musculus |
| 6 | 413 | 61.5 | 120 | 1 HV03 MOUSE | P01747 mus musculus |
| 7 | 408.5 | 60.8 | 139 | 1 HV07 MOUSE | P01751 mus musculus |
| 8 | 408 | 60.7 | 117 | 1 HV13 MOUSE | P01757 mus musculus |
| 9 | 394.5 | 58.7 | 120 | 1 HV50 MOUSE | P06329 mus musculus |
| 10 | 390 | 58.0 | 117 | 1 HV1A HUMAN | P01742 homo sapien |
| 11 | 388.5 | 57.8 | 137 | 1 HV11 MOUSE | P01755 mus musculus |
| 12 | 383 | 57.0 | 138 | 1 HV48 MOUSE | P03980 mus musculus |
| 13 | 378 | 56.2 | 125 | 1 HV1F HUMAN | P06326 homo sapien |
| 14 | 376 | 56.0 | 121 | 1 HV01 MOUSE | P01745 mus musculus |
| 15 | 372 | 55.4 | 117 | 1 HV52 MOUSE | P06327 mus musculus |
| 16 | 367.5 | 54.7 | 114 | 1 HV00 MOUSE | P01741 mus musculus |
| 17 | 365.5 | 54.4 | 120 | 1 HV1H HUMAN | P80421 homo sapien |
| 18 | 362 | 53.9 | 136 | 1 HV15 MOUSE | P01759 mus musculus |
| 19 | 354 | 52.7 | 117 | 1 HV09 MOUSE | P01753 mus musculus |
| 20 | 348 | 51.8 | 117 | 1 HV04 MOUSE | P01748 mus musculus |
| 21 | 347 | 51.6 | 117 | 1 HV06 MOUSE | P01750 mus musculus |
| 22 | 346 | 51.5 | 117 | 1 HV14 MOUSE | P01758 mus musculus |
| 23 | 342 | 50.9 | 117 | 1 HV49 MOUSE | P06328 mus musculus |
| 24 | 340.5 | 50.7 | 136 | 1 HV16 MOUSE | P01783 mus musculus |
| 25 | 338 | 50.3 | 117 | 1 HV10 MOUSE | P01754 mus musculus |
| 26 | 334.5 | 49.8 | 124 | 1 HV1D HUMAN | P01760 homo sapien |
| 27 | 334 | 49.7 | 117 | 1 HV05 MOUSE | P01749 mus musculus |
| 28 | 329.5 | 49.0 | 119 | 1 HV38 MOUSE | P01808 mus musculus |
| 29 | 329.5 | 48.4 | 114 | 1 HV3B HUMAN | P01763 homo sapien |
| 30 | 324.5 | 48.3 | 146 | 1 HV21 HUMAN | P06331 homo sapien |
| 31 | 324 | 48.2 | 121 | 1 HV31 HUMAN | P01771 homo sapien |
| 32 | 322.5 | 48.0 | 124 | 1 HV1E HUMAN | P01761 homo sapien |

34 320.5 47.7 122 1 HV3G HUMAN P01768 homo sapien
35 318 47.3 120 1 HV3E HUMAN P01766 homo sapien
36 318 47.3 142 1 HV01_EAT P01805 rattus norv
37 317.5 47.2 116 1 HV3T HUMAN P01781 homo sapien
38 317.5 47.2 126 1 HV3K HUMAN P01772 homo sapien
39 314.5 46.8 119 1 HV40 MOUSE P01810 mus musculus
40 313 46.6 115 1 HV3D HUMAN P01765 homo sapien
41 313 46.6 117 1 HV42 MOUSE P01812 mus musculus
42 313 46.6 119 1 HV3I HUMAN P01770 homo sapien
43 312.5 46.5 122 1 HV21_MOUSE P01790 mus musculus
44 312.5 46.5 122 1 HV3H HUMAN P01769 homo sapien
45 312 46.4 115 1 HV32_MOUSE P01801 mus musculus

ALIGNMENTS

RESULT 1
HV1C_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (In) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01789; MCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT DOMAIN 20 131 IG-LIKE.
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115 T -> V (IN REF. 2).
FT CONFLICT 21 21 IH -> HI (IN REF. 2).
FT CONFLICT 53 54 VG -> GV (IN REF. 2).
FT CONFLICT 67 68 MISSING (IN REF. 2).
FT CONFLICT 125 125
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 7.2e-42;

Matches 90; Conservative 16; Mismatches 19; Indels 3; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKASGYTFTSYDINVRQATGQGLEWMGNPNSGNTDY 60

```
Db 20 QTVLQSGAEVVRKPGASVVRKSGASGYTFIDSYIHWRQAPGHLEWVGWNPNSGGTNY 79
Qy 61 AQKFGQVMTTRDTSTSTAYMELSLRSDTAIYYCVRG--RGYSVNYDYVYGMVDVWGQ 117
Db 80 APKFGQVMTTRDTSTSTAYMELSLRSDTAIYYCVRG--RGYSVNYDYVYGMVDVWGQ 139
Qy 118 GTTVTVSS 125
Db 140 GTTVTVSS 147

RESULT 2
HV1G HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=2841108;
RX MEDLINE=86296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBO J. 7:1047-1051(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; J00240; AA52988.1; -
DR PIR; A02024; HVHUNG.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION H35.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC6CD1FE7 CRC64;

Query Match 65.6%; Score 441; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 3e-37;
Matches 84; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGINPNSGGTNY 79
Qy 61 AQKFGQVMTTRDTSTSTAYMELSLRSDTAIYYCVR 98
Db 80 AQKFGQVMTTRDTSTSTAYMELSLRSDTAIYYCVR 117

RESULT 3
HV1G HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=2841108;
RX MEDLINE=86296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBO J. 7:1047-1051(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07448; -; NOT ANNOTATED_CDS.
DR PIR; S00476; HVHJ35.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13009 MW; BB61CE63F8CE97BD CRC64;

Query Match 65.6%; Score 441; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 3e-37;
Matches 84; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGINPNSGGTNY 79
Qy 61 AQKFGQVMTTRDTSTSTAYMELSLRSDTAIYYCVR 98
Db 80 AQKFGQVMTTRDTSTSTAYMELSLRSDTAIYYCVR 117

RESULT 4
HV51 MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
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RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RL lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02040; MEMS38.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEB4C762A018 CRC64;

Query Match 62.3%; Score 418.5; DB 1; Length 118;
Best Local Similarity 63.2%; Pred. No. 5.4e-35;
Matches 79; Conservative 15; Mismatches 24; Indels 7; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWNPNSGNTDY 60
DB 1 EVQLQQSGPELVKPGASVKSCASGYTFTDYIMWVWKQSHGKSLWIGDINPNNGTGY 60
QY 61 AQKFGQRTVTRDTSISTAYMELSSLRSEDTAIYVCVRGFGSYNYDYVGMVWGQGT 120
DB 61 NQKFKGKATLTVDKSSATYMLRSLTSEDSAVYYCARGYGD-----PFDVWGTT 113
QY 121 VTSS 125
DB 114 VTSS 118

RESULT 5
HV12 MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02039; MEMS4E.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON TER 117

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SQ SEQUENCE 117 AA; 12983 MW; 3CFBACE4BE447E41 CRC64;

Query Match 61.6%; Score 414; DB 1; Length 117;
Best Local Similarity 63.2%; Pred. No. 1.5e-34;
Matches 79; Conservative 19; Mismatches 19; Indels 8; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWNPNSGNTDY 60
DB 1 EVQLQQSGPELVKPGASVKSCASGYTFTDYIMWVWKQSHGKSLWIGDINPNNGTGY 60
QY 61 AQKFGQRTVTRDTSISTAYMELSSLRSEDTAIYVCVRGFGSYNYDYVGMVWGQGT 120
DB 61 NQKFKGKATLTVDKSSATYMLRSLTSEDSAVYYCAR-----DYDWF--DVGAGTT 112
QY 121 VTSS 125
DB 113 VTSS 117

RESULT 6
HV03 MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131646; PubMed=6186498;
RA Siekevitz M., Geftex M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hydridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 61.5%; Score 413; DB 1; Length 120;
Best Local Similarity 62.7%; Pred. No. 1.9e-34;
Matches 79; Conservative 19; Mismatches 20; Indels 8; Gaps 2;

QY 2 VOLVQSGAEVKKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWNPNSGNTDYA 61
DB 1 VOLVQSGAEVKKPGASVKSCASGYTFTSYGINWVQKPGQGLEWIGYINPGNYTKYN 60
QY 62 QKFGQRTVTRDTSISTAYMELSSLRSEDTAIYVCVRG--FGSYNYDYVGMVWGQGT 119
DB 61 EKFGKATLTVDKSSATYMLRSLTSEDSAVYYGGSYYFDY-----WGQGT 114
QY 120 VTSS 125
DB 115 VTSS 120

RESULT 7

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HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6783376;
RA Bothwell A.L.M.; Paskind M.; Reth M.; Imanishi-Kari T.; Rajewsky K.;
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC -----
CC EMBL; J00529; AAA38170.1; -.
DR PIR; A90809; MHMS18.
DR PDB; 1A6U; 27-MAY-98.
DR PDB; 1A6W; 15-JUL-98.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 1541.9 MW; 1B57DD4FDC09F465 CRC64;

Query Match 60.8%; Score 408.5; DB 1; Length 139;
Best Local Similarity 63.0%; Pred. No. 6.4e-34;
Matches 80; Conservative 16; Mismatches 22; Indels 9; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSDYDINWVQATGQGLEWMGWINPNSGNTDY 60
DB 20 QVQLQPGAEVKKPGASVKLSCKASGYFTSDYDINWVQKQPGGLEWIGRIDPNSGGTKY 79
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSDETAIYCYVRGFGYSYNDYYG--MDVWQGG 118
DB 80 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYICAR-----YDYVGSFYDWQGG 132
QY 119 TTVTVSS 125
DB 133 TLTTVSS 139

RESULT 8
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```
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J.; Clevinger B.; Davie J.M.; Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MHMSJ5.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 60.7%; Score 408; DB 1; Length 117;
Best Local Similarity 62.4%; Pred. No. 5.9e-34;
Matches 78; Conservative 17; Mismatches 22; Indels 8; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSDYDINWVQATGQGLEWMGWINPNSGNTDY 60
DB 1 EVQLQSGGPELVKPGASVKMSCKASGYFTDYDMKWKVQSHGKSLGWIDINPNNGGTSY 60
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSDETAIYCYVRGFGYSYNDYYGMDVWQGGTT 120
DB 61 NQKFKSKATLTVDKSSSTAYMQLSLTSDSAVYICAR-----DRYWFYDWVGAGTT 112
QY 121 TTVVSS 125
DB 113 TTVVSS 117

RESULT 9
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J.; Rabbitts T.H.; Estess P.; Slaughter C.; Tucker P.W.;
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
```

```

RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL: J00493; AAA38128.1; --
DR PIR: A94264; HVMSG7.
DR HSSP: P01810; 2FSJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hyridoma; signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 60.7%; Score 408; DB 1; Length 140;
Best Local Similarity 60.8%; Pred. No. 7.3e-34;
Matches 76; Conservative 21; Mismatches 24; Indels 4; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGCGLEWGMWNPNSGNTDY 60
DB 20 EVQLQSGAEVLRAGSSVKKVSCKASGYTFTSYGINWVRQPGQGLEWIGYINPFGYNY 79
QY 61 AOKFGQVRVMTDRTSISTAYMELSSRLSEDTAIYVCVRGFGYSYNYDYGMVWGOGTT 120
DB 80 NEKFKSKATLTVDKSSATYMQLSPTSDSAVYFCARSHYVGGSYDP----DWVGQGT 135
QY 121 VTVSS 125
DB 136 LTVSS 140

RESULT 10
HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EWO J. 3:517-523(1984).
DR PIR: A02037; MEMS15.
DR HSSP: P01810; 2FBQ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT NON_TER 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.

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FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453P426F09834 CRC64;

Query Match 58.7%; Score 394.5; DB 1; Length 120;
Best Local Similarity 60.0%; Pred. No. 1.4e-32;
Matches 75; Conservative 20; Mismatches 25; Indels 5; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGCGLEWGMWNPNSGNTDY 60
DB 1 QVQLLPQGTETLVKPGASVNLKSKASGYTFTSYNMHWIRQPGQGLEWIGGINFSGNTNY 60
QY 61 AOKFGQVRVMTDRTSISTAYMELSSRLSEDTAIYVCVRGFGYSYNYDYGMVWGOGTT 120
DB 61 NEKFKSKATLTVDKSSATYMQLSPTSDSAVYFCAR---WDYEGDRYF--DWVGNTT 115
QY 121 VTVSS 125
DB 116 VTVSS 120

RESULT 11
HV1A_HUMAN STANDARD; PRT; 117 AA.
AC P01742;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A90563; G1HUEU.
DR HSSP: P01772; 2FB4.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding; NAS.
DR GO: GO:0008955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Pyrrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12472 MW; 99D60ADAEED52818 CRC64;

Query Match 58.0%; Score 390; DB 1; Length 117;
Best Local Similarity 67.2%; Pred. No. 3.7e-32;
Matches 84; Conservative 9; Mismatches 24; Indels 8; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGCGLEWGMWNPNSGNTDY 60

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Db 1 QVQLVQSGAEVKKPGSSVKVSCKASGFTFSRLIIVRQAPGQGLRWGIVPMFPPNY 60
Qy 61 AQKFGQVRVMTTRDTSISTAYMELSSLSRSEDTAIYVCVRGFGSYNYDYVGMVWGQGT 120
Db 61 AQKFGQVRVMTTRDTSISTAYMELSSLSRSEDTAIYVCVRGFGSYNYDYVGMVWGQGT 120
Qy 121 VTVSS 125
Db 113 VTVSS 117

RESULT 12
HV11 MOUSE
ID HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01753;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region S43 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00539; AAA38172.1; -
DR PIR; A02038; G2MS43.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 63 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF4B8EC9 CRC64;

Query Match 57.8%; Score 388.5; DB 1; Length 137;
Best Local Similarity 61.6%; Pred. No. 6.2e-32;
Matches 77; Conservative 15; Mismatches 26; Indels 7; Gaps 2;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLRWGIVPMNSGNTDY 60
Db 20 QVQLQPGAEVKKPGASVKLSCKASGYTFTSYLMEHWVNRQGRGLEWIGRIDPNSGTTY 79

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Qy 61 AQKFGQVRVMTTRDTSISTAYMELSSLSRSEDTAIYVCVRGFGSYNYDYVGMVWGQGT 120
Db 80 NEHFRSKATLIDKPSSTAYMQLSSLTSEDSAVTYCAR-----YRLGRYF--DYWGQGT 132
Qy 121 VTVSS 125
Db 133 VTVSS 137

RESULT 13
HV48 MOUSE
ID HV48 MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an Igd-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMS77.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 FRAMEWORK-4.
FT DOMAIN 128 138 BY SIMILARITY.
FT DISULFID 41 115
FT NON TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 57.0%; Score 383; DB 1; Length 138;
Best Local Similarity 59.2%; Pred. No. 2.2e-31;
Matches 74; Conservative 20; Mismatches 25; Indels 6; Gaps 2;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLRWGIVPMNSGNTDY 60
Db 20 QVQLQPGAEVKKPGASVKLSCKASGYTFTSYLMEHWVNRQGRGLEWIGRIDPNSGTY 79
Qy 61 AQKFGQVRVMTTRDTSISTAYMELSSLSRSEDTAIYVCVRGFGSYNYDYVGMVWGQGT 120
Db 80 NEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYICARSDGY---YDFV---YWGQGT 133
Qy 121 VTVSS 125
Db 134 VTVSS 138

RESULT 14
HV1F HUMAN
ID HV1F HUMAN STANDARD; PRT; 125 AA.
AC P06326;
DT 01-JAN-1988 (Rel. 06, Created)

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DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DI Ig heavy chain V-I region Mot.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86203277; PubMed=3084950;
RA Kojima M., Koide T., Odani S., Ono T.;
RT "Amino acid sequence of the variable region of heavy chain in
RI immunoglobulin (Mot) having unusual papain cleavage sites.";
RL Mol. Immunol. 23:169-174(1986).
DR PIR; A02025; HVHMO.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 107 D SEGMENT.
FT DOMAIN 108 125 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 125 125
SQ SEQUENCE 125 AA; 13579 MW; F4C4285D6DF0C8EA CRC64;

Query Match 56.2%; Score 378; DB 1; Length 125;
Best Local Similarity 58.4%; Pred. No. 6.3e-31;
Matches 73; Conservative 17; Mismatches 35; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGSSARLSCKVSGDDFNTYDIHWVRQAPGRGLEWMAVVPSPDRRTY 60

QY 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
DB 61 GPRQARPTVTRDSSTTVYMETALISADTAIYYCARGAHYSTDDSGTSLGPGWQGT 120

QY 121 VTVSS 125
DB 121 LIVSS 125

RESULT 15
HV01 MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RI region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -I- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
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CC FROM A MYELOMA THAT SECRETES IGG2B.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93708; GVM511.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 56.0%; Score 376; DB 1; Length 121;
Best Local Similarity 58.4%; Pred. No. 9.6e-31;
Matches 73; Conservative 19; Mismatches 29; Indels 4; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 EAQLQSGAEVLRPGTSVKISKAAGYFTNTYIGWVKRPGHGLEWIGDIYFGGGFTNY 60

QY 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
DB 61 NDNLKGATLTADTSSTAIYQLSLTSEDSAIYHCARGI---YINSSPYF---DSWGQGT 116

QY 121 VTVSS 125
DB 117 LIVSS 121

Search completed: April 21, 2004, 17:02:34
Job time : 26.2661 secs
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:28:28 ; Search time 19.2464 Seconds

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Title: SEQ3

Perfect score: 97

Sequence: 1 gfgysynydyvgmdv 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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2: /cgn2_6/ptodata/2/iaa/5B COMB.pdp.*

3: /cgn2_6/ptodata/2/iaa/6A COMB.pdp.*

4: /cgn2_6/ptodata/2/iaa/6B COMB.pdp.*

5: /cgn2_6/ptodata/2/iaa/PTCUT COMB.pdp.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
|------------|-------|-------|--------|--------------------|-------------------|
| 1 | 52 | 53.6 | 24 | US-09-142-732-4 | Sequence 4, Appli |
| 2 | 52 | 53.6 | 522 | US-09-142-732-2 | Sequence 2, Appli |
| 3 | 52 | 53.6 | 522 | US-08-945-826-2 | Sequence 2, Appli |
| 4 | 52 | 53.6 | 522 | US-09-197-503-2 | Sequence 2, Appli |
| 5 | 52 | 53.6 | 733 | US-09-328-352-5599 | Sequence 5599, Ap |
| 6 | 50.5 | 52.1 | 36 | US-08-053-131-84 | Sequence 84, Appl |
| 7 | 50.5 | 52.1 | 36 | US-08-645-641-84 | Sequence 84, Appl |
| 8 | 50.5 | 52.1 | 36 | US-07-853-408B-84 | Sequence 84, Appl |
| 9 | 50.5 | 52.1 | 36 | US-08-095-762-84 | Sequence 84, Appl |
| 10 | 50.5 | 52.1 | 36 | US-08-308-865-84 | Sequence 84, Appl |
| 11 | 50.5 | 52.1 | 36 | US-09-042-353-281 | Sequence 129, App |
| 12 | 50.5 | 52.1 | 36 | US-08-758-417A-129 | Sequence 129, App |
| 13 | 50.5 | 52.1 | 36 | PCT-US92-10983-84 | Sequence 84, Appl |
| 14 | 48 | 49.5 | 126 | US-08-983-607-48 | Sequence 48, Appl |
| 15 | 48 | 49.5 | 287 | US-08-862-124-17 | Sequence 17, Appl |
| 16 | 48 | 49.5 | 304 | US-08-862-124-14 | Sequence 14, Appl |
| 17 | 48 | 49.5 | 521 | US-08-945-826-4 | Sequence 4, Appli |
| 18 | 48 | 49.5 | 521 | US-09-197-503-4 | Sequence 4, Appli |
| 19 | 47.5 | 49.0 | 123 | US-08-652-816A-1 | Sequence 1, Appli |
| 20 | 47.5 | 49.0 | 123 | US-08-652-816A-6 | Sequence 6, Appli |
| 21 | 47.5 | 49.0 | 236 | US-09-456-090A-64 | Sequence 64, Appl |
| 22 | 47.5 | 49.0 | 236 | US-09-456-090A-104 | Sequence 104, App |
| 23 | 46 | 47.4 | 29 | US-08-053-131-73 | Sequence 73, Appl |
| 24 | 46 | 47.4 | 29 | US-08-645-641-73 | Sequence 73, Appl |
| 25 | 46 | 47.4 | 29 | US-07-853-408B-73 | Sequence 73, Appl |
| 26 | 46 | 47.4 | 29 | US-08-096-762-73 | Sequence 73, Appl |
| 27 | 46 | 47.4 | 29 | US-08-308-865-73 | Sequence 73, Appl |

Sequence 270, App
Sequence 118, App
Sequence 73, Appl
Sequence 80, Appl
Sequence 70, Appl
Sequence 282, App
Sequence 25, Appl
Sequence 26, Appl
Sequence 153, App
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 3, Appl
Sequence 96, Appl
Sequence 96, Appl
Sequence 34, Appl
Sequence 6014, App
Sequence 5, Appli

28 46 47.4 29 3 US-09-042-353-270
29 46 47.4 29 4 US-08-758-417A-118
30 46 47.4 29 5 PCT-US92-10983-73
31 46 47.4 167 4 US-09-472-087-80
32 46 47.4 451 4 US-09-472-087-70
33 46 47.4 633 4 US-09-976-594-282
34 45.5 46.9 126 3 US-09-240-274-45
35 45.5 46.9 126 3 US-09-240-274-153
36 45.5 46.9 126 3 US-09-004-139B-35
37 45 46.4 23 1 US-08-811-492-35
38 45 46.4 23 2 PCT-US96-10545A-35
39 45 46.4 23 5 US-08-082-623-3
40 45 46.4 123 1 US-08-478-039-96
41 45 46.4 128 1 US-08-478-039-96
42 45 46.4 391 4 US-09-721-870-34
43 45 46.4 408 4 US-09-328-352-6014
44 45 46.4 1326 4 US-09-147-236-5
45 44.5 45.9

ALIGNMENTS

RESULT 1

US-09-142-732-4
; Sequence 4, Application US/09142732
; Patent No. 6252045
; GENERAL INFORMATION:
; APPLICANT: James M. Anderson
; APPLICANT: Christina M. Van Itallie
; TITLE OF INVENTION: Human Occludin, Its Uses and
; TITLE OF INVENTION: Enhancement of Drug Absorption Using Occludin Inhibitors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Yale University Medical School
; ADDRESSEE: Section of Digestive Diseases
; ADDRESSEE: Department of Internal Medicine
; STREET: 333 Cedar Street, LCI 105
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8057
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/142,732
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/05909
; FILING DATE: March 14, 1997
; APPLICATION NUMBER: U.S. 60/013,625
; FILING DATE: March 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: 1751-P0016B.PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-324-6155
; TELEFAX: 203-327-1096
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: synthetic peptide
; FEATURE:

OTHER INFORMATION: construct used in experi-
OTHER INFORMATION: ments
US-09-142-732-4

Query Match 53.6%; Score 52; DB 3; Length 24;
Best Local Similarity 61.5%; Pred. No. 0.3;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 13
|:|:|:|:|:|
Db 6 GVGYGYGYG 18

RESULT 2

US-09-142-732-2
; Sequence 2, Application US/09142732
; Patent No. 6252045
; GENERAL INFORMATION:
; APPLICANT: James M. Anderson
; APPLICANT: Christina M. Van Itallie
; TITLE OF INVENTION: Human Occludin, Its Uses and
; TITLE OF INVENTION: Enhancement of Drug Absorption Using Occludin Inhibitors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yale University Medical School
; ADDRESSEE: Section of Digestive Diseases
; ADDRESSEE: Department of Internal Medicine
; STREET: 333 Cedar Street, LCI 105
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8057
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/142,732
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US97/05809
; APPLICATION NUMBER: PCT/US97/05809
; FILING DATE: March 14, 1997
; APPLICATION NUMBER: U.S. 60/013,625
; FILING DATE: March 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: 1751-P0016B.PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-324-6155
; TELEFAX: 203-327-1096
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 522
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; FRAGMENT TYPE: complete sequence
; FEATURE:
; NAME/KEY: human occludin
; US-09-142-732-2

Query Match 53.6%; Score 52; DB 3; Length 522;
Best Local Similarity 61.5%; Pred. No. 7.9;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 13
|:|:|:|:|:|
Db 117 GVGYGYGYG 129

RESULT 3

US-08-945-826-2
; Sequence 2, Application US/08945826
; Patent No. 6489460
; GENERAL INFORMATION:
; APPLICANT: TSUKITA, Shoichiro
; TITLE OF INVENTION: HUMAN ADHESION MOLECULE OCCLUDIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/945,826
; APPLICATION NUMBER: US/08/945,826
; FILING DATE: 05-NOV-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: PARACI, C. Joseph
; REGISTRATION NUMBER: 32,350
; REFERENCE/DOCKET NUMBER: 0425-0660P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 522 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-945-826-2

Query Match 53.6%; Score 52; DB 4; Length 522;
Best Local Similarity 61.5%; Pred. No. 7.9;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 13
|:|:|:|:|:|
Db 117 GVGYGYGYG 129

RESULT 4

US-09-197-503-2
; Sequence 2, Application US/09197503
; Patent No. 6559286
; GENERAL INFORMATION:
; APPLICANT: TSUKITA, Shoichiro
; TITLE OF INVENTION: HUMAN ADHESION MOLECULE OCCLUDIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,503
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/945,826
; FILING DATE: 05-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: FARACI, C. Joseph
; REGISTRATION NUMBER: 32,350
; REFERENCE/DOCKET NUMBER: 0425-0660P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 522 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-197-503-2

Query Match      53.6%; Score 52; DB 4; Length 522;
Best Local Similarity 61.5%; Pred. No. 7,9;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 GFGYSNYDYGG 13
Db      117 GYGVGYGYG 129

RESULT 5
US-09-328-352-5599
; Sequence 5599, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5599
; LENGTH: 733
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-5599

Query Match      53.6%; Score 52; DB 4; Length 733;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 GFGYSNYDYGG 12
Db      716 GYGVGYNAYAY 727

RESULT 6
US-08-053-131-84
; Sequence 84, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-053-131-84

Query Match      52.1%; Score 50.5; DB 1; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY      5 SYNDYYGMDV 16
Db      11 SYDY-YYGMDV 21

RESULT 7
US-08-645-641-84
; Sequence 84, Application US/08645641
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,641
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.

```

REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-000913
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-645-641-84

Query Match 52.1%; Score 50.5; DB 1; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 5 SYNDYYGMDV 16
||:|||||
Db 11 SYDY-YYGMDV 21

RESULT 8
US-07-853-408B-84
Sequence 84, Application US/07853408B
Patent No. 5789650
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,408B
FILING DATE: 19920318
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-853-408B-84

Query Match 52.1%; Score 50.5; DB 1; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 5 SYNDYYGMDV 16
||:|||||
Db 11 SYDY-YYGMDV 21

RESULT 9
US-08-096-762-84
Sequence 84, Application US/08096762
Patent No. 5814318
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-096-762-84

Query Match 52.1%; Score 50.5; DB 2; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 5 SYNDYYGMDV 16
||:|||||
Db 11 SYDY-YYGMDV 21

RESULT 10
US-08-308-865-84
Sequence 84, Application US/08308865
Patent No. 5877397
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils

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; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
;   Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,865
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,707
; FILING DATE:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-308-865-84

Query Match 52.1%; Score 50.5; DB 2; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 5 SYNDYYGMDV 16
DB 11 SYDY-YYGMDV 21

RESULT 11
US-09-042-353-281
; Sequence 281, Application US/09042353
; Patent No. 6255456
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; ADDRESSEE: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
;   Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16433
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,417
; FILING DATE: 02-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/21803
; FILING DATE: 01-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 014643-009040US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 281:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-042-353-281

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Query Match 52.1%; Score 50.5; DB 3; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

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QY 5 SYNDYYGMDV 16
||:|||||

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Db 11 SYDY-YYYGMDV 21

RESULT 12
US-08-758-417A-129
; Sequence 129, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,417A
; FILING DATE: 02-Dec-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Serafini, Andrew T.
; REGISTRATION NUMBER: 41,303
; REFERENCE/DOCKET NUMBER: 014643-009030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-08-758-417A-129
Query Match 52.1%; Score 50.5; DB 4; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Oy 5 SYNDY-YYYGMDV 16
||| |||||

Db 11 SYDY-YYYGMDV 21

RESULT 13
PCT-US92-10983-84
; Sequence 84, Application PC/TUS9210983
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic Non-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10983
; FILING DATE: 19921217
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US92-10983-84
Query Match 52.1%; Score 50.5; DB 5; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Oy 5 SYNDY-YYYGMDV 16
||| |||||

Db 11 SYDY-YYYGMDV 21

RESULT 14
US-08-983-607-48
; Sequence 48, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette

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;
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient)
; ORGANISM: immunized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lympho-
; INDIVIDUAL ISOLATE: cytes
; IMMEDIATE SOURCE:
; LIBRARY: VH antibodies obtained from FUSE5
; LIBRARY: fusion phage construct
; CLONE: P2
; FEATURE:
; NAME/KEY: heavy chain
;
US-08-983-607-48
;
Query Match 49.5%; Score 48; DB 3; Length 126;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DYVYGMVDV 16
Db 108 DYVYGMVDV 115

RESULT 15
US-08-862-124-17
; Sequence 17, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maiti, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,124
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-862-124-17
;
Query Match 49.5%; Score 48; DB 3; Length 287;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 NYDYYVGMVDV 16
Db 247 DYDHYVGLDV 256

Search completed: April 21, 2004, 17:40:04
Job time : 20.2464 secs
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:27:33 ; Search time 14.6087 Seconds
(without alignments)
105.353 Million cell updates/sec

Title: SEQ3

Perfect score: 97

Sequence: 1 gfgysynydyvgmdv 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 61 | 62.9 | 116 | 2 S37456 | Ig mu chain - huma |
| 2 | 58 | 59.8 | 205 | 2 P87623 | hypothetical prote |
| 3 | 55.5 | 57.2 | 19 | 2 PH1304 | Ig heavy chain DJ |
| 4 | 55 | 56.7 | 825 | 2 S64783 | probable membrane |
| 5 | 54.5 | 56.2 | 19 | 2 PH1307 | Ig heavy chain DJ |
| 6 | 53 | 54.6 | 45 | 2 PH0094 | Ig heavy chain V r |
| 7 | 52.5 | 54.1 | 132 | 2 PH0954 | Ig heavy chain V r |
| 8 | 52 | 53.6 | 522 | 2 G02533 | Occludin - human |
| 9 | 51 | 52.6 | 726 | 2 T44825 | hypothetical prote |
| 10 | 50.5 | 52.1 | 125 | 2 S24686 | Ig heavy chain V6 |
| 11 | 50 | 51.5 | 110 | 2 PH1655 | Ig heavy chain V r |
| 12 | 49.5 | 51.0 | 29 | 2 PH1328 | Ig heavy chain DJ |
| 13 | 49 | 50.5 | 153 | 2 S31689 | Ig heavy chain V r |
| 14 | 49 | 50.5 | 1044 | 2 H37186 | glycosyltransferas |
| 15 | 48.5 | 50.0 | 128 | 2 S48797 | Ig heavy chain V r |
| 16 | 48.5 | 50.0 | 131 | 2 S26792 | Ig heavy chain V r |
| 17 | 48 | 49.5 | 24 | 2 P70258 | Ig heavy chain CDR |
| 18 | 48 | 49.5 | 97 | 2 S24252 | Ig heavy chain V r |
| 19 | 48 | 49.5 | 121 | 2 S31106 | Ig heavy chain - h |
| 20 | 48 | 49.5 | 146 | 1 PH1HJ2 | Ig heavy chain DJ |
| 21 | 47.5 | 49.0 | 23 | 2 PH1361 | Ig heavy chain DJ |
| 22 | 47.5 | 49.0 | 105 | 2 H81723 | hypothetical prote |
| 23 | 47 | 48.5 | 23 | 2 PH1364 | Ig heavy chain DJ |
| 24 | 47 | 48.5 | 70 | 2 C83831 | hypothetical prote |
| 25 | 47 | 48.5 | 345 | 2 S23862 | hypothetical prote |
| 26 | 47 | 48.5 | 504 | 2 A49467 | occludin - chicken |
| 27 | 47 | 48.5 | 719 | 2 S63392 | probable membrane |
| 28 | 47 | 48.5 | 1048 | 2 H64459 | hypothetical prote |
| 29 | 46.5 | 47.9 | 45 | 2 S20776 | Ig heavy chain V r |

| | | | | | |
|----|------|------|-----|----------|--------------------|
| 30 | 46 | 47.4 | 119 | 2 E25114 | Ig heavy chain V r |
| 31 | 46 | 47.4 | 119 | 2 PH0961 | Ig heavy chain V r |
| 32 | 46 | 47.4 | 127 | 2 PH0955 | Ig heavy chain V r |
| 33 | 46 | 47.4 | 132 | 2 AB1125 | hypothetical prote |
| 34 | 46 | 47.4 | 201 | 2 S37847 | hypothetical prote |
| 35 | 46 | 47.4 | 210 | 2 C87305 | hypothetical prote |
| 36 | 46 | 47.4 | 483 | 2 E90159 | hypothetical prote |
| 37 | 46 | 47.4 | 633 | 2 T02673 | heterogeneous nucl |
| 38 | 45.5 | 46.9 | 27 | 2 PH1355 | Ig heavy chain DJ |
| 39 | 45.5 | 46.9 | 27 | 2 PH1371 | Ig heavy chain DJ |
| 40 | 45.5 | 46.9 | 113 | 2 S30515 | wound-induced prot |
| 41 | 45.5 | 46.9 | 136 | 2 PH0960 | Ig heavy chain V r |
| 42 | 45 | 46.4 | 69 | 2 A64961 | outer membrane por |
| 43 | 45 | 46.4 | 120 | 2 PH1650 | Ig heavy chain V r |
| 44 | 45 | 46.4 | 122 | 2 T05357 | ubiquinol-cytochro |
| 45 | 45 | 46.4 | 136 | 2 A49047 | Ig heavy chain V r |

ALIGNMENTS

RESULT 1

S37456
Ig mu chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37456
R:McIntosh, R.S.; Tandon, N.; Weetman, A.P.
Submitted to the EMBL Data Library, September 1993
A:Description: Cloning and analysis of human IGM anti-Thyroglobulin autoantibodies from I
A:Reference number: S37453
A:Accession: S37456
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <MC>
A:Cross-references: EMBL:X75024; NID:G404313; PIDN:CAA52932.1; PID:G758095
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:6-90/Domain: immunoglobulin homology <IMV>

Query Match 62.9%; Score 61; DB 2; Length 116;
Best Local Similarity 78.6%; Pred. No. 0.098; Mismatches 0; Gaps 0;
Matches 11; Conservative 0; Indels 3; Indels 0; Gaps 0;

| | | | |
|----|----|--------------|-----|
| QY | 3 | GYSYNYDYVYGM | 16 |
| DB | 92 | GYSYNYDYVYGM | 105 |

RESULT 2

P87623
hypothetical protein CC3024 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: F87623
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173696; PMID:11259647
A:Accession: F87623
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-205 <STO>
A:Cross-references: GB:AE005673; NID:G1342464; PIDN:AAK24986.1; GSPDB:GN00148
C:Genetics: CC3024

Query Match 59.8%; Score 58; DB 2; Length 205;
Best Local Similarity 58.8%; Pred. No. 0.46; Mismatches 2; Indels 1; Gaps 1;
Matches 10; Conservative 1; Indels 4; Gaps 1;

QY 1 GFGSYNYDY-----YVG 13
 DB 165 GYGVDYDYAPRPYTG 181

RESULT 3

PH1304
 Ig heavy chain DJ region (clone C439-111) - human (fragment)

C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

R/Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A/Reference number: PH1302; MUID:93094761; PMID:1460419

A/Accession: PH1304

A/Molecule type: DNA

A/Residues: 1-19 <WAS>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 57.2%; Score 55.5; DB 2; Length 19;

Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 GYSYNDYDYGGMDV 16

DB 2 GYFYDYDYGGMDV 14

RESULT 4

S64783

probable membrane protein YL032C - Yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein L0926

C/Species: Saccharomyces cerevisiae

C/Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002

R/Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.

submitted to the Protein Sequence Database, May 1996

A/Reference number: S64775

A/Accession: S64783

A/Molecule type: DNA

A/Residues: 1-825 <DUE>

A/Cross-references: EMBL:Z73137; NID:G1360217; PID:e245752; PID:G1360218; GSPDB:GN00012;

A/Experimental source: strain S288C

C/Genetics:

A/Gene: MIPS:YL032C

A/Cross-references: SGD:S0003955

A/Map position: 12L

C/Keywords: transmembrane protein

F/660-676/Domain: transmembrane #status predicted <TMM>

Query Match

Best Local Similarity 56.7%; Score 55; DB 2; Length 825;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGSYNYDYDY 12

DB 795 GYGTYDYDYNY 806

RESULT 5

PH1307

Ig heavy chain DJ region (clone C96-119) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

R/Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A/Reference number: PH1302; MUID:93094761; PMID:1460419

A/Accession: PH1307

A/Molecule type: DNA

A/Residues: 1-19 <WAS>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 56.2%; Score 54.5; DB 2; Length 19;

Matches 11; Conservative 0; Mismatches 3; Indels 1;

QY 3 GYSYNDYDYGGMDV 16

DB 4 GYSY---YYGGMDV 14

RESULT 6

PH0094

Ig heavy chain V region (6C4) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 30-May-1997

R/Meek, K.; Hagemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Cai

J. Exp. Med. 169, 519-533, 1989

A/Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are

A/Reference number: PH0080; MUID:89094248; PMID:2492056

A/Accession: PH0094

A/Molecule type: mRNA

A/Residues: 1-45 <MEB>

A/Note: the authors translated the codons AGC and AGU for residues 6 and 7 as Asp

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 54.6%; Score 53; DB 2; Length 45;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SYNDYDYGGMD 15

DB 23 SYGYDYGGMD 33

RESULT 7

PH0954

Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

R/Martin, I.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0952; MUID:92202880; PMID:1552291

A/Accession: PH0954

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-132 <MAR>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-30/Region: framework 1

F/15-98/Domain: immunoglobulin homology <IMM>

F/31-35/Region: complementarity-determining 1

F/36-50/Region: framework 2

F/51-67/Region: complementarity-determining 2

F/68-98/Region: framework 3

F/99-120/Region: complementarity-determining 3

Query Match

Best Local Similarity 54.1%; Score 52.5; DB 2; Length 132;

Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 GYSYNDYDYGGMDV 16

DB 109 GYFNY-YYGGMDV 121

```

RESULT 8
G02533
C:occludin - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 29-Sep-1999
C:Accession: G02533
R:Van Itallie, C.M.
submitted to the EMBL Data Library, April 1996
A:Reference number: H01403
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: G02533
A:Molecule type: mRNA
A:Residues: 1-522 <VAN>
A:Cross-references: EMBL:U53823; NID:g1322281; PIDN:AAB00195.1; PID:g1322282
C:Superfamily: occludin

Query Match      53.6%; Score 52; DB 2; Length 522;
Best Local Similarity 61.5%; Pred. No. 8.4;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GFGYSYNDYYG 13
Db 117 GYGYGYGYG 129

RESULT 9
T44825
Hypothetical protein wzc [imported] - Acinetobacter lwoffii
N:Alternate names: protein tyrosine kinase
C:Species: Acinetobacter lwoffii
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T44825
R:Nakar, D.; Gutnick, D.L.
submitted to the EMBL Data Library, July 1999
A:Description: Genomic organization of the wzc region of Acinetobacter lwoffii RAG-1 re
A:Reference number: Z22856
A:Accession: T44825
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-726 <NA>
A:Cross-references: EMBL:AJ243431; PIDN:CAB57193.1
A:Experimental source: strain RAG-1
C:Genetics:
A:Gene: wzc

Query Match      52.6%; Score 51; DB 2; Length 726;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GFGYSYNDYYG 12
Db 709 GAGYSYNAYAY 720

RESULT 10
S24686
Ig heavy chain V6 region - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S24686
R:van Es, J.H.
submitted to the EMBL Data Library, July 1992
A:Reference number: S24679
A:Accession: S24686
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-125 <VAN>
A:Cross-references: EMBL:X67880; NID:g37749; PIDN:CAA48079.1; PID:g37750
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-101/Domain: immunoglobulin homology <IMM>

Query Match      52.1%; Score 50.5; DB 2; Length 125;

```

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Best Local Similarity 71.4%; Pred. No. 3.1;
Matches 10; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 3 GYSYNDYYGMDV 16
Db 104 GYDY---YYGMDV 114

RESULT 11
PH1655
Ig heavy chain V region (clone 228) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1655
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1655
A:Molecule type: mRNA
A:Residues: 1-110 <HIL>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match      51.5%; Score 50; DB 2; Length 110;
Best Local Similarity 69.2%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 YSYNDYYGMDV 16
Db 87 YCAREDYYGMDV 99

RESULT 12
PH1328
Ig heavy chain DJ region (clone C113-148) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1328
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1328
A:Molecule type: DNA
A:Residues: 1-29 <WAS>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      51.0%; Score 49.5; DB 2; Length 29;
Best Local Similarity 71.4%; Pred. No. 0.92;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 3 GYSYNDYYGMDV 16
Db 12 GSCISY-YYGMDV 24

RESULT 13
S31689
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S31689
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31689
A:Status: preliminary
A:Molecule type: mRNA

```

A;Residues: 1-153 <CUI>
A;Cross-references: EMBL:Z14187; NID:G31041; PIDN:CAA78556.1; PID:G31042
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-121/Domain: immunoglobulin homology <IMM>

Query Match 50.5%; Score 49; DB 2; Length 153;
Best Local Similarity 56.2%; Pred. No. 6.1;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYGMDV 16
Db 127 GIAVAGTSDYYIGMDV 142

RESULT 14
H97186
glycosyltransferase domain containing protein [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: H97186
R;Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97186
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1044 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK0283.1; PID:G15025335; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2327

Query Match 50.5%; Score 49; DB 2; Length 1044;
Best Local Similarity 64.3%; Pred. No. 45;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 GYSYNDYYGMDV 16
Db 143 GYGQXD--YGMDI 154

RESULT 15
S48797
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C;Accession: S48797; S26893
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S48797
A;Molecule type: mRNA
A;Residues: 1-128 <MAH>
A;Cross-references: EMBL:Z46379; NID:G587147; PIDN:CAA86512.1; PID:G1340168
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V regions
A;Reference number: S26885; MUID:33021117; PMID:1404388
A;Accession: S26893
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12350; NID:G32922; PIDN:CAA78220.1; PID:G32923
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 50.0%; Score 48.5; DB 2; Length 128;
Best Local Similarity 71.4%; Pred. No. 5.9;
Matches 10; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 3 GYSYNDYYGMDV 16
Db 107 GYY---YYGMDV 117

Search completed: April 21, 2004, 17:38:28
Job time : 15.6087 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:27:33 ; Search time 10.9565 Seconds
(without alignments)
105.353 Million cell updates/sec

Title: SEQ4
Perfect score: 53
Sequence: 1 rasqsvsssyia 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 53 | 100.0 | 83 | 2 | I30607 |
| 2 | 53 | 100.0 | 87 | 2 | I16823 |
| 3 | 53 | 100.0 | 89 | 2 | S34096 |
| 4 | 53 | 100.0 | 91 | 2 | S37520 |
| 5 | 53 | 100.0 | 91 | 2 | S67940 |
| 6 | 53 | 100.0 | 92 | 2 | S37513 |
| 7 | 53 | 100.0 | 92 | 2 | S37519 |
| 8 | 53 | 100.0 | 92 | 2 | S37517 |
| 9 | 53 | 100.0 | 92 | 2 | S37514 |
| 10 | 53 | 100.0 | 92 | 2 | S37518 |
| 11 | 53 | 100.0 | 93 | 2 | S37526 |
| 12 | 53 | 100.0 | 93 | 2 | S37528 |
| 13 | 53 | 100.0 | 96 | 2 | A30601 |
| 14 | 53 | 100.0 | 100 | 1 | K3HUNG |
| 15 | 53 | 100.0 | 104 | 2 | PH0964 |
| 16 | 53 | 100.0 | 107 | 2 | PH0965 |
| 17 | 53 | 100.0 | 108 | 2 | C30608 |
| 18 | 53 | 100.0 | 108 | 2 | H41451 |
| 19 | 53 | 100.0 | 109 | 2 | PH0963 |
| 20 | 53 | 100.0 | 109 | 2 | B30601 |
| 21 | 53 | 100.0 | 109 | 2 | A30608 |
| 22 | 53 | 100.0 | 109 | 2 | D30601 |
| 23 | 53 | 100.0 | 109 | 2 | F30607 |
| 24 | 53 | 100.0 | 109 | 2 | C30601 |
| 25 | 53 | 100.0 | 109 | 2 | H30601 |
| 26 | 53 | 100.0 | 116 | 2 | B27594 |
| 27 | 53 | 100.0 | 121 | 2 | S40327 |
| 28 | 53 | 100.0 | 129 | 1 | K3HUHA |
| 29 | 53 | 100.0 | 129 | 1 | K3HUHI |

| | | | | | | |
|----|----|-------|-----|---|--------|--------------------|
| 30 | 53 | 100.0 | 129 | 2 | S46369 | IG light chain var |
| 31 | 53 | 100.0 | 134 | 2 | S38643 | IG kappa chain V r |
| 32 | 52 | 98.1 | 114 | 2 | S46375 | IG kappa chain V-J |
| 33 | 50 | 94.3 | 47 | 2 | B30607 | IG kappa chain V-I |
| 34 | 50 | 94.3 | 62 | 2 | I30601 | IG kappa chain V-I |
| 35 | 50 | 94.3 | 92 | 2 | S37510 | IG kappa chain V r |
| 36 | 50 | 94.3 | 96 | 2 | S45441 | IG kappa chain V r |
| 37 | 50 | 94.3 | 109 | 1 | K3HUSI | IG kappa chain V-I |
| 38 | 50 | 94.3 | 116 | 2 | C27594 | IG kappa chain pre |
| 39 | 50 | 94.3 | 116 | 2 | S41817 | IG kappa chain V r |
| 40 | 50 | 94.3 | 119 | 2 | S41816 | IG kappa chain V r |
| 41 | 49 | 92.5 | 87 | 2 | S16843 | IG kappa chain V r |
| 42 | 49 | 92.5 | 92 | 2 | S37524 | IG kappa chain V r |
| 43 | 49 | 92.5 | 93 | 2 | S37508 | IG kappa chain V r |
| 44 | 49 | 92.5 | 109 | 1 | K3HUPM | IG kappa chain V-I |
| 45 | 49 | 92.5 | 110 | 2 | S44120 | IG kappa chain V-J |

ALIGNMENTS

RESULT 1

I30607
IG kappa chain V-III region (Wei) - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-May-1997
C;Accession: I30607
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solor
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantib
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: I30607
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-83 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 2

S16823
IG kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16823
R;Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(Kappa)III variable regions of polyclonal rheumatoid fac
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16823
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-87 <BLA>
C;Cross-references: EMBL:X54821
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;7-82/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 53; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 15 RASQSVSSSYLA 26

RESULT 3

S34096
Ig kappa chain V region - human

C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34096

R;Wagner, S.D.; Luzzatto, L.

Eur. J. Immunol. 23, 391-397, 1993

A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed

A:Reference number: S34076; MUID:93170387; PMID:8436174

A:Accession: S34096

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-89 <WAG>

A:Cross-references: EMBL:X67180

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:9-84/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 53; DB 2; Length 89;

Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12

|||||

Db 17 RASQSVSSSYLA 28

RESULT 4

S37520
Ig kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

R;Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37501

A:Accession: S37520

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-91 <KLE>

A:Cross-references: EMBL:Z26612; NID:g405682; PIDN:CAA81365.1; PID:g405693

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 91;

Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12

|||||

Db 7 RASQSVSSSYLA 18

RESULT 5

S67940
Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998

C:Accession: S67940

R;Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.

Autoimmunity 12, 135-141, 1992

A:Title: Cloning of a human autoimmune response: preparation and sequencing of a human

A:Reference number: S67940; MUID:92314301; PMID:1617110

A:Accession: S67940

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-91 <HEX>

A:Cross-references: EMBL:X73852

C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 100.0%; Score 53; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12

|||||

Db 5 RASQSVSSSYLA 16

RESULT 6

S37513
Ig kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37513

R;Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37513

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-references: EMBL:Z26598; NID:g405668; PIDN:CAA81362.1; PID:g405669

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 0.0016;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12

|||||

Db 7 RASQSVSSSYLA 18

RESULT 7

S37519
Ig kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37519

R;Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37519

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-references: EMBL:Z26613; NID:g405680; PIDN:CAA81366.1; PID:g405681

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 0.0016;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12

|||||

Db 7 RASQSVSSSYLA 18

RESULT 8

S37517
Ig kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37517

R;Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501
 A:Accession: S37517
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-92 <KLE>

A:Cross-references: EMBL:Z26615; NID:g405676; PIDN:CAA81368.1; PID:g405677
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 DB 7 RASQSVSSSYLA 18

RESULT 9

S37514

IG kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S37514

R:Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37501

A:Accession: S37514

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-references: EMBL:Z26597; NID:g405670; PIDN:CAA81351.1; PID:g405671

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 DB 7 RASQSVSSSYLA 18

RESULT 10

S37518

IG kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S37518

R:Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37501

A:Accession: S37518

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-references: EMBL:Z26614; NID:g405678; PIDN:CAA81367.1; PID:g405679

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 DB 7 RASQSVSSSYLA 18

RESULT 11

S37526

IG kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
 C:Accession: S37526

R:Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37501

A:Accession: S37526

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-93 <KLE>

A:Cross-references: EMBL:Z26618; NID:g405694; PIDN:CAA81371.1; PID:g405695

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 DB 7 RASQSVSSSYLA 18

RESULT 12

S37528

IG kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S37528

R:Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37528

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-93 <KLE>

A:Cross-references: EMBL:Z26616; NID:g405698; PIDN:CAA81369.1; PID:g405699

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 DB 7 RASQSVSSSYLA 18

RESULT 13

A30601

IG kappa chain V-III region (KV325) - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C:Accession: A30601

R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soli

J. Immunol. 142, 3158-3163, 1989

A:Title: Structural and idiotypic characterization of the L chains of human IGM autoant:

A:Reference number: A30601; MUID:89215279; PMID:2496160

A:Accession: A30601

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-96 <GON>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 53; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.0016;

Thu Apr 22 05:59:17 2004

seq4.open.rpr

Db 22 RASQSVSSSYLA 33

Search completed: April 21, 2004, 17:38:28
Job time : 10.9565 secs

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 14

K3HUNG
Ig kappa chain precursor V-III region (NG9) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 21-Jan-2000
C:Accession: A01894
R:Bentley, D.L.
Nature 307, 77-80, 1984
A:Title: Most kappa immunoglobulin mRNA in human lymphocytes is homologous to a small fa
A:Reference number: A01894; PMID:84093600; PMID:6419127
A:Accession: A01894
A:Molecule type: DNA
A:Residues: 1-100 <BEN>
A:Note: the sequence was determined from the germline gene
C:Comment: This gene was isolated from the NG9/9.1 hybridoma.
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; hybridoma; immunoglobulin
F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F:5-100/Product: Ig kappa chain V-III region (NG9) #status predicted <MAT>
F:20-95/Domain: immunoglobulin homology <IMM>
F:27-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 53; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 28 RASQSVSSSYLA 39

RESULT 15

PH0964
Ig kappa chain V region (G6+ CLL-SIC) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C:Accession: PH0964
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; PMID:9220280; PMID:1552291
A:Accession: PH0964
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-104 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-21/Region: framework 1
F:14-89/Domain: immunoglobulin homology <IMM>
F:22-32/Region: complementarity-determining 1
F:33-48/Region: framework 2
F:49-54/Region: complementarity-determining 2
F:55-87/Region: framework 3
F:88-92/Region: complementarity-determining 3

Query Match 100.0%; Score 53; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:48 ; Search time 6.08696 Seconds

(without alignments)
102.653 Million cell updates/sec

Title: SEQ4

Perfect score: 53

Sequence: 1 rasqsvssyla 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 53 | 100.0 | 100 | 1 KV3C_HUMAN | P01621 homo sapien |
| 2 | 53 | 100.0 | 129 | 1 KV3L_HUMAN | P18135 homo sapien |
| 3 | 53 | 100.0 | 129 | 1 KV3M_HUMAN | P18136 homo sapien |
| 4 | 50 | 94.3 | 109 | 1 KV3B_HUMAN | P01620 homo sapien |
| 5 | 49 | 92.5 | 109 | 1 KV3F_HUMAN | P01624 homo sapien |
| 6 | 49 | 92.5 | 116 | 1 KV3J_HUMAN | P04434 homo sapien |
| 7 | 46 | 86.8 | 109 | 1 KV3D_HUMAN | P01622 homo sapien |
| 8 | 45 | 84.9 | 109 | 1 KV3E_HUMAN | P01623 homo sapien |
| 9 | 43 | 81.1 | 108 | 1 KV3A_HUMAN | P01619 homo sapien |
| 10 | 39 | 73.6 | 129 | 1 KV4A_MOUSE | P01680 mus musculu |
| 11 | 38.5 | 72.6 | 115 | 1 KV3I_HUMAN | P04433 homo sapien |
| 12 | 38 | 71.7 | 447 | 1 G6PI_LACLA | P81181 lactococcus |
| 13 | 35 | 66.0 | 108 | 1 KV3V_MOUSE | P01674 mus musculu |
| 14 | 35 | 66.0 | 128 | 1 KV3K_HUMAN | P06311 homo sapien |
| 15 | 35 | 66.0 | 449 | 1 G6PI_STR3 | Q863X1 streptococc |
| 16 | 35 | 66.0 | 449 | 1 G6PI_STRWU | Q9x670 streptococc |
| 17 | 35 | 66.0 | 449 | 1 G6PI_STRP3 | Q8x896 streptococc |
| 18 | 35 | 66.0 | 449 | 1 G6PI_STRP8 | Q9p2r3 streptococc |
| 19 | 35 | 66.0 | 449 | 1 G6PI_STRPN | Q97n90 streptococc |
| 20 | 35 | 66.0 | 449 | 1 G6PI_STRPY | Q9a1l1 streptococc |
| 21 | 35 | 66.0 | 449 | 1 G6PI_STRP6 | Q8qn74 streptococc |
| 22 | 35 | 66.0 | 449 | 1 G6PI_STRTR | Q8vnb7 streptococc |
| 23 | 35 | 66.0 | 735 | 1 AD02_CAVFO | Q80411 cavia porce |
| 24 | 35 | 66.0 | 759 | 1 AL16_SCHPO | P87244 schizosacch |
| 25 | 34.5 | 65.1 | 108 | 1 KV1H_HUMAN | P01600 homo sapien |
| 26 | 34 | 64.2 | 450 | 1 G6PI_LACPE | Q83xm3 lactobacill |
| 27 | 34 | 64.2 | 450 | 1 G6PI_LISIN | Q928r6 listeria in |
| 28 | 34 | 64.2 | 450 | 1 G6PI_LISNO | Q8v4r7 listeria mo |
| 29 | 34 | 64.2 | 476 | 1 TRZA_RHOCO | Q57275 rhodococcus |
| 30 | 34 | 64.2 | 782 | 1 OSTA_PASMU | Q9ck12 pasteurella |
| 31 | 34 | 64.2 | 1177 | 1 Y307_MYCCE | P47549 mycoplasma |
| 32 | 33 | 62.3 | 117 | 1 KV1J_HUMAN | P01602 homo sapien |
| 33 | 33 | 62.3 | 450 | 1 G6PI_CLOPE | Q8xi54 clostridium |

| | | | | | |
|----|----|------|------|--------------|--------------------|
| 34 | 33 | 62.3 | 1478 | 1 BUD3_ASHGO | Q9hf61 ashbya goes |
| 35 | 32 | 60.4 | 129 | 1 KV3H_HUMAN | P04207 homo sapien |
| 36 | 32 | 60.4 | 235 | 1 ICLN_CANFA | P35521 canis famil |
| 37 | 32 | 60.4 | 236 | 1 ICLN_MOUSE | Q61189 mus musculu |
| 38 | 32 | 60.4 | 236 | 1 ICLN_RAT | Q04753 rattus norv |
| 39 | 32 | 60.4 | 237 | 1 ICLN_HUMAN | P54105 homo sapien |
| 40 | 32 | 60.4 | 433 | 1 MCRB_METBA | P07955 methanosarc |
| 41 | 32 | 60.4 | 445 | 1 G6PB_BACST | P13376 bacillus st |
| 42 | 32 | 60.4 | 474 | 1 ATZA_PSESD | P72156 pseudomonas |
| 43 | 32 | 60.4 | 546 | 1 YQ44_CAEEL | Q09460 caenorhabdi |
| 44 | 31 | 58.5 | 111 | 1 KV3R_MOUSE | P01670 mus musculu |
| 45 | 31 | 58.5 | 111 | 1 KV3S_MOUSE | P01671 mus musculu |

ALIGNMENTS

RESULT 1
KV3C_HUMAN STANDARD; PRT; 100 AA.
ID KV3C_HUMAN
AC P01621;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region NG9 precursor (fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093600; PubMed=6419127;
RA Bentley D.L.;
RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to a small family of germ-line V genes."
RC Nature 307:77-80(1984).
CL -I- MISCELLANEOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR PIR; A01894; K3HUNG.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; Hybridoma.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION NG9.
FT DISULFID 27 93 BY SIMILARITY.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 10729 MW; 5D9AF363CC52632F CRC64;
Query Match 100.0%; Score 53; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQSVSSSYLA 12
DB 28 RASQSVSSSYLA 39
RESULT 2
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID KV3L_HUMAN
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).


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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A. PubMed=3127527;
RX MEDLINE=88171307; Chen P.P., Carson D.A.;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR; PLO022; K3HUHA.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 JKI SEGMENT.
FT NON_TER 129 129 BY SIMILARITY.
SQ SEQUENCE 129 AA; 14073 MW; D3C5529277774D0 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
DB 44 RASQSVSSSYLA 55

RESULT 3
KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR; PLO021; K3HUHI.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.

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DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 JKI SEGMENT.
FT NON_TER 129 129 BY SIMILARITY.
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2B74D6 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
DB 44 RASQSVSSSYLA 55

RESULT 4
KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IGM anti-gamma-globulins of the Wa
RT Group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01892; K3HUSI.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7699C3BCD646FFB4 CRC64;

Query Match 94.3%; Score 50; DB 1; Length 109;
Best Local Similarity 91.7%; Pred. No. 0.0022;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
DB 44 RASQSVSSSYLA 55

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Db      24 RASQSVSNLYA 35
RESULT 5
KV3F HUMAN
ID_KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig kappa chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "the amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive IgM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
CC PIR; A01897; K3HUPM.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT SIGNAL 1 20
FT CHAIN 21 >116
FT DOMAIN 21 43
FT DOMAIN 44 55
FT DOMAIN 56 70
FT DOMAIN 71 77
FT DOMAIN 78 109
FT DOMAIN 110 116
FT DISULFID 43 109
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;
Query Match 92.5%; Score 49; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYL 11
Db 44 RASQSVSSSYL 54

RESULT 7
KV3D HUMAN
ID_KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
Ti). IV. The complete amino acid sequence and its significance for
the mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01895; K3HUTI.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;
Query Match 92.5%; Score 49; DB 1; Length 109;
Best Local Similarity 83.3%; Pred. No. 0.0036;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYL 12
Db 24 RASQSVSSSYL 35

RESULT 6
KV3J HUMAN
ID_KV3J_HUMAN STANDARD; PRT; 116 AA.
AC P04434;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region VH precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
within the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).
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-----NOT ANNOTATED_CDS-----

CC EMBL; X02725; -; NOT ANNOTATED_CDS.
 CC PIR; A01901; K3HUVH.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 >116
 FT DOMAIN 21 43
 FT DOMAIN 44 55
 FT DOMAIN 56 70
 FT DOMAIN 71 77
 FT DOMAIN 78 109
 FT DOMAIN 110 116
 FT DISULFID 43 109
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;

Query Match 92.5%; Score 49; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0038;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYL 11

Db 44 RASQSVSSSYL 54

RESULT 7

KV3D_HUMAN
 ID_KV3D_HUMAN STANDARD; PRT; 109 AA.
 AC P01622;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region Ti.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RA MEDLINE=72188439; PubMed=5027703;
 RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
 Ti). IV. The complete amino acid sequence and its significance for
 the mechanism of antibody production."
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01895; K3HUTI.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 23 89
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

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Query Match      86.8%; Score 46; DB 1; Length 109;
Best Local Similarity 83.3%; Pred. No. 0.015;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
   |||||:|:|
Db 24 RASQSVNSFLA 35

RESULT 8
KV3E HUMAN
ID KV3E HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01896; K3HUWL.
DR HSSP; P80362; LWTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115B69CBEE CRC64;

Query Match      84.9%; Score 45; DB 1; Length 109;
Best Local Similarity 90.9%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSYL 11
   |||||:|:|
Db 24 RASQSVSSGYL 34

RESULT 9
KV3A HUMAN
ID KV3A HUMAN STANDARD; PRT; 108 AA.
AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
RT of Bence Jones proteins Rad, Fr4 and B6."

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RL FBBS Lett. 2:301-304(1969).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01891; K3HUB6.
DR HSSP; P80362; LWTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match      81.1%; Score 43; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 0.063;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
   |||||:|:|
Db 24 RASQSLSGNYLA 35

RESULT 10
KV4A MOUSE
ID KV4A MOUSE STANDARD; PRT; 129 AA.
AC P01680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region S107B precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82115300; PubMed=6799208;
RA Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107."
RL Cell 26:57-66(1981).
CC -1- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
CC NORMAL KAPPA CHAIN S107.
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DR EMBL; J00577; AAA38780.1; -.
DR EMBL; V00780; CAA24157.1; -.
DR PIR; A01943; KVMS7B.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129
FT DOMAIN 23 45
FT DOMAIN 46 57
FT DOMAIN 58 72
FT DOMAIN 73 79
FT DOMAIN 80 111
FT DOMAIN 112 118
FT DOMAIN 119 128

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FT DISULFID 45 111 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 13833 MW; E4BB73072DC6BEE4 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 129;
Best Local Similarity 90.0%; Pred. No. 0.53;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQSVSSSYL 11
Db 47 ASSSVSSSYL 56

RESULT 11
KV31 HUMAN STANDARD; PRT; 115 AA.
AC P04433.
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE IG kappa chain V-III region VG precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus."
RL Nucleic Acids Res. 12:9229-9236(1984).
CC
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CC
CC EMBL; X01668; -; NOT ANNOTATED_CDS.
DR PIR; A01900; K3HUVG.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 54 FRAMEWORK-2.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 72.6%; Score 38.5; DB 1; Length 115;
Best Local Similarity 91.7%; Pred. No. 0.59;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 RASQSVSSSYLA 12
Db 44 RASQSV-SSSYLA 54

RESULT 12
G6PI LACLA STANDARD; PRT; 447 AA.
ID G6PI LACLA
AC P81181;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN PGI OR PGIA OR LL2168.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Winkler P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
RN [2]
RP SEQUENCE OF 1-19.
RX MEDLINE=97312580; PubMed=9169021;
RX Nomura M., Nakajima I., Matsuzaki M., Kimoto H., Suzuki I., Aso H.;
RA "The N-terminal sequence of Lactococcus lactis phosphoglucose
RA isomerase purified by affinity chromatography differs from the other
RA species."
RL Arch. Biochem. Biophys. 341:315-320(1997).
CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC phosphate.
CC -1- PATHWAY: Involved in glycolysis and in gluconeogenesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GPI family.
CC
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CC
CC EMBL; AE006445; AA06266.1; -.
DR PIR; H86895; H86895.
DR HSSP; P13376; 2PGI.
DR HAMAP; MF_00473; -; 1.
DR InterPro; IPR001672; G6P_Isomerase.
DR Pfam; PF00342; PGI; 1.
DR PRINTS; PS00662; G6PISOMERASE.
DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT INIT MET 0
FT ACT SITE 310 310 BY SIMILARITY.
FT ACT SITE 424 424 BY SIMILARITY.
SQ SEQUENCE 447 AA; 49463 MW; 40DD4FC7D106FD29 CRC64;

Query Match 71.7%; Score 38; DB 1; Length 447;
Best Local Similarity 72.7%; Pred. No. 3.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASQSVSSSYLA 12
Db 115 AGNSISSSYLA 125

RESULT 13
KV3V MOUSE STANDARD; PRT; 108 AA.
ID KV3V MOUSE
AC P01674;
```

HSP: P01607; IRE1.
GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 20 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT CHAIN 21 128
FT DOMAIN 21 43 FRAMEWORK-1
FT DOMAIN 41 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
FT SEQUENCE 128 AA; 14070 MW; CQ9557F0FE3B9012 CRC64;
SQ
Query Match 66.0%; Score 35; DB 1; Length 128;
Best Local Similarity 88.9%; Pred.No.3.6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps
QY 1 RASQSVSS 9
|||||:
44 RASQSVSSN 52
Db
RESULT 15
G6PI STRA3
ID _G6PI STRA3 STANDARD; PRT; 449 AA.
AC Q8B6X1; Q8B1F3;
DC 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).
DE PGI OR GBS0437 OR SAG0402.
GN Streptococcus agalactiae (serotype III), and
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC Streptococcus.
ON NCBI_TaxID=216495, 216466;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=2242508; PubMed=12354221;
RA Glaser P., Rouniok C., Buchrieser C., Chevalier F., Prangeul L.,
RA Meadek I., Zouine M., Couve E., Lalloui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RA "Genome sequence of Streptococcus agalactiae, a pathogen causing
RA invasive neonatal disease."
RL Mol. Microbiol. 45:1499-1513(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolanay J.F., Khodup R., Lewis M.R.,
RA Radu D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni P., Malone D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RA "Complete genome sequence and comparative genomic analysis of an
RA emerging human pathogen, serotype V Streptococcus agalactiae."
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).

```

CC -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC phosphate.
CC -!- PATHWAY: Involved in glycolysis and in gluconeogenesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the GPI family.
CC -----
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CC -----
CC EMBL; AL766845; CAD46081.1; -.
CC EMBL; AB014209; AAM99308.1; -.
CC SagsList; gbs0437; -.
CC TIGR; SAG0402; -.
CC HAMAP; MF_00473; -.
CC InterPro; IPR001672; G6P_Isomerase.
CC Pfam; PF00342; PGI; 1.
CC PRINTS; PR00662; G6PISOMERASE.
CC PROSITE; PS00765; P_GLUCOSE_ISOMERASE 1; 1.
CC PROSITE; PS00174; P_GLUCOSE_ISOMERASE 2; 1.
CC KJ Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
CC ACT_SITE 312 312 BY SIMILARITY.
CC ACT_SITE 426 426 BY SIMILARITY.
CC SEQUENCE 449 AA; 49585 MW; 5199E72DE0CDE1B CRC64;
CC -----
Query Match 66.0%; Score 35; DB 1; Length 449;
Best Local Similarity 63.6%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 ASQSVSSSYLA 12
DB 117 AGNSISSTYLA 127

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Search completed: April 21, 2004, 17:33:59
Job time : 7.08696 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:26:23 ; Search time 32 Seconds
(without alignments)
118.319 Million cell updates/sec

Title: SEQ4

Perfect score: 53

Sequence: 1 rasqvssysla 12

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 53 | 100.0 | 109 | 4 Q9UL86 | Q9ul86 homo sapien |
| 2 | 53 | 100.0 | 109 | 4 Q9UL78 | Q9ul78 homo sapien |
| 3 | 44 | 83.0 | 114 | 11 Q8K1F1 | Q8k1f1 mus musculus |
| 4 | 39 | 73.6 | 131 | 11 Q811C3 | Q811c3 mus musculus |
| 5 | 38 | 71.7 | 449 | 2 Q8GQP6 | Q8gqp6 streptococc |
| 6 | 37 | 69.8 | 363 | 16 Q8XKS7 | Q8xks7 clostridium |
| 7 | 35 | 66.0 | 101 | 11 Q9UL78 | Q9ul78 mus musculus |
| 8 | 35 | 66.0 | 108 | 4 Q9UL83 | Q9ul83 homo sapien |
| 9 | 35 | 66.0 | 124 | 11 Q8C3A7 | Q8c3a7 mus musculus |
| 10 | 35 | 66.0 | 195 | 2 Q8G9K4 | Q8g9k4 streptococc |
| 11 | 35 | 66.0 | 388 | 12 Q8J871 | Q8j871 spodoptera |
| 12 | 35 | 66.0 | 449 | 2 Q8SP79 | Q8sp79 streptococc |
| 13 | 35 | 66.0 | 449 | 16 Q835G1 | Q835g1 enterococcu |
| 14 | 35 | 66.0 | 782 | 4 Q96A82 | Q96a82 homo sapien |
| 15 | 35 | 66.0 | 1055 | 10 Q9SVF0 | Q9svf0 arabidopsis |
| 16 | 35 | 66.0 | 4753 | 16 Q8PLI3 | Q8pli3 xanthomonas |

| | | | | | |
|----|------|------|------|-----------|---------------------|
| 17 | 34 | 64.2 | 112 | 17 Q9YFH8 | Q9yfh8 aeropyrum p |
| 18 | 34 | 64.2 | 203 | 10 Q65720 | Q65720 arabidopsis |
| 19 | 34 | 64.2 | 263 | 10 Q9LX95 | Q9ly95 arabidopsis |
| 20 | 34 | 64.2 | 276 | 17 Q8PZG7 | Q8pzg7 methanosarc |
| 21 | 34 | 64.2 | 282 | 10 Q8S7V3 | Q8s7v3 oryza sativ |
| 22 | 34 | 64.2 | 341 | 16 Q7UEG1 | Q7ueg1 rhodospirell |
| 23 | 34 | 64.2 | 384 | 3 Q12283 | Q12283 saccharomyc |
| 24 | 34 | 64.2 | 450 | 2 Q83XM3 | Q83xm3 lactobacill |
| 25 | 34 | 64.2 | 510 | 16 Q7UX00 | Q7ux00 rhodospirell |
| 26 | 34 | 64.2 | 518 | 13 Q42436 | Q42436 notopithalm |
| 27 | 34 | 64.2 | 603 | 3 Q9C2D7 | Q9c2d7 neurospora |
| 28 | 34 | 64.2 | 1465 | 10 Q9LQH4 | Q9lqh4 arabidopsis |
| 29 | 33.5 | 63.2 | 107 | 4 Q96SA9 | Q96sa9 homo sapien |
| 30 | 33.5 | 63.2 | 108 | 4 Q9UL77 | Q9ul77 homo sapien |
| 31 | 33.5 | 63.2 | 234 | 4 Q72473 | Q72473 homo sapien |
| 32 | 33 | 62.3 | 72 | 5 Q8INL7 | Q8inl7 drosophila |
| 33 | 33 | 62.3 | 115 | 6 Q9BE38 | Q9be38 cryptotlagus |
| 34 | 33 | 62.3 | 133 | 12 Q8JTH4 | Q8jth4 little cher |
| 35 | 33 | 62.3 | 162 | 13 Q9PT33 | Q9pt33 oncorhynch |
| 36 | 33 | 62.3 | 174 | 16 Q7ULI4 | Q7uli4 rhodospirell |
| 37 | 33 | 62.3 | 210 | 8 Q8W9Q9 | Q8w9q9 mesostigma |
| 38 | 33 | 62.3 | 236 | 10 Q23193 | Q23193 arabidopsis |
| 39 | 33 | 62.3 | 241 | 17 Q96ZP0 | Q96zp0 sulfolobus |
| 40 | 33 | 62.3 | 309 | 16 Q7VA08 | Q7va08 prochloroco |
| 41 | 33 | 62.3 | 361 | 13 Q8AWC6 | Q8awc6 brachydanio |
| 42 | 33 | 62.3 | 475 | 5 Q8MPT2 | Q8mpt2 caenorhabdi |
| 43 | 33 | 62.3 | 487 | 5 Q9U2B7 | Q9u2b7 caenorhabdi |
| 44 | 33 | 62.3 | 510 | 11 Q8BUC9 | Q8buc9 mus musculu |
| 45 | 33 | 62.3 | 525 | 10 Q8LCP6 | Q8lcp6 arabidopsis |

ALIGNMENTS

RESULT 1

| | | | |
|---|--------------|------|---------|
| Q9UL86 | PRELIMINARY; | PRT; | 109 AA. |
| ID Q9UL86 | | | |
| AC Q9UL86; | | | |
| DT 01-MAY-2000 (TREMREL. 13, Created) | | | |
| DT 01-MAY-2000 (TREMREL. 13, Last sequence update) | | | |
| DT 01-OCT-2003 (TREMREL. 25, Last annotation update) | | | |
| DE Myosin-reactive immunoglobulin kappa chain variable region (fragment). | | | |
| OS Homo sapiens (Human). | | | |
| OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX NCBI_TaxID=9606; | | | |
| RN [1] | | | |
| RP SEQUENCE FROM N.A. | | | |
| RX MEDLINE=98277139; PubMed=9614934; | | | |
| RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., | | | |
| RA Young D.C.; | | | |
| RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus." | | | |
| RL Clin. Immunol. Immunopathol. 87:184-192(1998). | | | |
| DR EMBL; AF035028; AAD56264.1; - | | | |
| DR PIR; B30807; B30607. | | | |
| DR PIR; I30601; I30601. | | | |
| DR HSP; P80362; IWTI. | | | |
| DR InterPro; IPR007110; Ig-like. | | | |
| DR InterPro; IPR003596; Ig_v. | | | |
| DR Pfam; PF00047; Ig; 1. | | | |
| DR SMART; SM00406; IGV; 1. | | | |
| DR PROSITE; PS00835; IG_LIKE; 1. | | | |
| FT NON_TER | | | |
| FT 109 | | | |
| SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64; | | | |

Query Match 100.0%; Score 53; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12

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Db          24 RASQSVSSSYLA 35
|||||
RESULT 2
Q9UL78      PRELIMINARY;      PRT;      109 AA.
AC          01-MAY-2000 (TREMBlrel. 13, Created)
DT          01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT          01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE          Myosin-reactive immunoglobulin light chain variable region
DE          (Fragment).
OS          Homo sapiens (Human).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX          NCBI_TaxID=9606;
RN          [1]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=96277139; PubMed=9614934;
RA          Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA          Young D.C.;
RT          "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT          fetus.";
RL          Clin. Immunol. Immunopathol. 87:184-192(1998).
DR          EMBL; AF035036; AAD56272.1; -
DR          PIR; A30601; A30601.
DR          PIR; A30608; A30608.
DR          PIR; B30601; B30601.
DR          PIR; B30607; B30607.
DR          PIR; C30601; C30601.
DR          PIR; C30607; C30607.
DR          PIR; C30608; C30608.
DR          PIR; D30601; D30601.
DR          PIR; D30607; D30607.
DR          PIR; D30608; D30608.
DR          PIR; F30607; F30607.
DR          PIR; F30608; F30608.
DR          PIR; G30601; G30601.
DR          PIR; G30608; G30608.
DR          PIR; H30607; H30607.
DR          PIR; H30608; H30608.
DR          PIR; I30601; I30601.
DR          PIR; PH0963; PH0963.
DR          PIR; PH0965; PH0965.
DR          PIR; S34096; S34096.
DR          HSSP; P80362; 1WTL.
DR          InterPro; IPR007110; Ig-like.
DR          InterPro; IPR003596; Ig_v.
DR          Pfam; PF00047; Ig; 1.
DR          SMART; SM00406; IGV; 1.
DR          PROSITE; PS50835; IG_LIKE; 1.
FT          NON_TER 1
FT          NON_TER 109
SQ          SEQUENCE 109 AA; 11646 MW; 5P675C52EC7EE197 CRC64;

Query Match      100.0%; Score 53; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 RASQSVSSSYLA 12
|||||
Db          24 RASQSVSSSYLA 35
|||||
RESULT 3
Q8K1F1      PRELIMINARY;      PRT;      114 AA.
AC          08K1F1
DT          01-OCT-2002 (TREMBlrel. 22, Created)
DT          01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT          01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE          Anti-VIPase light chain variable region (Fragment).
OS          Mus musculus (Mouse).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX          NCBI_TaxID=10090;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA          Zhou Y.-X., Taguchi H., Plaque S., Katle S., Nishiyama Y., Paul S.;
RT          "Innate proteolytic antibodies: Failed D-VIPase response to the D-
RT          subunit of VIP and identification of L-VIPase VL domains.";
RL          Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR          EMBL; AF516284; AAM64202.1; -
DR          PIR; A33933; A33933.
DR          InterPro; IPR003599; Ig.
DR          InterPro; IPR007110; Ig-like.
DR          InterPro; IPR003596; Ig_v.
DR          Pfam; PF00047; Ig; 1.
DR          SMART; SM00409; IGV; 1.
DR          SMART; SM00406; IGV; 1.
DR          PROSITE; PS50835; IG_LIKE; 1.
FT          NON_TER 1
FT          NON_TER 114
SQ          SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3EEFD1 CRC64;

Query Match      83.0%; Score 44; DB 11; Length 114;
Best Local Similarity 90.9%; Pred. No. 0.32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 RASQSVSSSYL 11
|||||
Db          24 RASQSVSSSYL 34
|||||
RESULT 4
Q811C3      PRELIMINARY;      PRT;      131 AA.
AC          Q811C3
DT          01-JUN-2003 (TREMBlrel. 24, Created)
DT          01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT          01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE          Immunoglobulin gamma-3 kappa chain precursor (Fragment).
OS          Mus musculus (Mouse).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX          NCBI_TaxID=10090;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          STRAIN=MRL/MpJ-lpr/lpr; TISSUE=Spleen;
RX          MEDLINE=93156722; PubMed=8429833;
RA          Takahashi S., Itoh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;
RT          "Cloning and cDNA sequence analysis of nephritogenic monoclonal
RT          antibodies derived from an MRL/lpr lupus mouse.";
RL          Mol. Immunol. 30:177-182(1993).
DR          EMBL; DJ4629; BAA03482.1; -
DR          InterPro; IPR003599; Ig.
DR          InterPro; IPR007110; Ig-like.
DR          InterPro; IPR003596; Ig_v.
DR          Pfam; PF00047; Ig; 1.
DR          SMART; SM00409; IGV; 1.
DR          SMART; SM00406; IGV; 1.
DR          PROSITE; PS50835; IG_LIKE; 1.
KW          Signal.
FT          SIGNAL 1 22
FT          CHAIN 23 >131
FT          NON_TER 131
SQ          SEQUENCE 131 AA; 14083 MW; 5B83656954666E9E CRC64;

Query Match      73.6%; Score 39; DB 11; Length 131;
Best Local Similarity 81.8%; Pred. No. 4.1;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY          1 RASQSVSSSYL 11
|||||

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DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSSP; P80362; 1WT1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 66.0%; Score 35; DB 4; Length 108;
Best Local Similarity 88.9%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSS 9
Db 24 RASQSVSSN 32

RESULT 9
O8C3A7 PRELIMINARY; PRT; 124 AA.
AC O8C3A7;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN D930030005RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CS7BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
  60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK086466; BAC39674.1; -.
DR MGD; MGI:2443927; D930030005RIK.
KW Hypothetical protein.
SQ SEQUENCE 124 AA; 13208 MW; 23EBAEBBC01083E1 CRC64;

Query Match 66.0%; Score 35; DB 11; Length 124;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 70 RGSQNSSSWLA 81

RESULT 10
O8G9K4 PRELIMINARY; PRT; 195 AA.
AC O8G9K4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative glucose-6-phosphate isomerase (Fragment).
GN PGI.
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=G 39072;
RX MEDLINE=22269278; PubMed=12381468;
RX Sachse S., Seidel P., Gerlach D., Guenther E., Roedel J., Straube E.,
  Schmidt K.H.;
RA "Superantigen like gene(s) in human pathogenic Streptococcus
  dysgalactiae, subsp. equisimilis: Genomic localization of the gene
  encoding streptococcal pyrogenic exotoxin G (speG).";
RL FEMS Immunol. Med. Microbiol. 34:159-167(2002).
DR EMBL; AJ489606; CAD33905.1; -.
DR GO; GO:0004347; F:glucose-6-phosphate isomerase activity; IEA.
DR GO; GO:0016853; P:isomerase activity; IEA.
DR GO; GO:0006094; P:gluconeogenesis; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR001672; G6P_isomerase.
DR Pfam; PF00342; PGI; 1.
KW isomerase.
FT NON_TER 195
FT NON_TER 195
SQ SEQUENCE 195 AA; 21515 MW; 52C0182D022B1F45 CRC64;

Query Match 66.0%; Score 35; DB 2; Length 195;
Best Local Similarity 63.8%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQSVSSSYLA 12
Db 117 AGNSISSTYLA 127

RESULT 11
Q9J871 PRELIMINARY; PRT; 388 AA.
ID Q9J871;
AC Q9J871;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE ORF64.
OS Spodoptera exigua nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10454;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20036646; PubMed=10567663;
RX Iukel W.F.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D.,
  Goldbach R.W., Vlak J.M.;
RA "Sequence and organization of the spodoptera exigua multicapsid
  nucleopolyhedrovirus genome."
RT nucleopolyhedrovirus genome.
RL J. Gen. Virol. 80:3289-3304(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Iukel W.F.J., van Strien E.A., Heldens J.G.M., Broer R., Zuidema D.,
  Goldbach R.W., Vlak J.M.;
RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF169823; AAF33594.1; -.
DR InterPro; IPR008562; DUF844.
DR Pfam; PF05815; DUF844; 1.
SQ SEQUENCE 388 AA; 43654 MW; 9DDA0BCBCEFC9777 CRC64;

Query Match 66.0%; Score 35; DB 12; Length 388;
Best Local Similarity 75.0%; Pred. No. 94;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 370 RASQSVSSSYNA 381

RESULT 12
Q9RP79 PRELIMINARY; PRT; 449 AA.
ID Q9RP79;
AC Q9RP79;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

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E
i

RP SEQUENCE FROM N.A.
 RA Bevan M., Wedler H., Kutzner M., Wambutt R., Bancroft I., Mewes H.W.,
 RA Mayer K.F.X., Schueller C.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP PARTIAL SEQUENCE FROM N.A.
 RA Wedler H., Kutzner M., Wambutt R., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL035539; CAB37491.1; -;
 DR EMBL; AL161593; CAB80500.1; -;
 DR PIR; T05663; T05663.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0008158; F: hedgehog receptor activity; IEA.
 DR GO; GO:0030301; P: cholesterol transport; IEA.
 DR InterPro; IPR004765; NP_C type.
 DR InterPro; IPR003392; Patched.
 DR InterPro; IPR000731; SSD 5TM.
 DR Pfam; PF02460; Patched; 1.
 DR TIGRFAMs; TIGR00917; 2A060601; 1.
 DR PROSITE; PS50156; SSD; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1055 AA; 116148 MW; 15E154A61DC936BC CRC64;

Query Match 66.0%; Score 35; DB 10; Length 1055;
 Best Local Similarity 58.3%; Pred. No. 2.8e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 DB 778 RASQASDTSYIA 789

Search completed: April 21, 2004, 17:37:18
 Job time : 34 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:18 ; Search time 48 Seconds
(without alignments)
70.637 Million cell updates/sec

Title: SEQ4

Perfect score: 53

Sequence: 1 rasqsvassyla 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 53 | 100.0 | 12 | 2 | AAR15375 IGM-RF G1 |
| 2 | 53 | 100.0 | 12 | 5 | AU70331 Human Kap |
| 3 | 53 | 100.0 | 12 | 5 | AU83718 MS-GPC-6 |
| 4 | 53 | 100.0 | 12 | 5 | AB57480 HLA-DR-sp |
| 5 | 53 | 100.0 | 12 | 5 | AB57475 HLA-DR-sp |
| 6 | 53 | 100.0 | 12 | 5 | AB57469 HLA-DR-sp |
| 7 | 53 | 100.0 | 12 | 5 | AB57472 HLA-DR-sp |
| 8 | 53 | 100.0 | 12 | 6 | Aae38096 Human COU |
| 9 | 53 | 100.0 | 12 | 6 | Aae38067 Human 17G |
| 10 | 53 | 100.0 | 12 | 6 | ADA90302 MS-Roche |
| 11 | 53 | 100.0 | 12 | 6 | ADA90308 MS-Roche |
| 12 | 53 | 100.0 | 12 | 6 | ADA90317 MS-Roche |
| 13 | 53 | 100.0 | 12 | 6 | ADA90323 MS-Roche |
| 14 | 53 | 100.0 | 12 | 6 | ADA90324 MS-Roche |
| 15 | 53 | 100.0 | 12 | 6 | ADA90641 MS-Roche |
| 16 | 53 | 100.0 | 12 | 6 | ADA90751 MS-Roche |
| 17 | 53 | 100.0 | 12 | 6 | ADA90867 MS-Roche |
| 18 | 53 | 100.0 | 12 | 6 | ADA90869 MS-Roche |
| 19 | 53 | 100.0 | 12 | 6 | ADA91097 MS-R Fab/ |
| 20 | 53 | 100.0 | 12 | 6 | ADA90322 MS-Roche |
| 21 | 53 | 100.0 | 12 | 6 | ADA90487 MS-Roche |
| 22 | 53 | 100.0 | 12 | 6 | ADA90497 MS-Roche |
| 23 | 53 | 100.0 | 12 | 6 | ADA90871 MS-Roche |
| 24 | 53 | 100.0 | 12 | 6 | ADA90953 MS-R Fab/ |
| 25 | 53 | 100.0 | 12 | 6 | ADA91010 MS-R Fab/ |

| | | | | | |
|----|----|-------|----|---|--------------------|
| 26 | 53 | 100.0 | 12 | 6 | ADA91235 MS-R Fab/ |
| 27 | 53 | 100.0 | 12 | 6 | ADA91241 MS-R Fab/ |
| 28 | 53 | 100.0 | 12 | 6 | ADA90301 MS-Roche |
| 29 | 53 | 100.0 | 12 | 6 | ADA90309 MS-Roche |
| 30 | 53 | 100.0 | 12 | 6 | ADA90488 MS-Roche |
| 31 | 53 | 100.0 | 12 | 6 | ADA90637 MS-Roche |
| 32 | 53 | 100.0 | 12 | 6 | ADA90756 MS-Roche |
| 33 | 53 | 100.0 | 12 | 6 | ADA90313 MS-Roche |
| 34 | 53 | 100.0 | 12 | 6 | ADA90320 MS-Roche |
| 35 | 53 | 100.0 | 12 | 6 | ADA90484 MS-Roche |
| 36 | 53 | 100.0 | 12 | 6 | ADA90490 MS-Roche |
| 37 | 53 | 100.0 | 12 | 6 | ADA90631 MS-Roche |
| 38 | 53 | 100.0 | 12 | 6 | ADA90643 MS-Roche |
| 39 | 53 | 100.0 | 12 | 6 | ADA90989 MS-R Fab/ |
| 40 | 53 | 100.0 | 12 | 6 | ADA91339 MS-R Fab/ |
| 41 | 53 | 100.0 | 12 | 6 | ADA90315 MS-Roche |
| 42 | 53 | 100.0 | 12 | 6 | ADA90321 MS-Roche |
| 43 | 53 | 100.0 | 12 | 6 | ADA90325 MS-Roche |
| 44 | 53 | 100.0 | 12 | 6 | ADA90479 MS-Roche |
| 45 | 53 | 100.0 | 12 | 6 | ADA90495 MS-Roche |

ALIGNMENTS

RESULT 1
AAR15375
ID AAR15375 standard; protein; 12 AA.

XX AAR15375;
XX
DT 25-MAR-2003 (revised)
DT 05-MAR-1992 (first entry)
XX IGM-RF Glo.
XX Rheumatoid factor; RF; antigen; CDR; Igm.
XX Synthetic.
XX US068177-A.
XX 26-NOV-1991.
XX 05-AUG-1985; 85US-00762698.
XX 05-AUG-1985; 85US-00762698.
XX (SCRI) SCRIPPS CLINIC & RES FOUND.
XX Carson DA, Fong S, Chen PP;
XX WPI; 1991-368612/50.
XX Synthetic polypeptide(s) for inducing anti-idiotypic antibodies - useful
XX for treating auto immune-, endocrine- and rheumatic-diseases and
XX myasthenia gravis.
XX Claim 10; Page 42; 44pp; English.
XX Three rabbits were inoculated with two s.c. injections of PGL1 (synthetic
XX peptide) conjugated to KLH as an immunogen, and their sera were analysed
XX for anti-peptide antibody activity by ELISA. All three immunised rabbits
XX produced anti-PGL1 antibody. Antisera drawn from a rabbit on two
XX different days reacted significantly with the corresp. intact IGM-RF Glo.
XX See also AAR15365-74 and AAR15375. (Updated on 25-MAR-2003 to correct PA
XX field.)

XX Sequence 12 AA;

Query Match 100.0%; Score 53; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 Db 1 RASQSVSSSYLA 12

RESULT 2

AAU70331
 ID AAU70331 standard; peptide; 12 AA.
 AC AAU70331;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human Kappa III light chain CDR1.
 XX
 KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
 KW IgD; IgE; IgY; IgW; kappa; lambda; CHBP.
 XX
 OS Homo sapiens.
 XX
 FN WO200183806-A1.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US014349.
 XX
 PR 02-MAY-2000; 2000US-00563222.
 XX
 PA (EPIC-) EPICYTE PHARM INC.
 XX
 PI Hiatt AC, Hein MB;
 XX
 DR WPI; 2002-055482/07.
 XX
 PT Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array.
 XX
 PS Disclosure; Page 14; 129pp; English.

The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides encoding different immunoglobulin binding protein (IgBP) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transfected cells, to generate an IgBP that binds to a ligand, and transformed plant cells are selected, and preparing an IgBP array in plant cells. At least one peptide sequence has at least 75% sequence identity to a framework region (FR) of a native IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein array, preferably heavy chain binding protein (CHBP) array in eukaryotic cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammalian cells). The CHBP is useful for discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian immunoglobulin derived peptide that may be incorporated into an IgBP of the invention

Sequence 12 AA;

Query Match 100.0%; Score 53; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. NO. 0.0013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 Db 1 RASQSVSSSYLA 12

RESULT 3

AAU83718
 ID AAU83718 standard; peptide; 12 AA.
 XX
 AC AAU83718;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE MS-GPC-6 light chain variable region CD1 sequence.
 XX
 KW Human; antibody-based antigen; HLA-DR; CDR; antibody;
 KW human leukocyte antigen; cell proliferative disorder; lymphoma;
 KW MHC class II antigen disorder; lymphoma; B cell lymphoma; leukaemia;
 KW acute myeloid leukaemia; rheumatoid arthritis; multiple sclerosis;
 KW Grave's disease; insulin-dependent diabetes; transplant rejection;
 KW systemic lupus erythematosus; graft vs. host disease; myasthenia gravis;
 KW irritable bowel disease; Sjogren's syndrome; interleukin-2 secretion;
 KW IL-2; MS-GPC; complementarity determining region.
 XX
 OS Homo sapiens.
 XX
 FN WO200187337-A1.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US015625.
 XX
 PR 12-MAY-2000; 2000EP-00110065.
 PR 06-OCT-2000; 2000US-0238492P.
 XX
 PA (GPCB-) GPC BIOTECH AG.
 XX
 PI (MORP-) MORPHOSYS AG.
 XX
 PI Nagy Z, Brunner C, Tesar M, Thomassen-Wolf E;
 XX
 DR WPI; 2002-075288/10.
 XX
 PT Polypeptide compositions which bind to cell surface epitopes, which in
 PT multivalent form kills lymphoid tumor cells and in monovalent form causes
 PT immunosuppression or inhibits activation of lymphocytes.
 XX
 PS Example 4; Page 66; 150pp; English.

The invention relates to a composition which includes a polypeptide or a multivalent polypeptide comprising one or more antibody-based antigen - binding domain of human composition with binding specificity for an antigen expressed on surface of a human cell, especially HLA-DR (human leukocyte antigen DR), where treating cells expressing HLA-DR with the multivalent polypeptide causes or leads to killing of cells without need of cytotoxic entities or immunological mechanisms. Also included are the nucleic acid encoding the polypeptide, a vector comprising the nucleic acid and a host cell harbouring vector or nucleic acid. The polypeptide and the host cell are useful for preparing a pharmaceutical preparation for the treatment of cell proliferative disorders, disorders involving transformed cells expressing MHC class II antigens, B cell non-Hodgkin's lymphoma, B cell lymphoma, B cell acute lymphoid leukaemia, Burkitt's lymphoma, Hodgkin's lymphoma, hairy cell leukaemia, acute myeloid leukaemia, T cell lymphoma, T cell non-Hodgkin's lymphoma, chronic myeloid leukaemia, chronic lymphoid leukaemia or multiple myeloid leukaemia, disorders involving unwanted activation of the cells of the immune system, such as lymphoid cells expressing MHC class II, rheumatoid arthritis, juvenile arthritis, multiple sclerosis, Grave's disease, insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus erythematosus, ankylosing spondylitis, transplant rejection, graft vs. host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris, glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. The antigen is useful for suppressing activation or proliferation of a cell of the immune system, suppressing interleukin-2 (IL-2) secretion by a cell of the immune system, such as expressing HLA-DR, the interaction of the cell of the immune system with another cell, immunosuppressing a patient and for killing a cell expressing an antigen, HLA-DR on the surface of the cell, where neither cytotoxic entities nor immunological

CC mechanisms are needed to cause or lead to the killing. The killing is
 CC dependent on the action of non-caspase proteases and/or cannot be
 CC inhibited by zVAD-fmk or zDEVD-fmk. The present sequence is a
 CC complementarity determining region (CDR) based on the human antigen
 CC binding polypeptides of the invention MS-GPC-1, 6, 8 and 10. The CDRs are
 CC either the native sequence or have been optimised/mutated to alter their
 CC antigen binding capabilities
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 53; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASQSVSSSYLA 12
 DB 1 RASQSVSSSYLA 12
 |||||
 RESULT 4
 ABB57480
 ID ABB57480 standard; peptide; 12 AA.
 AC ABB57480;
 DT 18-MAR-2002 (first entry)
 DE HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-6.
 XX
 XX Immunomodulatory human MHC class II antigen-binding protein; HLA;
 KW human leukocyte antigen; immune system; immunosuppression; antibody;
 KW major histocompatibility complex; antirheumatic; antiarthritic;
 KW neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
 KW immunosuppressive; dermatological; antichyroid; nephrotropic; psoriasis;
 KW thymimetic; hepatotropic; immune response suppressor; narcolepsy;
 KW rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;
 KW Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
 KW systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
 KW transplant rejection; graft versus host disease; pemphigus vulgaris;
 KW glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
 KW irritable bowel disease; Sjogren's syndrome.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX WO200187338-A1.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US015626.
 XX
 PR 12-MAY-2000; 2000EP-00110063.
 PR 06-OCT-2000; 2000US-0238762P.
 XX
 XX (GPCB-) GPC BIOTECH AG.
 PA (MORP-) MORPHOSYS AG.
 XX
 XX Nagy Z, Tesar M, Thomassen-Wolf E;
 PI WPI; 2002-075289/10.
 DR
 XX Composition for suppressing immune response, treating diseases of immune
 PT system, has polypeptide comprising antibody-based antigen-binding domain
 PT of human composition, which binds antigen expressed on a cell surface.
 XX
 XX Example; Page 60; 139pp; English.
 PS
 CC The present invention describes a composition (I), comprising a
 CC polypeptide comprising an antibody-based antigen-binding domain of human
 CC composition with binding specificity for an antigen expressed on the
 CC surface of a cell, where treating cells expressing the antigen with the
 CC polypeptides leads to suppression of an immune response, and the IC50 for
 CC the suppression of immune response is 1 microM or less. (I) has

CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
 CC antidiabetic, antipsoriatic, immunosuppressive, dermatological,
 CC antichyroid, nephrotropic, thymimetic and hepatotropic activities, and
 CC can be used as a suppressor of immune response. (I) is useful for
 CC suppressing activation or proliferation of a cell of the immune system,
 CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
 CC immune system with another cell, immunosuppressing a patient and for
 CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on
 CC the surface of the cell, where neither cytotoxic entities nor
 CC immunological mechanisms are needed to cause or lead to the killing. (I)
 CC (optionally linked to cytotoxic or immunogenic agent) is useful for
 CC preparing a pharmaceutical preparation for the treatment of rheumatoid
 CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
 CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
 CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus
 CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
 CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
 CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
 CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 53; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASQSVSSSYLA 12
 DB 1 RASQSVSSSYLA 12
 |||||
 RESULT 5
 ABB57475
 ID ABB57475 standard; peptide; 12 AA.
 AC ABB57475;
 DT 18-MAR-2002 (first entry)
 DE HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-4.
 XX
 XX Immunomodulatory human MHC class II antigen-binding protein; HLA;
 KW human leukocyte antigen; immune system; immunosuppression; antibody;
 KW major histocompatibility complex; antirheumatic; antiarthritic;
 KW neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
 KW immunosuppressive; dermatological; antichyroid; nephrotropic; psoriasis;
 KW thymimetic; hepatotropic; immune response suppressor; narcolepsy;
 KW rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;
 KW Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
 KW systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
 KW transplant rejection; graft versus host disease; pemphigus vulgaris;
 KW glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
 KW irritable bowel disease; Sjogren's syndrome.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX WO200187338-A1.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US015626.
 XX
 PR 12-MAY-2000; 2000EP-00110063.
 PR 06-OCT-2000; 2000US-0238762P.
 XX
 XX (GPCB-) GPC BIOTECH AG.
 PA (MORP-) MORPHOSYS AG.
 XX
 XX Nagy Z, Tesar M, Thomassen-Wolf E;
 PI WPI; 2002-075289/10.
 DR

XX Composition for suppressing immune response, treating diseases of immune
PT system, has polypeptide comprising antibody-based antigen-binding domain
PT of human composition, which binds antigen expressed on a cell surface.
XX
XX
XX Example; Page 60; 139pp; English.
XX
XX The present invention describes a composition (I), comprising a
CC polypeptide comprising an antibody-based antigen-binding domain of human
CC composition with binding specificity for an antigen expressed on the
CC surface of a cell, where treating cells expressing the antigen with the
CC polypeptides leads to suppression of an immune response, and the IC50 for
CC the suppression of immune response is 1 microM or less. (I) has
CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
CC antidiabetic, antipsoriatic, immunosuppressive, dermatological,
CC antithyroid, nephrotropic, thymimetic and hepatotropic activities, and
CC can be used as a suppressor of immune response. (I) is useful for
CC suppressing activation or proliferation of a cell of the immune system,
CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
CC immune system with another cell, immunosuppressing a patient and for
CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on
CC the surface of the cell, where neither cytotoxic entities nor
CC immunological mechanisms are needed to cause or lead to the killing. (I)
CC (optionally linked to cytotoxic or immunogenic agent) is useful for
CC preparing a pharmaceutical preparation for the treatment of rheumatoid
CC arthritis, juvenile arthritis, multiple sclerosis, psoriasis, systemic lupus
CC erythematosus, ankylosing spondylitis, narcolepsy, psoriasis, systemic lupus
CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
CC the exemplification of the present invention
XX
XX Sequence 12 AA;

Query Match 100.0%; Score 53; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12

RESULT 6
ABB57469
ID ABB57469 standard; peptide; 12 AA.
XX
XX ABB57469;
XX
XX 18-MAR-2002 (first entry)
XX
XX HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-2.

XX Immunomodulatory human MHC class II antigen-binding protein; HLA;
KW human leukocyte antigen; immune system; immunosuppression; antibody;
KW major histocompatibility complex; antirheumatic; antithyroid;
KW neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
KW immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis;
KW thymimetic; hepatotropic; immune response suppressor; narcolepsy;
KW rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;
KW Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
KW systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
KW transplant rejection; graft versus host disease; pemphigus vulgaris;
KW glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
KW irritable bowel disease; Sjogren's syndrome.

XX Homo sapiens.
OS Synthetic.
XX
XX WO200187338-A1.

PD 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US015626.
XX
XX 12-MAY-2000; 2000EP-00110063.
PR 06-OCT-2000; 2000US-0238762P.
XX
XX (GPCB-) GPC BIOTECH AG.
PA (MORP-) MORPHOSYS AG.
XX
XX Nagy Z, Teseur M, Thomassen-Wolf E;
XX
XX WPI; 2002-075289/10.
XX
XX Composition for suppressing immune response, treating diseases of immune
PT system, has polypeptide comprising antibody-based antigen-binding domain
PT of human composition, which binds antigen expressed on a cell surface.
XX
XX Example; Page 60; 139pp; English.

XX The present invention describes a composition (I), comprising a
CC polypeptide comprising an antibody-based antigen-binding domain of human
CC composition with binding specificity for an antigen expressed on the
CC surface of a cell, where treating cells expressing the antigen with the
CC polypeptides leads to suppression of an immune response, and the IC50 for
CC the suppression of immune response is 1 microM or less. (I) has
CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
CC antidiabetic, antipsoriatic, immunosuppressive, dermatological,
CC antithyroid, nephrotropic, thymimetic and hepatotropic activities, and
CC can be used as a suppressor of immune response. (I) is useful for
CC suppressing activation or proliferation of a cell of the immune system,
CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
CC immune system with another cell, immunosuppressing a patient and for
CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on
CC the surface of the cell, where neither cytotoxic entities nor
CC immunological mechanisms are needed to cause or lead to the killing. (I)
CC (optionally linked to cytotoxic or immunogenic agent) is useful for
CC preparing a pharmaceutical preparation for the treatment of rheumatoid
CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
CC erythematosus, ankylosing spondylitis, narcolepsy, psoriasis, systemic lupus
CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
CC the exemplification of the present invention
XX

Sequence 12 AA;
Query Match 100.0%; Score 53; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12
RESULT 7
ABB57472
ID ABB57472 standard; peptide; 12 AA.
XX
XX ABB57472;
XX
XX 18-MAR-2002 (first entry)
XX
XX HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-3.

XX Immunomodulatory human MHC class II antigen-binding protein; HLA;
KW human leukocyte antigen; immune system; immunosuppression; antibody;
KW major histocompatibility complex; antirheumatic; antithyroid;
KW neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
KW immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis;

KW thyromimetic; hepatotropic; immune response suppressor; narcolepsy;
KW rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;
KW Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
KW systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
KW transplant rejection; graft versus host disease; pemphigus vulgaris;
KW glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
KW irritable bowel disease; Sjogren's syndrome.
XX
XX Homo sapiens.
OS Synthetic.
XX WO200197338-A1.
PN
XX 22-NOV-2001.
PD
XX 14-MAY-2001; 2001WO-US015626.
PF
XX 12-MAY-2000; 2000EP-00110063.
PR
XX 06-OCT-2000; 2000US-0238762P.
XX
XX (GPCB-) GPC BIOTECH AG.
PA (MORP-) MORPHOSYS AG.
PA
XX Nagy Z, Tesar M, Thomassen-Wolf E;
PI WPI; 2002-075289/10.
DR
XX Composition for suppressing immune response, treating diseases of immune
PT system, has polypeptide comprising antibody-based antigen-binding domain
PT of human composition, which binds antigen expressed on a cell surface.
XX
XX Example; Page 60; 139pp; English.
PS
XX The present invention describes a composition (I), comprising a
CC polypeptide comprising an antibody-based antigen-binding domain of human
CC composition with binding specificity for an antigen expressed on the
CC surface of a cell, where treating cells expressing the antigen with the
CC polypeptides leads to suppression of an immune response, and the IC50 for
CC the suppression of immune response is 1 microm or less. (I) has
CC antiarheumatic, antiarthritic, neuroprotective, antiinflammatory,
CC antidiabetic, antipsoriatic, immunosuppressive, dermatological,
CC antithyroid, nephrotropic, thyromimetic and hepatotropic activities, and
CC can be used as a suppressor of immune response. (I) is useful for
CC suppressing activation or proliferation of a cell of the immune system,
CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
CC immune system with another cell, immunosuppressing a patient and for
CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on
CC the surface of the cell, where neither cytotoxic entities nor
CC immunological mechanisms are needed to cause or lead to the killing. (I)
CC (optionally linked to cytotoxic or immunogenic agent) is useful for
CC preparing a pharmaceutical preparation for the treatment of rheumatoid
CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus
CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
XX the exemplification of the present invention
XX
XX Sequence 12 AA;

Query Match 100.0%; Score 53; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
|||
DB 1 RASQSVSSSYLA 12

RESULT 8
AAE38096

ID AAE38096 standard; peptide; 12 AA.
XX
AC AAE38096;
XX
XX 06-NOV-2003 (first entry)
XX
XX Human COU-1 antibody VL CDR1 peptide #1.
DE
XX
XX Human; cancer-associated epitope; cytokeatin K8; cytokeatin K18; VL;
KW adenocarcinoma; therapy; cancer; antibody; light chain variable region;
KW complementarity determining region; CDR.
XX
XX Homo sapiens.
XX WO2003057168-A2.
PN
XX 17-JUL-2003.
PD
XX 03-JAN-2003; 2003WO-US000297.
PF
XX 03-JAN-2002; 2002US-0345208P.
PR
XX (SCRI) SCRIPPS RES INST.
XX
XX Ditzel H, Jensenius JC;
PI WPI; 2003-598315/56.
DR
XX Novel isolated cancer-associated epitope comprising two separate
PT polypeptides, a cytokeatin 8 polypeptide and a cytokeatin 18
PT polypeptide, useful as component of vaccine for preventing or treating
PT adenocarcinoma.
XX
XX Claim 15; Page 36; 155pp; English.
PS
XX The invention provides a cancer-associated epitope comprising two
CC separate polypeptides, a cytokeatin 8 polypeptide and a cytokeatin 18
CC polypeptide. Vaccine composition of the invention is useful for treating
CC or preventing colon adenocarcinoma, ovarian adenocarcinoma, renal
CC adenocarcinoma, mammary adenocarcinoma, lung adenocarcinoma, pancreatic
CC adenocarcinoma or non-seminoma testis carcinoma. The invention is also
CC useful for preparing a medicament for treating or preventing cancer in a
CC mammal. The present sequence is human COU-1 cancer-associated epitope
CC antibody VL (light chain variable region) CDR (complementarity
CC determining region) peptide
XX
XX Sequence 12 AA;

Query Match 100.0%; Score 53; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
|||
DB 1 RASQSVSSSYLA 12

RESULT 9
AAE38067
ID AAE38067 standard; peptide; 12 AA.
XX
AC AAE38067;
XX
XX 06-NOV-2003 (first entry)
XX
XX Human 17G1 CD30 antibody VL CDR1 peptide.

XX Human; antibody; CD30; tumour; autoimmune disease; rheumatoid arthritis;
KW systemic lupus erythematosus; systemic sclerosis; Grave's disease; AICL;
KW atopic dermatitis; Hashimoto's thyroiditis; chronic renal failure; AILD;
KW acute infectious mononucleosis; angioimmunoblastic lymphadenopathy; HIV;
KW Hodgkin's disease; Castleman's disease; Kaposi's sarcoma; lymphoma; ATL;
KW adult T cell lymphoma; human immunodeficiency virus; carcinoma; therapy;
KW

KW Wegner's granulomatosis; anaplastic large cell lymphoma; Omen's syndrome;
 KW light chain variable domain; VL; complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 XX WO2003059282-A2.
 XX
 XX 24-JUL-2003.
 XX
 XX 07-JAN-2003; 2003WO-US000440.
 XX
 XX 09-JAN-2002; 2002US-0347649P.
 PR
 PR 19-AUG-2002; 2002US-0404427P.
 PR
 PR 06-DEC-2002; 2002US-0431684P.
 XX
 XX (MEDA-) MEDAREX INC.
 XX
 XX Keler T, Graziano R, Trembl J;
 XX
 XX WPI: 2003-598476/56.
 DR N-PSDB; AAD57379.
 XX
 XX New human monoclonal antibody that binds to human CD30, useful for
 PT treating or preventing tumor or autoimmune disease, e.g., rheumatoid
 PT arthritis.
 PT
 XX Disclosure; Page 117; 122pp; English.
 XX
 XX The invention relates to human monoclonal antibody that binds to human
 CC CD30. The antibody is useful for treating or preventing tumor or
 CC autoimmune disease e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, systemic sclerosis, atopic dermatitis, Grave's disease,
 CC Hashimoto's thyroiditis, Wegner's granulomatosis, Omen's syndrome,
 CC chronic renal failure, acute infectious mononucleosis, herpes or HIV
 CC (human immunodeficiency virus) virus-associated diseases. The antibody is
 CC also useful for treating Hodgkin's disease, anaplastic large cell
 CC lymphoma (ALCL), adult T cell lymphoma, HIV associated body cavity
 CC lymphadenopathy (AILD)-like T cell lymphoma, undifferentiated carcinomas of the
 CC based lymphomas, embryonal carcinomas, Castleman's disease, Kaposi's
 CC rhino-pharynx (e.g. Schinckel's tumour), Castleman's disease, Kaposi's
 CC Sarcoma and other T-cell or B-cell lymphomas. The present sequence is
 CC human CD30 antibody VL (light chain variable domain) CDR (complementarity
 CC determining region) peptide
 XX
 XX Sequence 12 AA;
 XX
 XX Query Match 100.0%; Score 53; DB 6; Length 12;
 XX Best Local Similarity 100.0%; Pred. No. 0.0013;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RASQSVSSSYLA 12
 Db |||||
 1 RASQSVSSSYLA 12
 RESULT 10
 ADA90302
 ID ADA90302 standard; peptide; 12 AA.
 XX
 XX ADA90302;
 XX
 XX 20-NOV-2003 (first entry)
 XX
 XX MS-Roche #3.2 L-CDR1 amino acid sequence.
 XX
 XX antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
 KW nootropic; antiparkinsonian; gene therapy; amyloidogenesis;
 KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
 KW Alzheimer's disease; motor neuropathy; Down's syndrome;
 KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
 KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
 KW neuronal disorder; aging.
 XX

OS Synthetic.
 OS Homo sapiens.
 XX WO2003070760-A2.
 XX
 XX 28-AUG-2003.
 XX
 XX 20-FEB-2003; 2003WO-BP001759.
 XX
 XX 20-FEB-2002; 2002EP-00003844.
 PR
 PR (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA (MORP-) MOREPHOSYS AG.
 XX
 XX Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretschmar T;
 PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
 PI
 XX WPI: 2003-663848/62.
 DR
 XX
 XX New antibody molecule capable of specifically recognizing two regions of
 PT the beta-A4 peptide, useful for diagnosing, preventing or treating
 PT diseases associated with amyloidogenesis or amyloid-plaque formation
 PT (e.g. dementia).
 XX
 XX Example 5; Page 64; 312pp; English.
 XX
 XX The present invention describes an antibody molecule (I) capable of
 CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
 CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
 CC Ser-Gly-Tyr ADA98986 or its fragment, and the second region comprises the
 CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Ala-Glu-Asp-Val-
 CC Gly ADA98987 or its fragment. Also described: (1) a nucleic acid molecule
 CC encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host
 CC cell comprising the vector of (2); (4) preparing (I), comprising
 CC culturing the host cell of (3) under conditions that allow synthesis of
 CC (I) and recovering (I) from the culture; (5) a composition comprising (I)
 CC or an antibody molecule produced by method (4); (6) a kit comprising (I),
 CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
 CC (I); (8) testing the resulting Fab optimisation library by panning
 CC against Abeta/Abeta4; (9) identifying optimised clones; (10) expressing
 CC of selected, optimised clones; (11) preparing a pharmaceutical
 CC composition, comprising optimisation of (I), and formulating the
 CC optimised antibody/antibody molecule with a carrier; and (12) a
 CC pharmaceutical composition prepared by method (8). (I) has
 CC neuroprotective, nootropic and antiparkinsonian activities, and can be
 CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,
 CC vector or host is useful in preparing a pharmaceutical composition for
 CC the prevention and/or treatment of a disease associated with
 CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
 CC may also be used in preparing a diagnostic composition for the detection
 CC of the disease mentioned above. The antibody is used for the
 CC disintegration of beta-amyloid plaques or for passive immunisation
 CC against beta-amyloid plaque formation. In particular, the disease is
 CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
 CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
 CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
 CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
 CC present sequence is used in the exemplification of the present invention.
 XX
 XX Sequence 12 AA;
 XX
 XX Query Match 100.0%; Score 53; DB 6; Length 12;
 XX Best Local Similarity 100.0%; Pred. No. 0.0013;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RASQSVSSSYLA 12
 Db |||||
 1 RASQSVSSSYLA 12
 RESULT 11
 ADA90308
 ID ADA90308 standard; peptide; 12 AA.

| | |
|----|--|
| XX | ADA90308; |
| AC | |
| XX | |
| DT | 20-NOV-2003 (first entry) |
| XX | |
| DE | MS-Roche #3.2.H2 L-CDR1 amino acid sequence. |
| XX | |
| KW | antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; |
| KW | neurotropic; antiparkinsonian; gene therapy; amyloidogenesis; |
| KW | amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; |
| KW | Alzheimer's disease; motor neuropathy; Down's syndrome; |
| KW | Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; |
| KW | Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; |
| KW | neuronal disorder; aging. |
| XX | |
| OS | Synthetic. |
| OS | Homo sapiens. |
| XX | |
| PN | WO2003070760-A2. |
| XX | |
| PD | 28-AUG-2003. |
| XX | |
| XX | 20-FEB-2003; 2003WO-EP001759. |
| XX | |
| PR | 20-FEB-2002; 2002EP-00003844. |
| XX | |
| PA | (HOFF) HOFFMANN LA ROCHE & CO AG F. |
| PA | (MORP-) MORPHOSYS AG. |
| XX | |
| PI | Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T; |
| PI | Loehning C, Loetscher H, Nordstedt C, Rothe C; |
| XX | |
| DR | WPI; 2003-663848/62. |
| XX | |
| XX | New antibody molecule capable of specifically recognizing two regions of |
| PT | the beta-A4 peptide, useful for diagnosing, preventing or treating |
| PT | diseases associated with amyloidogenesis or amyloid-plaque formation |
| PT | (e.g. dementia). |
| XX | |
| PS | Example 5; Page 64; 312pp; English. |
| XX | |
| CC | The present invention describes an antibody molecule (I) capable of |
| CC | specifically recognising two regions of the beta-A4 peptide/Abeta4. The |
| CC | first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp- |
| CC | Ser-Gly-Tyr ADA8986 or its fragment, and the second region comprises the |
| CC | amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Ala-Glu-Asp-Val- |
| CC | Gly ADA8987 or its fragment. Also described: (1) a nucleic acid molecule |
| CC | encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host |
| CC | cell comprising the vector of (2); (4) preparing (I), comprising |
| CC | culturing the host cell of (3) under conditions that allow synthesis of |
| CC | (I) and recovering (I) from the culture; (5) a composition comprising (I), |
| CC | or an antibody molecule produced by method (4); (6) a kit comprising (I), |
| CC | nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising |
| CC | (I); (8) testing the resulting Fab optimisation library by panning |
| CC | against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing |
| CC | of selected, optimised clones; (11) preparing a pharmaceutical |
| CC | composition, comprising optimisation of (I), and formulating the |
| CC | optimised antibody/antibody molecule with a carrier; and (12) a |
| CC | pharmaceutical composition prepared by method (8). (I) has |
| CC | neuroprotective, neurotropic and antiparkinsonian activities, and can be |
| CC | used in gene therapy. The antibody molecule (I), nucleic acid molecule, |
| CC | vector or host is useful in preparing a pharmaceutical composition for |
| CC | the prevention and/or treatment of a disease associated with |
| CC | amyloidogenesis and/or amyloid-plaque formation. The antibody molecule |
| CC | may also be used in preparing a diagnostic composition for the detection |
| CC | of the disease mentioned above. The antibody is used for the |
| CC | disintegration of beta-amyloid plaques or for passive immunisation |
| CC | against beta-amyloid plaque formation. In particular, the disease is |
| CC | dementia, Alzheimer's disease, hereditary cerebral haemorrhage with |
| CC | Creutzfeldt Jacob disease, Parkinson's disease, HIV-related dementia, |
| CC | amyloidosis Duch type, Parkinson's disease, HIV-related dementia, |
| CC | amyotrophic lateral sclerosis or neuronal disorders related to aging. The |
| CC | present sequence is used in the exemplification of the present invention. |

pharmaceutical composition prepared by method (8). (1) has neuroprotective, neurotropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.

Sequence 12 AA;

Query Match 100.0%; Score 53; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12

RESULT 13
ADA90323
ID ADA90323 standard; peptide; 12 AA.
XX ADA90323;
AC
XX
XX
XX 20-NOV-2003 (first entry)
XX
XX MS-Roche #3.4.H12 L-CDR1 amino acid sequence.
XX
KW antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
KW neurotropic; antiparkinsonian; gene therapy; amyloidogenesis;
KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
KW Alzheimer's disease; motor neuropathy; Down's syndrome;
KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
KW neuronal disorder; aging.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO2003070760-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-EP001759.
XX
XX 20-FEB-2002; 2002EP-00003844.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX (MORP-) MORPHOSYS AG.
XX
XX Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T;
XX Loehning C, Loetscher H, Nordstedt C, Rothe C;
XX WPI; 2003-663848/62.
XX
XX
XX New antibody molecule capable of specifically recognizing two regions of
PT the beta-A4 peptide, useful for diagnosing, preventing or treating
PT diseases associated with amyloidogenesis or amyloid-plaque formation
PT (e.g. dementia).
XX
XX Example 5; Page 64; 312pp; English.
XX
XX The present invention describes an antibody molecule (I) capable of
CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The

first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA9886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Val-Gly ADA8987 or its fragment. Also described: (1) a nucleic acid molecule encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (1), comprising culturing the host cell of (3) under conditions that allow synthesis of (1) and recovering (1) from the culture; (5) a composition comprising (1) or an antibody molecule produced by method (4); (6) a kit comprising (1), nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1); (8) testing the resulting Fab optimisation library by panning against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing of selected, optimised clones; (11) preparing a pharmaceutical composition, comprising optimisation of (1), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a pharmaceutical composition prepared by method (8). (1) has neuroprotective, neurotropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.

Sequence 12 AA;

Query Match 100.0%; Score 53; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

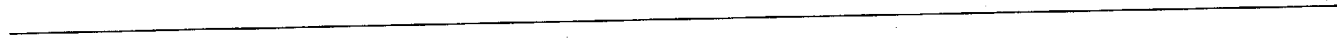
QY 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12

RESULT 14
ADA90324
ID ADA90324 standard; peptide; 12 AA.
XX ADA90324;
AC
XX
XX 20-NOV-2003 (first entry)
XX
XX MS-Roche #3.4.H13 L-CDR1 amino acid sequence.
XX
KW antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
KW neurotropic; antiparkinsonian; gene therapy; amyloidogenesis;
KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
KW Alzheimer's disease; motor neuropathy; Down's syndrome;
KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
KW neuronal disorder; aging.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO2003070760-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-EP001759.
XX
XX 20-FEB-2002; 2002EP-00003844.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX (MORP-) MORPHOSYS AG.

XX
PI Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T;
PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
XX WPI; 2003-663848/62.
XX
XX New antibody molecule capable of specifically recognizing two regions of
PT the beta-A4 peptide, useful for diagnosing, preventing or treating
PT diseases associated with amyloidogenesis or amyloid-plaque formation
PT (e.g. dementia).
XX
XX Example 5; Page 64; 312pp; English.
XX
XX The present invention describes an antibody molecule (I) capable of
CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
CC Ser-Gly-Tyr ADA9886 or its fragment, and the second region comprises the
CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Ala-Glu-Asp-Val-
CC Gly ADA9887 or its fragment. Also described: (1) a nucleic acid molecule
CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host
CC cell comprising the vector of (2); (4) preparing (1), comprising
CC culturing the host cell of (3) under conditions that allow synthesis of
CC (1) and recovering (1) from the culture; (5) a composition comprising (1)
CC or an antibody molecule produced by method (4); (6) a kit comprising (1),
CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
CC (1); (8) testing the resulting Fab optimisation library by panning
CC against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing
CC of selected, optimised clones; (11) preparing a pharmaceutical
CC composition, comprising optimisation of (1), and formulating the
CC optimised antibody/antibody molecule with a carrier; and (12) a
CC pharmaceutical composition prepared by method (8). (1) has
CC neuroprotective, neurotropic and antiparkinsonian activities, and can be
CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,
CC vector or host is useful in preparing a pharmaceutical composition for
CC the prevention and/or treatment of a disease associated with
CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
CC may also be used in preparing a diagnostic composition for the detection
CC of the disease mentioned above. The antibody is used for the
CC disintegration of beta-amyloid plaques or for passive immunisation
CC against beta-amyloid plaque formation. In particular, the disease is
CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 53; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. NO. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12
RESULT 15
ADA90641
ID ADA90641 standard; peptide; 12 AA.
XX
XX ADA90641;
XX
XX
DT 20-NOV-2003 (first entry)
XX
DE MS-Roche #7.9.H1 L-CDR1 amino acid sequence.
XX
XX antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
KW neurotropic; antiparkinsonian; gene therapy; amyloidogenesis;
KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
KW Alzheimer's disease; motor neuropathy; Down's syndrome;
KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;

KW neuronal disorder; aging.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070760-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-BF001759.
XX
PR 20-FEB-2002; 2002EP-00003844.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (MORP-) MORPHOSYS AG.
XX
PI Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T;
PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
XX WPI; 2003-663848/62.
XX
XX New antibody molecule capable of specifically recognizing two regions of
PT the beta-A4 peptide, useful for diagnosing, preventing or treating
PT diseases associated with amyloidogenesis or amyloid-plaque formation
PT (e.g. dementia).
XX
XX Example 5; Page 66; 312pp; English.
XX
XX The present invention describes an antibody molecule (I) capable of
CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
CC Ser-Gly-Tyr ADA9886 or its fragment, and the second region comprises the
CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Ala-Glu-Asp-Val-
CC Gly ADA9887 or its fragment. Also described: (1) a nucleic acid molecule
CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host
CC cell comprising the vector of (2); (4) preparing (1), comprising
CC culturing the host cell of (3) under conditions that allow synthesis of
CC (1) and recovering (1) from the culture; (5) a composition comprising (1)
CC or an antibody molecule produced by method (4); (6) a kit comprising (1),
CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
CC (1); (8) testing the resulting Fab optimisation library by panning
CC against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing
CC of selected, optimised clones; (11) preparing a pharmaceutical
CC composition, comprising optimisation of (1), and formulating the
CC optimised antibody/antibody molecule with a carrier; and (12) a
CC pharmaceutical composition prepared by method (8). (1) has
CC neuroprotective, neurotropic and antiparkinsonian activities, and can be
CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,
CC vector or host is useful in preparing a pharmaceutical composition for
CC the prevention and/or treatment of a disease associated with
CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
CC may also be used in preparing a diagnostic composition for the detection
CC of the disease mentioned above. The antibody is used for the
CC disintegration of beta-amyloid plaques or for passive immunisation
CC against beta-amyloid plaque formation. In particular, the disease is
CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 53; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. NO. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12

Search completed: April 21, 2004, 17:33:12



| | | | | | | |
|----|----|-------|----|----|---------------------|--------------------|
| 1 | 53 | 100.0 | 12 | 1 | PCT-US01-14349-11 | Sequence 11, Appl |
| 2 | 53 | 100.0 | 12 | 1 | PCT-US03-10788-38 | Sequence 38, Appl |
| 3 | 53 | 100.0 | 12 | 1 | PCT-US03-10788-40 | Sequence 40, Appl |
| 4 | 53 | 100.0 | 12 | 1 | PCT-US03-10788-41 | Sequence 41, Appl |
| 5 | 53 | 100.0 | 12 | 1 | PCT-US03-10788-42 | Sequence 42, Appl |
| 6 | 53 | 100.0 | 12 | 1 | PCT-US03-00297-15 | Sequence 15, Appl |
| 7 | 53 | 100.0 | 12 | 1 | PCT-US03-00440-20 | Sequence 20, Appl |
| 8 | 53 | 100.0 | 12 | 1 | PCT-US03-06155-4 | Sequence 4, Appl |
| 9 | 53 | 100.0 | 12 | 1 | PCT-US03-33678-38 | Sequence 38, Appl |
| 10 | 53 | 100.0 | 12 | 1 | PCT-US03-38871-38 | Sequence 38, Appl |
| 11 | 53 | 100.0 | 12 | 1 | PCT-US03-36126-38 | Sequence 38, Appl |
| 12 | 53 | 100.0 | 12 | 1 | PCT-US03-38230-194 | Sequence 194, Appl |
| 13 | 53 | 100.0 | 12 | 1 | PCT-US98-24303-124 | Sequence 124, Appl |
| 14 | 53 | 100.0 | 12 | 15 | US-09-191-817-124 | Sequence 11, Appl |
| 15 | 53 | 100.0 | 12 | 19 | US-09-563-222-11 | Sequence 11, Appl |
| 16 | 53 | 100.0 | 12 | 19 | US-09-563-222C-11 | Sequence 38, Appl |
| 17 | 53 | 100.0 | 12 | 23 | US-09-828-708-38 | Sequence 40, Appl |
| 18 | 53 | 100.0 | 12 | 23 | US-09-828-708-40 | Sequence 41, Appl |
| 19 | 53 | 100.0 | 12 | 23 | US-09-828-708-41 | Sequence 42, Appl |
| 20 | 53 | 100.0 | 12 | 23 | US-09-828-708-42 | Sequence 62, Appl |
| 21 | 53 | 100.0 | 12 | 26 | US-10-001-934-62 | Sequence 19, Appl |
| 22 | 53 | 100.0 | 12 | 28 | US-10-375-046-19 | Sequence 20, Appl |
| 23 | 53 | 100.0 | 12 | 29 | US-10-338-366-20 | Sequence 8, Appl |
| 24 | 53 | 100.0 | 12 | 29 | US-10-374-932-8 | Sequence 8, Appl |
| 25 | 53 | 100.0 | 12 | 29 | US-10-379-741-8 | Sequence 8, Appl |
| 26 | 53 | 100.0 | 12 | 31 | US-10-684-957-38 | Sequence 38, Appl |
| 27 | 53 | 100.0 | 12 | 32 | US-10-714-353-38 | Sequence 38, Appl |
| 28 | 53 | 100.0 | 12 | 32 | US-10-726-332-194 | Sequence 194, Appl |
| 29 | 53 | 100.0 | 28 | 1 | PCT-US03-32243-68 | Sequence 68, Appl |
| 30 | 53 | 100.0 | 28 | 28 | US-10-469-711-57 | Sequence 57, Appl |
| 31 | 53 | 100.0 | 28 | 31 | US-10-684-109-68 | Sequence 68, Appl |
| 32 | 53 | 100.0 | 28 | 33 | US-60-418-031-57 | Sequence 57, Appl |
| 33 | 53 | 100.0 | 66 | 33 | US-60-196-718-5772 | Sequence 5772, Ap |
| 34 | 53 | 100.0 | 74 | 1 | PCT-US03-12202-23 | Sequence 23, Appl |
| 35 | 53 | 100.0 | 74 | 27 | US-10-425-687-23 | Sequence 23, Appl |
| 36 | 53 | 100.0 | 80 | 22 | US-09-791-537-35418 | Sequence 35418, A |
| 37 | 53 | 100.0 | 80 | 22 | US-09-791-537-36133 | Sequence 36133, A |
| 38 | 53 | 100.0 | 81 | 22 | US-09-791-537-35334 | Sequence 35334, A |
| 39 | 53 | 100.0 | 81 | 22 | US-09-791-537-35348 | Sequence 35348, A |
| 40 | 53 | 100.0 | 81 | 22 | US-09-791-537-35453 | Sequence 35453, A |
| 41 | 53 | 100.0 | 81 | 22 | US-09-791-537-35493 | Sequence 35493, A |
| 42 | 53 | 100.0 | 81 | 22 | US-09-791-537-36105 | Sequence 36105, A |
| 43 | 53 | 100.0 | 81 | 22 | US-09-791-537-36107 | Sequence 36107, A |
| 44 | 53 | 100.0 | 81 | 22 | US-09-791-537-36163 | Sequence 36163, A |
| 45 | 53 | 100.0 | 81 | 22 | US-09-791-537-36683 | Sequence 36683, A |

ALIGNMENTS

```

RESULT 1
PCT-US01-14349-11
; Sequence 11, Application PC/TUS0114349
; GENERAL INFORMATION:
; APPLICANT: EPICYTE Pharmaceuticals, Inc.
; APPLICANT: Hiatt, Andrew C.
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406PC
; CURRENT APPLICATION NUMBER: PCT/US01/14349
; CURRENT FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapien
PCT-US01-14349-11

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Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | Score | Match | Length | DB | ID | Description |
|--------|-------|-------|-------|--------|----|----|-------------|
| No. | | | | | | | |

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QY      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 2
PCT-US02-10788-38
; Sequence 38, Application PC/TUS0210788
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Antibodies inhibiting autoimmune disease
; FILE REFERENCE: 1361.005W01
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-10788-38

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 3
PCT-US02-10788-40
; Sequence 40, Application PC/TUS0210788
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Antibodies inhibiting autoimmune disease
; FILE REFERENCE: 1361.005W01
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-10788-40

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 4
PCT-US02-10788-41
; Sequence 41, Application PC/TUS0210788
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Antibodies inhibiting autoimmune disease
; FILE REFERENCE: 1361.005W01
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-10788-41

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 5
PCT-US02-10788-42
; Sequence 42, Application PC/TUS0210788
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Antibodies inhibiting autoimmune disease
; FILE REFERENCE: 1361.005W01
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-10788-42

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 6
PCT-US03-00297-15
; Sequence 15, Application PC/TUS0300297
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, Henrik
; APPLICANT: Jensenius, Jens
; TITLE OF INVENTION: Cancer-Associated Epitope
; FILE REFERENCE: 1361.017W01
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,208
; PRIOR FILING DATE: 2002-01-03
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15

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; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-00297-15

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 7
PCT-US03-00440-20
; Sequence 20, Application PC/TUS0300440
; GENERAL INFORMATION:
; APPLICANT: Medarex, Inc. et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
; FILE REFERENCE: MXI-180PC
; CURRENT APPLICATION NUMBER: PCT/US03/00440
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/347649
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/404427
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/431684
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-00440-20

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 8
PCT-US03-06155-4
; Sequence 4, Application PC/TUS0306155
; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: Antagonistic Anti-hFas Ligand Human Antibodies and Fragments Thereof
; FILE REFERENCE: X15450
; CURRENT APPLICATION NUMBER: PCT/US03/06155
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-06155-4

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 9
PCT-US03-32678-38
; Sequence 38, Application PC/TUS0332678
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamm
; FILE REFERENCE: 01-1635-G
; CURRENT APPLICATION NUMBER: PCT/US03/32678
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-32678-38

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 10
PCT-US03-32871-38
; Sequence 38, Application PC/TUS0332871
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Medarex, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamm
; FILE REFERENCE: 01-1635-G
; CURRENT APPLICATION NUMBER: PCT/US03/32871
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-32871-38

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 11
PCT-US03-36126-38
; Sequence 38, Application PC/TUS0336126

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GENERAL INFORMATION:
; APPLICANT: Genmab A/S
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD25
; FILE REFERENCE: GMI-059PC
; CURRENT APPLICATION NUMBER: PCT/US03/36126
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426690
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-36126-38

Query Match 100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
| | | | | | | | | | | |
DB 1 RASQSVSSSYLA 12

RESULT 12
PCT-US03-38234-194
; Sequence 194, Application PC/TUS0338234
; GENERAL INFORMATION:
; APPLICANT: Abgenix, Inc.
; APPLICANT: Lexicon Genetics Incorporated
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 AND USES THEREOF
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: PCT/US03/38234
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38234-194

Query Match 100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
| | | | | | | | | | | |
DB 1 RASQSVSSSYLA 12

RESULT 13
PCT-US98-24303-124
; Sequence 124, Application PC/TUS9824303
; GENERAL INFORMATION:
; APPLICANT: Purdue Pharma L.P.
; TITLE OF INVENTION: MODIFIED ANTIBODIES WITH ENHANCED ABILITY TO ELICIT AN
; FILE REFERENCE: 6750-015-228
; CURRENT APPLICATION NUMBER: PCT/US98/24303
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/081,403

; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/065,716
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 124
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-24303-124

Query Match 100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
| | | | | | | | | | | |
DB 1 RASQSVSSSYLA 12

RESULT 14
US-09-191-817-124
; Sequence 124, Application US/09191817
; GENERAL INFORMATION:
; APPLICANT: Burch, R.M.
; TITLE OF INVENTION: MODIFIED ANTIBODIES WITH ENHANCED ABILITY TO ELICIT AN
; FILE REFERENCE: 6750-015
; CURRENT APPLICATION NUMBER: US/09/191,817
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/081,403
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/065,716
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 124
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-191-817-124

Query Match 100.0%; Score 53; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
| | | | | | | | | | | |
DB 1 RASQSVSSSYLA 12

RESULT 15
US-09-563-222-11
; Sequence 11, Application US/09563222
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-11

Query Match 100.0%; Score 53; DB 19; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
| | | | | | | | | |
Db 1 RASQSVSSSYLA 12

Search completed: April 21, 2004, 17:57:23
Job time : 179.435 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2004, 17:37:29 ; Search time 36.1739 Seconds
(without alignments)
91.715 Million cell updates/sec

Title:

SEQ4

Perfect score: 53

Sequence: 1 rasqsvssyla 12

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 13: /cgn2_6/ptodata/2/pubaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 53 | 100.0 | 12 | 9 US-09-828-708-38 | Sequence 38, Appl |
| 2 | 53 | 100.0 | 12 | 9 US-09-828-708-40 | Sequence 40, Appl |
| 3 | 53 | 100.0 | 12 | 9 US-09-828-708-41 | Sequence 41, Appl |
| 4 | 53 | 100.0 | 12 | 9 US-09-828-708-42 | Sequence 42, Appl |
| 5 | 53 | 100.0 | 12 | 10 US-09-563-222-11 | Sequence 11, Appl |
| 6 | 53 | 100.0 | 12 | 10 US-10-379-741-8 | Sequence 8, Appl |
| 7 | 53 | 100.0 | 12 | 14 US-10-001-934-62 | Sequence 62, Appl |
| 8 | 53 | 100.0 | 12 | 15 US-10-374-932-8 | Sequence 8, Appl |
| 9 | 53 | 100.0 | 12 | 15 US-10-338-366-20 | Sequence 20, Appl |
| 10 | 53 | 100.0 | 12 | 15 US-10-275-046-19 | Sequence 19, Appl |
| 11 | 53 | 100.0 | 28 | 12 US-10-269-711-57 | Sequence 57, Appl |
| 12 | 53 | 100.0 | 74 | 14 US-10-125-687-23 | Sequence 23, Appl |
| 13 | 53 | 100.0 | 95 | 14 US-09-948-939-5 | Sequence 5, Appl |
| 14 | 53 | 100.0 | 95 | 14 US-10-041-860-371 | Sequence 371, Appl |
| 15 | 53 | 100.0 | 96 | 12 US-10-453-698-29 | Sequence 29, Appl |

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| 16 | 53 | 100.0 | 96 | 14 US-10-194-975-82 | Sequence 82, Appl |
| 17 | 53 | 100.0 | 96 | 14 US-10-153-382-22 | Sequence 22, Appl |
| 18 | 53 | 100.0 | 96 | 14 US-10-041-860-10 | Sequence 10, Appl |
| 19 | 53 | 100.0 | 96 | 14 US-10-041-860-370 | Sequence 370, Appl |
| 20 | 53 | 100.0 | 96 | 14 US-10-041-860-376 | Sequence 376, Appl |
| 21 | 53 | 100.0 | 96 | 14 US-10-041-860-377 | Sequence 377, Appl |
| 22 | 53 | 100.0 | 96 | 15 US-10-308-817-29 | Sequence 29, Appl |
| 23 | 53 | 100.0 | 96 | 15 US-10-309-762-35 | Sequence 35, Appl |
| 24 | 53 | 100.0 | 101 | 14 US-10-010-729-31 | Sequence 31, Appl |
| 25 | 53 | 100.0 | 104 | 9 US-09-828-708-6 | Sequence 6, Appl |
| 26 | 53 | 100.0 | 105 | 9 US-09-828-708-3 | Sequence 3, Appl |
| 27 | 53 | 100.0 | 105 | 9 US-09-828-708-5 | Sequence 5, Appl |
| 28 | 53 | 100.0 | 105 | 9 US-09-828-708-7 | Sequence 7, Appl |
| 29 | 53 | 100.0 | 106 | 15 US-10-309-762-163 | Sequence 163, Appl |
| 30 | 53 | 100.0 | 107 | 15 US-10-309-762-38 | Sequence 38, Appl |
| 31 | 53 | 100.0 | 107 | 15 US-10-309-762-44 | Sequence 44, Appl |
| 32 | 53 | 100.0 | 107 | 15 US-10-309-762-80 | Sequence 80, Appl |
| 33 | 53 | 100.0 | 108 | 10 US-09-300-425B-21 | Sequence 21, Appl |
| 34 | 53 | 100.0 | 108 | 12 US-10-292-088-113 | Sequence 113, Appl |
| 35 | 53 | 100.0 | 108 | 12 US-10-269-711-21 | Sequence 21, Appl |
| 36 | 53 | 100.0 | 108 | 14 US-10-041-860-47 | Sequence 47, Appl |
| 37 | 53 | 100.0 | 108 | 14 US-10-041-860-49 | Sequence 49, Appl |
| 38 | 53 | 100.0 | 108 | 14 US-10-041-860-225 | Sequence 225, Appl |
| 39 | 53 | 100.0 | 108 | 14 US-10-041-860-226 | Sequence 226, Appl |
| 40 | 53 | 100.0 | 108 | 14 US-10-041-860-259 | Sequence 259, Appl |
| 41 | 53 | 100.0 | 108 | 14 US-10-041-860-260 | Sequence 260, Appl |
| 42 | 53 | 100.0 | 108 | 14 US-10-041-860-369 | Sequence 369, Appl |
| 43 | 53 | 100.0 | 108 | 14 US-10-041-860-375 | Sequence 375, Appl |
| 44 | 53 | 100.0 | 108 | 14 US-10-127-890-150 | Sequence 150, Appl |
| 45 | 53 | 100.0 | 108 | 14 US-10-321-558-32 | Sequence 32, Appl |

ALIGNMENTS

RESULT 1

US-09-828-708-38
; Sequence 38, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-38

Query Match 100.0%; Score 53; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12

Db 1 RASQSVSSSYLA 12

RESULT 2

US-09-828-708-40
; Sequence 40, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-40

Query Match 100.0%; Score 53; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12

RESULT 3
US-09-828-708-41
; Sequence 41, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-41

Query Match 100.0%; Score 53; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12

RESULT 4
US-09-828-708-42
; Sequence 42, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-42

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Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RASQSVSSSYLA 12

RESULT 5
US-09-563-222-11
; Sequence 11, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-11

Query Match 100.0%; Score 53; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12

RESULT 6
US-10-379-741-8
; Sequence 8, Application US/10379741
; Publication No. US20040071702A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus Antonius
; APPLICANT: Schuurman, Janine
; APPLICANT: Gerritsen, Arnout F.
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Petersen, Jorgen
; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
; FILE REFERENCE: GMI-024CP2
; CURRENT APPLICATION NUMBER: US/10/379,741
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 10/226615
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-741-8

Query Match 100.0%; Score 53; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12

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; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
; FILE REFERENCE: MXI-180
; CURRENT APPLICATION NUMBER: US/10/338,366
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/347649
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/404427
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/431684
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-366-20

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 RASQSVSSSYLA 12

RESULT 10
US-10-275-046-19
; Sequence 19, Application US/10275046
; Publication No. US20040019187A1
; GENERAL INFORMATION:
; APPLICANT: Nagy et al.
; TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPTIDES
; FILE REFERENCE: GPCG-P01-260
; CURRENT APPLICATION NUMBER: US/10/275,046
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 00110063.5
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-DR specific polypeptide
US-10-275-046-19

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Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 RASQSVSSSYLA 12

RESULT 11
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; Sequence 57, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; FILE REFERENCE: 6989.US.01
; CURRENT APPLICATION NUMBER: US/10/269,711

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; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-57

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Best Local Similarity 100.0%; Pred. No. 0.014; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12

RESULT 12
US-10-125-687-23
; Sequence 23, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/125,697
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-687-23

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Best Local Similarity 100.0%; Pred. No. 0.038; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 17 RASQSVSSSYLA 28

RESULT 13
US-09-948-939-5
; Sequence 5, Application US/09948939
; Publication No. US20020086014A1
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
; APPLICANT: Haik, Edward L.
; APPLICANT: Lonberg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/09/948,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 05/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: light chain variable region predicted sequence for
; OTHER INFORMATION: Vx A-27 germline
US-09-948-939-5

Query Match 100.0%; Score 53; DB 12; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.05; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 14
US-10-041-860-371
; Sequence 371, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 371
; LENGTH: 95
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 54
; OTHER INFORMATION: Xaa = Any Amino Acid
; NAME/KEY: VARIANT
; LOCATION: 54
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-371

Query Match 100.0%; Score 53; DB 14; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.05; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 15
US-10-453-698-29
; Sequence 29, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 96
; TYPE: PRT
; ORGANISM: human
US-10-453-698-29

Query Match 100.0%; Score 53; DB 12; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.05; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | | | | | | |
Db 24 RASQVSSSYLA 35

Search completed: April 21, 2004, 18:02:06
Job time : 36.1739 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:28:28 ; Search time 14.4348 Seconds
(without alignments)
42.918 Million cell updates/sec

Title: SRQ4

Perfect score: 53

Sequence: 1 rasqvssvssyla 12

Scoring table: BLOSUM62

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 3 | 53 | 100.0 | 108 | 1 | US-08-488-113B-150 |
| 4 | 53 | 100.0 | 108 | 1 | US-08-477-484B-150 |
| 5 | 53 | 100.0 | 108 | 2 | US-08-646-360-150 |
| 6 | 53 | 100.0 | 108 | 2 | US-08-232-081B-42 |
| 7 | 53 | 100.0 | 108 | 3 | US-08-839-765-150 |
| 8 | 53 | 100.0 | 108 | 3 | US-09-136-389-150 |
| 9 | 53 | 100.0 | 108 | 4 | US-09-610-838-150 |
| 10 | 53 | 100.0 | 108 | 4 | US-09-711-485-150 |
| 11 | 53 | 100.0 | 109 | 4 | US-09-025-769B-16 |
| 12 | 53 | 100.0 | 110 | 4 | US-09-025-769B-30 |
| 13 | 53 | 100.0 | 110 | 4 | US-09-025-769B-47 |
| 14 | 53 | 100.0 | 116 | 1 | US-08-053-131-183 |
| 15 | 53 | 100.0 | 116 | 2 | US-08-096-762-183 |
| 16 | 53 | 100.0 | 116 | 3 | US-09-042-353-46 |
| 17 | 53 | 100.0 | 116 | 4 | US-08-758-417A-311 |
| 18 | 53 | 100.0 | 150 | 3 | US-08-862-124-5 |
| 19 | 53 | 100.0 | 224 | 4 | US-09-456-090A-40 |
| 20 | 53 | 100.0 | 224 | 4 | US-09-456-090A-52 |
| 21 | 53 | 100.0 | 224 | 4 | US-09-456-090A-76 |
| 22 | 53 | 100.0 | 226 | 4 | US-09-456-090A-38 |
| 23 | 53 | 100.0 | 226 | 4 | US-09-456-090A-42 |
| 24 | 53 | 100.0 | 226 | 4 | US-09-456-090A-50 |
| 25 | 53 | 100.0 | 226 | 4 | US-09-456-090A-80 |
| 26 | 53 | 100.0 | 226 | 4 | US-09-456-090A-86 |
| 27 | 53 | 100.0 | 287 | 3 | US-08-862-124-17 |

| | | | | | | |
|----|----|-------|-----|---|--------------------|-------------------|
| 28 | 53 | 100.0 | 304 | 3 | US-08-862-124-14 | Sequence 14, Appl |
| 29 | 52 | 98.1 | 108 | 3 | US-09-240-274-178 | Sequence 178, App |
| 30 | 50 | 94.3 | 107 | 4 | US-08-635-109-5 | Sequence 5, Appl |
| 31 | 50 | 94.3 | 109 | 1 | US-08-278-852-147 | Sequence 147, App |
| 32 | 50 | 94.3 | 109 | 1 | US-08-899-575-147 | Sequence 147, App |
| 33 | 50 | 94.3 | 109 | 1 | US-08-899-575-147 | Sequence 147, App |
| 34 | 50 | 94.3 | 109 | 5 | PCT-US95-08743-147 | Sequence 147, App |
| 35 | 50 | 94.3 | 224 | 4 | US-09-456-090A-44 | Sequence 44, Appl |
| 36 | 50 | 94.3 | 224 | 4 | US-09-456-090A-78 | Sequence 78, Appl |
| 37 | 49 | 92.5 | 112 | 1 | US-08-276-852-151 | Sequence 151, App |
| 38 | 49 | 92.5 | 112 | 1 | US-08-899-575-151 | Sequence 151, App |
| 39 | 49 | 92.5 | 112 | 1 | US-08-899-575-151 | Sequence 151, App |
| 40 | 49 | 92.5 | 112 | 5 | PCT-US95-08743-151 | Sequence 151, App |
| 41 | 49 | 92.5 | 226 | 4 | US-09-456-090A-72 | Sequence 72, Appl |
| 42 | 49 | 92.5 | 226 | 4 | US-09-456-090A-74 | Sequence 74, Appl |
| 43 | 48 | 90.6 | 129 | 2 | US-08-480-774A-4 | Sequence 4, Appl |
| 44 | 48 | 90.6 | 141 | 4 | US-09-472-087-88 | Sequence 88, Appl |
| 45 | 48 | 90.6 | 235 | 4 | US-09-472-087-14 | Sequence 14, Appl |

ALIGNMENTS

RESULT 1
US-09-472-087-87
; Sequence 87, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-87

Query Match 100.0%; Score 53; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 2
US-08-652-558-49
; Sequence 49, Application US/08652558
; Patent No. 5861155
; GENERAL INFORMATION:
; APPLICANT: LIN, AUGUSTINE YEE-THARN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF
; STREET: 75 STATE STREET, 23RD FLOOR
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA

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;
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/552,558
; FILING DATE: JUNE 6, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB94/00387
; FILING DATE: NOVEMBER 21, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, LEON R.
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,497-L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-652-558-49

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Query Match      100.0%; Score 53; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. NO. 0.0072;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 RASQSVSSSYLA 12
DB      24 RASQSVSSSYLA 35

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RESULT 3

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US-08-488-113B-150
; Sequence 150, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992

```

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-150

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Query Match      100.0%; Score 53; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. NO. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 RASQSVSSSYLA 12
DB      24 RASQSVSSSYLA 35

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RESULT 4

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US-08-477-484B-150
; Sequence 150, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567

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FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-150

Query Match 100.0%; Score 53; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 5
US-08-646-360-150
Sequence 150, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studzika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: US/08/646.360
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064.691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988.430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901.707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787.567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-150

Query Match 100.0%; Score 53; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 6
US-08-232-081B-42
Sequence 42, Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WUJENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-232-081B-42

Query Match 100.0%; Score 53; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 7
US-08-839-765-150
; Sequence 150, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELEPHONE: 312/707-8899
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-839-765-150
Query Match 100.0%; Score 53; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. NO. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 8
US-09-136-389-150
; Sequence 150, Application US/09136389
; Patent No. 6146850

GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-136-389-150
Query Match 100.0%; Score 53; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. NO. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 9
US-09-610-938-150
; Sequence 150, Application US/09610938
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.

```
/
/ APPLICANT: Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ TITLE OF INVENTION: Proteins
/ NUMBER OF SEQUENCES: 173
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/610,838
/ FILING DATE: 06-JUL-2000
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/136,389
/ FILING DATE: 18-AUG-1998
/ APPLICATION NUMBER: 08/646,360
/ FILING DATE: 13-MAY-1996
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70-P4
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70-P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-9155
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 150:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 108 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-610-838-150

Query Match 100.0%; Score 53; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 10
US-09-711-485-150
; Sequence 150, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
```

```
/
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ TITLE OF INVENTION: Proteins
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/711,485
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/839,765
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70-P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 150:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 108 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-711-485-150

Query Match 100.0%; Score 53; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 11
US-09-025-769B-16
; Sequence 16, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
```

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10021
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769B
;; FILING DATE: 18-FEB-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 109 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-025-769B-16

Query Match 100.0%; Score 53; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 12
US-09-025-769B-30
; Sequence 30, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Illeg, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0

;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 30:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 110 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-025-769B-30

Query Match 100.0%; Score 53; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 13
US-09-025-769B-47
; Sequence 47, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Illeg, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-47

Query Match 100.0%; Score 53; DB 4; Length 110;

Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
| | | | | | | |
Db 24 RASQSVSSSYLA 35

RESULT 14
US-08-053-131-183
; Sequence 183, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lomberg, Nils
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELEPHONE: 415-326-2422
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-053-131-183

Query Match 100.0%; Score 53; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
| | | | | | | |
Db 44 RASQSVSSSYLA 55

RESULT 15
US-08-096-762-183
; Sequence 183, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lomberg, Nils

APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELEPHONE: 415-326-2422
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-096-762-183

Query Match 100.0%; Score 53; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
| | | | | | | |
Db 44 RASQSVSSSYLA 55

Search completed: April 21, 2004, 17:40:04
Job time : 14.4348 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:48 ; Search time 3.55072 Seconds
(without alignments)
102.653 Million cell updates/sec

Title: SEQ5
Perfect score: 31
Sequence: 1 atserat 7
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 31 | 100.0 | 497 | 1 KPYC ARATH | O65595 arabidopsis |
| 2 | 28 | 90.3 | 5703 | 1 MUSB HUMAN | Q9hc84 homo sapien |
| 3 | 27 | 87.1 | 249 | 1 MABC BOVIN | O02659 bos taurus |
| 4 | 27 | 87.1 | 283 | 1 NI42 ARATH | O84036 arabidopsis |
| 5 | 27 | 87.1 | 475 | 1 MMR STRCO | P11545 streptomyce |
| 6 | 27 | 87.1 | 676 | 1 VGP EBOSB | Q66814 ebola virus |
| 7 | 27 | 87.1 | 676 | 1 VGP EBOSB | Q66798 ebola virus |
| 8 | 27 | 87.1 | 695 | 1 PLB2 CANGA | Q8t906 candida gla |
| 9 | 27 | 87.1 | 777 | 1 RTN1 RAT | Q64548 rattus norv |
| 10 | 27 | 87.1 | 888 | 1 STU2 YEAST | O13339 schizosacch |
| 11 | 27 | 87.1 | 988 | 1 TERT SCHPO | P35228 homo sapien |
| 12 | 27 | 87.1 | 1153 | 1 NS2A HUMAN | P35436 mus musculu |
| 13 | 27 | 87.1 | 1464 | 1 NME1 MOUSE | Q00959 rattus norv |
| 14 | 27 | 87.1 | 1464 | 1 NME1 RAT | P78346 homo sapien |
| 15 | 26 | 83.9 | 268 | 1 RP30 HUMAN | P23949 mus musculu |
| 16 | 26 | 83.9 | 367 | 1 TISD MOUSE | O13326 schizosacch |
| 17 | 26 | 83.9 | 429 | 1 CYSD SCHPO | Q9ux32 scifolobos |
| 18 | 26 | 83.9 | 444 | 1 ARLY SULSO | O9z8m8 arabidopsis |
| 19 | 26 | 83.9 | 856 | 1 EZAL ARATH | P37335 schizopyll |
| 20 | 26 | 83.9 | 928 | 1 MAY4 SCHCO | P31999 l genome po |
| 21 | 26 | 83.9 | 3255 | 1 POLG LMV0 | P89876 l genome po |
| 22 | 26 | 83.9 | 3255 | 1 POLG LMVE | O94686 schizosacch |
| 23 | 25 | 80.6 | 94 | 1 RL43 SCHPO | O52984 rhizobium m |
| 24 | 25 | 80.6 | 156 | 1 PHS FAGGE | O22077 fagus crena |
| 25 | 25 | 80.6 | 182 | 1 PHS FAGGE | P48144 clarias mac |
| 26 | 25 | 80.6 | 195 | 1 PACA CLAMA | P45705 bacillus st |
| 27 | 25 | 80.6 | 210 | 1 XINA BACST | P50538 mus musculu |
| 28 | 25 | 80.6 | 215 | 1 Y215 ADE02 | Q01622 helobdella |
| 29 | 25 | 80.6 | 229 | 1 MAD MOUSE | P40688 drosophila |
| 30 | 25 | 80.6 | 427 | 1 HML2 HELRO | P22757 paracentrot |
| 31 | 25 | 80.6 | 548 | 1 SWA DROME | O33137 mycobacteri |
| 32 | 25 | 80.6 | 587 | 1 HE EARLI | |
| 33 | 25 | 80.6 | 587 | 1 RECN MYCTU | |

| | | | | | |
|----|----|------|------|--------------|--------------------|
| 34 | 25 | 80.6 | 1018 | 1 YDIJ ECOLI | P77748 escherichia |
| 35 | 25 | 80.6 | 1027 | 1 YDIJ HABIN | Q57252 haemophilus |
| 36 | 24 | 77.4 | 119 | 1 YPAA LACLA | Q02009 lactococcus |
| 37 | 24 | 77.4 | 180 | 1 PSP2 CAEEL | O62193 caenorhabdi |
| 38 | 24 | 77.4 | 202 | 1 COAT ELV | P35927 erysimum la |
| 39 | 24 | 77.4 | 229 | 1 YI67 CAEEL | Q11083 caenorhabdi |
| 40 | 24 | 77.4 | 265 | 1 HMEC XENLA | P52729 xenopus lae |
| 41 | 24 | 77.4 | 325 | 1 YHU3 YEAST | P38844 saccharomyc |
| 42 | 24 | 77.4 | 328 | 1 SGS3 DROER | P13730 drosophila |
| 43 | 24 | 77.4 | 337 | 1 CAHE MOUSE | Q9wvt6 mus musculu |
| 44 | 24 | 77.4 | 361 | 1 COL9 ARATH | O22800 arabidopsis |
| 45 | 24 | 77.4 | 374 | 1 RECA STRCO | O50487 streptomyce |

ALIGNMENTS

RESULT 1
KPYC_ARATH STANDARD; PRT; 497 AA.
ID AC O65595;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable pyruvate kinase, cytosolic isozyme (EC 2.7.1.40) (PK).
GN A14G36390 OR M3E9.180
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
EN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RC MEDLINE=20083486; PubMed=10617198;
RA Mayer K.F.X., Schueeller C., Wambutt R., Murphy G., Volckaert G.,
Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
Weicheelgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
Kraus M., Delsen M., Pulgomech P., Watson M., Schmidheini T.,
Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
Vos P., Hohnel J., Zimmermann W., Wedler H., Ridley P.,
Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F.,
Van der Schueren J., Grymonprez B., Chuang Y.-J., Bastiaens I., Aert R.,
Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
Weitzenecker T., Bothe G., Ransperger U., Hilbert H., Braun M.,
Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
Berneser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
De Keyser A., Buysshaert C., Giesen J., Villarroel R., De Clercq R.,
Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Alen S.,
Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
Petrett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fartmann B., Granderath K., Pauner D., Herzl A.,
Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,
Massenat O., Quigley F., Claubald G., Muendlein A., Felber R.,
Schnebl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
Chedof F., Cooke R., Berger C., Monfort A., Casacuberta E.,
Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielek C.,
Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
Parnell L., Dedhia N., Gnoj L., Schutz K., Huang B., Spiegel L.,
Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
Stonking T., Kalicki J., Graves T., Harmon G., Edwards J.,
Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
Kramer J., Fulton L., Mardis E., Dance M., Pepin K., Hillier L.W.,
Nelson J., Speth J., Ryan E., Andrews S., Geisel C., Layman D.,
Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,

RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekhar M., Maturo A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Gracat S., Shohdy N., Hasegawa A., Hameed A., Lodi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:769-777(1999).
RN
CC -1- CATALYTIC ACTIVITY: ATP + pyruvate = ADP + phosphoenolpyruvate.
CC -1- COFACTOR: Requires magnesium and potassium.
CC -1- PATHWAY: Glycolysis; final step.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the pyruvate kinase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC
CC -----
DR ENBL; AL022223; CAA18231.1; -;
DR ENBL; AL161565; CAB79494.1; -;
DR HSP; T05065; T05065.
DR InterPro; IPR001697; Pyruvate_kinase.
DR Pfam; PF02287; PK_C1.
DR PRINTS; PR01050; PYRUVATE_KINASE.
DR PRODOM; PD001009; Pyruvate_kinase; 1.
DR TIGRFAMs; TIGR01064; PYRUV_KIN; 1.
DR TRANSFAS; PS00110; PYRUVATE_KINASE; 1.
KW Transferase; Kinase; Glycolysis; Magnesium.
FT ACT_SITE 227 227 BY SIMILARITY.
FT METAL 229 229 MAGNESIUM (BY SIMILARITY).
FT METAL 250 250 MAGNESIUM (BY SIMILARITY).
FT METAL 251 251 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 497 AA; 54319 MW; 45D43EF54A99F62 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 497;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 377 ATSSRAT 383

RESULT 2
ID MUC5B_HUMAN STANDARD; PRT; 5703 AA.
AC Q9HC64; Q00447; Q00573; Q14985; Q15494; Q95291; Q95451; Q14881;
AC Q9552; Q9UE28;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mucin 5B precursor (Mucin 5 subtype B, tracheobronchial) (High
DE molecular weight salivary mucin MGI) (Sublingual gland mucin).
GN MUC5B OR MUC5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 1-1594 FROM N.A.
RA Chen Y., Di Y.P., Wu R.;
RT "Molecular cloning of the amino-terminal and 5'-flanking region of the
RT human MUC5B mucin gene.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-1325 FROM N.A.

RX MEDLINE=99009274; PubMed=9790959;
RA Offner G.D., Nunes D.P., Keates A.C., Afdhal N.H., Troxler R.F.;
RT "The amino-terminal sequence of MUC5B contains conserved
RT functional D domains: implications for tissue-specific mucin
RT functions.";
RL Biochem. Biophys. Res. Commun. 251:350-355(1998).
RN [3]
RP SEQUENCE OF 40-1324 FROM N.A.
RX MEDLINE=99029327; PubMed=9804771;
RA Desseyn J.-L., Buisine M.P., Porchet N., Aubert J.-P., Laine A.;
RT "Genomic organization of the human mucin gene MUC5B: cDNA and genomic
RT sequences upstream of the large central exon.";
RL J. Biol. Chem. 273:30157-30164(1998).
RN [4]
RP SEQUENCE OF 1326-4895 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97166151; PubMed=9013550;
RA Desseyn J.-L., Guyonnet-Duperrat V., Porchet N., Aubert J.-P.,
RA Laine A.;
RT "Human mucin gene MUC5B, the 10.7 kb large central exon encodes
RT various alternate subdomains resulting in a super-repeat. Structural
RT evidence for a 1p15.5 gene family.";
RL J. Biol. Chem. 272:3168-3178(1997).
RN [5]
RP SEQUENCE OF 4057-4480 FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=97292540; PubMed=9147051;
RA Nielsen P.A., Bennett E.P., Wandall H.H., Therkildsen M.H.,
RA Hannibal J., Clausen H.;
RT "Identification of a major human high molecular weight salivary mucin
RT (MGI) as tracheobronchial mucin MUC5B.";
RL Glycobiology 7:413-419(1997).
RN [6]
RP SEQUENCE OF 4721-5703 FROM N.A.
RC TISSUE=Gall bladder;
RX MEDLINE=97293229; PubMed=9164870;
RA Keates A.C., Nunes D.P., Afdhal N.H., Troxler R.F., Offner G.D.;
RT "Molecular cloning of a novel human gall bladder mucin: complete C-
RT terminal sequence and genomic organization of MUC5B.";
RL Biochem. J. 324:295-303(1997).
RN [7]
RP SEQUENCE OF 4809-5687 FROM N.A.
RC TISSUE=Sublingual gland;
RX MEDLINE=96125355; PubMed=8554565;
RA Troxler R.F., Offner G.D., Zhang F., Iontcheva I., Oppenheim F.G.;
RT "Molecular cloning of a novel high molecular weight mucin (MGI)
RT from human sublingual gland.";
RL Biochem. Biophys. Res. Commun. 217:1112-1119(1995).
RN [8]
RP SEQUENCE OF 4859-5703 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97347489; PubMed=9201995;
RA Desseyn J.-L., Aubert J.-P., Porchet N., Laine A.;
RT "Genomic organization of the 3 region of the human MUC5B mucin.";
RL J. Biol. Chem. 272:16873-16883(1997).
CC -1- FUNCTION: Salivary mucin that is thought to contribute to the
CC lubricating and viscoelastic properties of whole saliva.
CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- TISSUE SPECIFICITY: Expressed mainly in bronchus glands and also
CC in submaxillary glands, endocervix, gall bladder, and pancreas.
CC -1- PTM: Highly glycosylated.
CC -1- SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.
CC -1- SIMILARITY: Contains 3 VWFC domains.
CC -1- SIMILARITY: Contains 4 VWFC domains.
CC -1- SIMILARITY: Contains 1 C-terminal cysteine knot-like (CTCK) domain.
CC
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CC or send an email to license@isb-sib.ch).

| | | | | | | | |
|----|---|----|----------|------|------|--------------------------------|---------------|
| CC | EMBL; AF107890; AAG33673.1; - | FT | CARBOHYD | 5037 | 5037 | N-LINKED (GLCNAC. . .) | (POTENTIAL) . |
| DR | EMBL; AF086604; AAC67545.1; - | FT | CARBOHYD | 5052 | 5052 | N-LINKED (GLCNAC. . .) | (POTENTIAL) . |
| DR | EMBL; AF004862; CAA06167.1; - | FT | CARBOHYD | 5156 | 5156 | N-LINKED (GLCNAC. . .) | (POTENTIAL) . |
| DR | EMBL; X72496; CAA96577.1; - | FT | CARBOHYD | 5427 | 5427 | N-LINKED (GLCNAC. . .) | (POTENTIAL) . |
| DR | EMBL; X74955; CAA52910.1; - | FT | CARBOHYD | 5467 | 5467 | N-LINKED (GLCNAC. . .) | (POTENTIAL) . |
| DR | EMBL; U63836; AAB61398.1; - | FT | CARBOHYD | 5506 | 5506 | N-LINKED (GLCNAC. . .) | (POTENTIAL) . |
| DR | EMBL; U63836; AAB61398.1; - | FT | CARBOHYD | 5507 | 5507 | N-LINKED (GLCNAC. . .) | (POTENTIAL) . |
| DR | EMBL; U78554; AAC51344.1; - | FT | CARBOHYD | 5543 | 5543 | N-LINKED (GLCNAC. . .) | (POTENTIAL) . |
| DR | EMBL; U78552; AAC51344.1; JOINED. | FT | CARBOHYD | 5553 | 5553 | N-LINKED (GLCNAC. . .) | (POTENTIAL) . |
| DR | EMBL; U78553; AAC51344.1; - | FT | CARBOHYD | 5604 | 5604 | N-LINKED (GLCNAC. . .) | (POTENTIAL) . |
| DR | EMBL; U78551; AAC51343.1; - | FT | CARBOHYD | 5618 | 5618 | N-LINKED (GLCNAC. . .) | (POTENTIAL) . |
| DR | EMBL; U95031; AAB65151.1; - | FT | CARBOHYD | 5662 | 5662 | N-LINKED (GLCNAC. . .) | (POTENTIAL) . |
| DR | EMBL; Y09788; CAA70926.1; - | FT | VARIANT | 5137 | 5137 | T -> S (in dBSNP:2672788) . | |
| DR | Genew; HGNC:7516; MUC5B. | FT | CONFLICT | 34 | 34 | /FTID=VAR_014123. | |
| DR | MIM; 600770; - | FT | CONFLICT | 95 | 100 | G -> E (IN REF. 2) . | |
| DR | GO; GO:0005515; F:protein binding; IPI. | FT | CONFLICT | 104 | 104 | FPGLCN -> LPCLCK (IN REF. 2) . | |
| DR | InterPro; IPR006208; Cys_knot.C. | FT | CONFLICT | 142 | 142 | S -> C (IN REF. 2) . | |
| DR | InterPro; IPR006207; Cys_knot.C. | FT | CONFLICT | 225 | 225 | E -> K (IN REF. 1) . | |
| DR | InterPro; IPR009041; PMP_inhibitor. | FT | CONFLICT | 330 | 331 | R -> S (IN REF. 2) . | |
| DR | InterPro; IPR002919; TIL_Cysrich. | FT | CONFLICT | 337 | 337 | PL -> T (IN REF. 2) . | |
| DR | InterPro; IPR006552; VC_out. | FT | CONFLICT | 356 | 356 | E -> N (IN REF. 2) . | |
| DR | InterPro; IPR001007; VWF_C. | FT | CONFLICT | 362 | 362 | E -> K (IN REF. 2) . | |
| DR | InterPro; IPR001846; VWF_D. | FT | CONFLICT | 369 | 369 | G -> R (IN REF. 2) . | |
| DR | Pfam; PF01826; TIL; 1. | FT | CONFLICT | 374 | 374 | MISSING (IN REF. 2 AND 3) . | |
| DR | Pfam; PF00093; vwc; 1. | FT | CONFLICT | 393 | 394 | D -> N (IN REF. 2) . | |
| DR | Pfam; PF00094; vwd; 4. | FT | CONFLICT | 468 | 469 | RT -> TR (IN REF. 2) . | |
| DR | SMART; SM00214; VWC; 6. | FT | CONFLICT | 512 | 512 | RK -> GR (IN REF. 2) . | |
| DR | SMART; SM00215; VWC_out; 4. | FT | CONFLICT | 585 | 587 | L -> P (IN REF. 2) . | |
| DR | SMART; SM00216; VWD; 4. | FT | CONFLICT | 601 | 601 | GAA -> AH (IN REF. 3) . | |
| DR | PROSITE; PS01185; CTCK_1; 1. | FT | CONFLICT | 628 | 629 | A -> S (IN REF. 3) . | |
| DR | PROSITE; PS01285; CTCK_2; 1. | FT | CONFLICT | 633 | 633 | DP -> RS (IN REF. 2) . | |
| DR | PROSITE; PS01208; VWF_C_1; 2. | FT | CONFLICT | 676 | 676 | F -> L (IN REF. 2) . | |
| DR | PROSITE; PS01208; VWF_C_2; 2. | FT | CONFLICT | | | A -> P (IN REF. 3) . | |
| DR | PROSITE; PS0184; VWF_C_1; 2. | FT | CONFLICT | | | | |
| KW | Glycoprotein; Repeat; Signal; Polymorphism. | | | | | | |
| FT | SIGNAL 1 25 | | | | | | |
| FT | GLYCOPROTEIN; Repeat; Signal; Polymorphism. | | | | | | |
| FT | MUCIN 5B. | | | | | | |
| FT | CHAIN 26 5703 | | | | | | |
| FT | DOMAIN 77 225 | | | | | | |
| FT | DOMAIN 329 386 | | | | | | |
| FT | DOMAIN 426 580 | | | | | | |
| FT | DOMAIN 858 918 | | | | | | |
| FT | DOMAIN 896 1044 | | | | | | |
| FT | DOMAIN 1457 1603 | | | | | | |
| FT | DOMAIN 1609 4873 | | | | | | |
| FT | DOMAIN 5005 5178 | | | | | | |
| FT | DOMAIN 5353 5425 | | | | | | |
| FT | DOMAIN 5462 5528 | | | | | | |
| FT | DOMAIN 5594 5683 | | | | | | |
| FT | DISULFID 5594 5646 | | | | | | |
| FT | DISULFID 5622 5660 | | | | | | |
| FT | DISULFID 5626 5676 | | | | | | |
| FT | DISULFID 5643 5678 | | | | | | |
| FT | DISULFID 5645 5682 | | | | | | |
| FT | CARBOHYD 145 145 | | | | | | |
| FT | CARBOHYD 201 201 | | | | | | |
| FT | CARBOHYD 254 254 | | | | | | |
| FT | CARBOHYD 402 402 | | | | | | |
| FT | CARBOHYD 516 516 | | | | | | |
| FT | CARBOHYD 806 806 | | | | | | |
| FT | CARBOHYD 930 930 | | | | | | |
| FT | CARBOHYD 1277 1277 | | | | | | |
| FT | CARBOHYD 1293 1293 | | | | | | |
| FT | CARBOHYD 1557 1557 | | | | | | |
| FT | CARBOHYD 1775 1775 | | | | | | |
| FT | CARBOHYD 2192 2192 | | | | | | |
| FT | CARBOHYD 2721 2721 | | | | | | |
| FT | CARBOHYD 3419 3419 | | | | | | |
| FT | CARBOHYD 3948 3948 | | | | | | |
| FT | CARBOHYD 4745 4745 | | | | | | |
| FT | CARBOHYD 4901 4901 | | | | | | |
| FT | CARBOHYD 4958 4958 | | | | | | |
| FT | CARBOHYD 4965 4965 | | | | | | |
| FT | CARBOHYD 4987 4987 | | | | | | |

Query Match 90.3%; Score 28; DB 1; Length 5703;
Best Local Similarity 85.7%; Pred. No. 3,4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSRAT 7
Db 3006 ATSSRAT 3012
RESULT 3
MABC BOVIN
ID MABC BOVIN STANDARD; PRT; 249 AA.
AC 002659,
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mannose-binding protein C precursor (MBP-C) (Mannan-binding protein) .
GN MBL.
OS Bos taurus (Bovine) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RA MEDLINE=97228413; PubMed=9074491;
RA Kawai T., Suzuki Y., Eda S., Ohtani K., Kase T., Fujinaga Y.,
RA Sakamoto T., Kurimura T., Wakamiya N.;
RT "Cloning and characterization of a cDNA encoding bovine mannan-binding
protein.";
RL Gene 186:161-165(1997) .
CC -!- FUNCTION: Binds mannose and N-acetylglucosamine in a calcium-
dependent manner. Is capable of host defense against pathogens, by
activating the classical complement pathway independently of the
antibody (By similarity).
CC -!- SUBUNIT: Oligomeric complex of 6 set of homotrimers.
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

RC STRAIN=A3(2);
RX MEDLINE=88112873; PubMed=2828187;
RA "Nucleotide sequence analysis reveals similarities between proteins
RT determining methylenomycin A resistance in Streptomyces and
RT tetracycline resistance in eubacteria";
RL Gene 58:229-241(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bruton C.J., Wietzorrek A., Hartley N., Woodburn L., Chater K.F.;
RT "Genes involved in methylenomycin biosynthesis from plasmid SCP1 of
RT Streptomyces coelicolor A3(2)";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble L., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)";
RL Nature 417:141-147(2002).
CC -!- FUNCTION: RESISTANCE TO THE EPOXIDE ANTIBIOTIC METHYLENOMYCIN A;
CC NATURE 417:141-147(2002).
CC PROBABLY BY MEDIATING ITS EFFLUX.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
CC AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M18263; AAA98341.1; -;
CC EMBL; A3276673; CAB82871.1; -;
CC EMBL; AL589148; CAC32711.1; -;
CC EMBL; AL590464; CAC36763.1; -;
CC FIC; B29606; B29606.
CC InterPro; IPR007114; MFS.
CC PROSITE; PS50850; MFS; 1.
CC Plasmid; Antibiotic resistance; Transmembrane; Transport;
CC Complete proteome.
FT TRANSMEM 28 48 POTENTIAL.
FT TRANSMEM 65 85 POTENTIAL.
FT TRANSMEM 93 113 POTENTIAL.
FT TRANSMEM 123 143 POTENTIAL.
FT TRANSMEM 152 172 POTENTIAL.
FT TRANSMEM 173 193 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 285 305 POTENTIAL.
FT TRANSMEM 314 334 POTENTIAL.
FT TRANSMEM 346 366 POTENTIAL.
FT TRANSMEM 371 391 POTENTIAL.
FT TRANSMEM 416 436 POTENTIAL.
FT TRANSMEM 439 459 POTENTIAL.
SQ SEQUENCE 475 AA; 49238 MW; CF35F49BA9535102 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 475;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ATSSRAT 7
Db 204 ATESRAT 210
RESULT 6
VGP_EBOB
ID VGP_EBOB STANDARD; PRT; 676 AA.
AC Q66814;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Structural glycoprotein precursor (Viron spike glycoprotein)
DE [Contains: GP1; GP2].
GN GP.
OS Ebola virus (strain Sudan Boniface) (Ebo).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
OC Ebola-like viruses.
OX NCBI_TaxID=128948;
RN [1]
RP SEQUENCE FROM N.A. AND RNA EDITING.
RX MEDLINE=96195018; PubMed=8622982;
RA Sanchez A., Trappier S.G., Mahy B.W.J., Peters C.J., Nichol S.T.;
RT "The virion glycoproteins of Ebola viruses are encoded in two reading
RT frames and are expressed through transcriptional editing";
RL Proc. Natl. Acad. Sci. U.S.A. 93:3602-3607(1996).
CC -!- FUNCTION: Structural protein that forms the virion spike and which
CC is responsible for binding to target cells and subsequent fusion
CC of the viral and host-cell membranes. In cell receptor recognition
CC and in fusion.
CC -!- SUBUNIT: Homotrimer; each monomer consist of a GP1 and a GP2
CC subunit linked by disulfide bonds (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. GP1 can also be
CC shed by the virus after proteolytic processing (By similarity).
CC -!- PTM: N-glycosylated, could also be O-glycosylated (By similarity).
CC -!- PTM: Processing into GP1 and GP2 is effected by the host furin (By
CC similarity).
CC -!- RNA EDITING: Modified positions=295; Note=Partially edited. RNA
CC editing at this position consists of an insertion of one adenine
CC nucleotide. The sequence displayed here is the full-length
CC transmembrane glycoprotein, derived from the edited RNA. The
CC unedited RNA gives rise to the small secreted glycoprotein (AC
CC P60172).
CC -!- SIMILARITY: Belongs to the filoviruses glycoprotein family.
CC -----
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CC -----
CC EMBL; U28134; AAB37096.1; -;
CC HSP; Q05320; 2EBO.
CC InterPro; IPR002561; Filo.glycop.
CC Pfam; PF01611; Filo.glycop; 1
CC Transmembrane; Envelope protein; Glycoprotein; Signal; RNA editing.
CC SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 676 STRUCTURAL GLYCOPROTEIN.
FT CHAIN 33 501 GP1.
FT CHAIN 502 676 GP2.
FT DOMAIN 33 649 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 650 672 POTENTIAL.
FT DOMAIN 673 676 CYTOPLASMIC (POTENTIAL).
FT DISULFID 601 608 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 563 563 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 676 AA; 74986 MW; 700029BFD67F5E9A CRC64;

Query Match 87.1%; Score 27; DB 1; Length 676;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
Db 321 ATSSRAT 327

RESULT 7
VGP_EBOSM
ID_VGP_EBOSM STANDARD; PRT; 676 AA.
AC Q66798;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Structural glycoprotein precursor (Viron spike glycoprotein)
DE [Contains: GPI; GP2].
GN GP.
OS Ebola virus (strain Sudan Maleo-79) (Ebo).
OC Viruses; sRNA negative-strand viruses; Mononegavirales; Filoviridae;
OC Ebola-like viruses.
OX NCBI_TaxID=128949;
RN [1]
SEQUENCE FROM N.A., AND RNA EDITING.
RX MEDLINE=96195018; PubMed=8622982;
RA Sanchez A., Trappier S.G., Mahy B.W.J., Peters C.J., Nichol S.T.;
RT "The virion glycoproteins of Ebola viruses are encoded in two reading
frames and are expressed through transcriptional editing.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:3602-3607(1996).
CC -!- FUNCTION: Structural protein that forms the virion spike and which
is responsible for binding to target cells and subsequent fusion
of the viral and host-cell membranes. In cell receptor recognition
and in fusion.
CC -!- SUBUNIT: Homotrimer; each monomer consist of a GP1 and a GP2
subunit linked by disulfide bonds (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. GPI can also be
shed by the virus after proteolytic processing (By similarity).
CC -!- PTM: N-glycosylated, could also be O-glycosylated (By similarity).
CC -!- PTM: Processing into GP1 and GP2 is effected by the host furin (By
similarity).
CC -!- RNA EDITING: Modified positions=295; Note=Partially edited. RNA
editing at this position consists of an insertion of one adenine
nucleotide. The sequence displayed here is the full-length
transmembrane glycoprotein, derived from the edited RNA. The
unedited RNA gives rise to the small secreted glycoprotein (AC
P60173).
CC -!- SIMILARITY: Belongs to the filoviruses glycoprotein family.

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EMBL; U23069; AAC54882.1; --
DR HSP3; Q05320; ZEB0.
DR InterPro; IPR002561; Filo_glycop.
DR Pfam; PF01611; Envlope protein; 1.
KW Transmembrane; Envelope protein; Glycoprotein; Signal; RNA editing.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 676 STRUCTURAL GLYCOPROTEIN.
FT CHAIN 33 501 GPI.
FT CHAIN 502 676 GP2.

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FT DOMAIN 33 649 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 650 672 POTENTIAL.
FT DOMAIN 673 676 CYTOPLASMIC (POTENTIAL).
FT DISULFID 601 608 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 563 563 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 676 AA; 74970 MW; 1DAB9EB78CF755C8 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 676;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
Db 321 ATSSRAT 327

RESULT 8
PLB2_CANGA
ID_PLB2_CANGA STANDARD; PRT; 695 AA.
AC Q8TG06;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lysophospholipase 2 precursor (EC 3.1.1.5) (Phospholipase B 2).
GN PLB2.
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
SEQUENCE FROM N.A.
RA Clancy C., Cheng S., Chekley M.A., Lewin A., Nguyen M.-H.;
RT "Cloning and characterization of phospholipase B gene (PLB2) of Candida
glabrata".
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the release of fatty acids from
lysophospholipids. Phospholipase B may well contribute to
pathogenicity by abetting the fungus in damaging and traversing
host cell membranes, processes which likely increase the rapidity
of disseminated infection (By similarity).
CC -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
glycerophosphocholine + a fatty acid anion.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the lysophospholipase family.

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EMBL; AF498582; AAM19335.1; --
DR InterPro; IPR02642; PLAC.
DR Pfam; PF01735; PLA2_B; 1.
DR SMART; SM00022; PLAC; 1.
KW Lipid degradation; Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 695 LYSPHOSPHOLIPASE 2.
FT CHAIN 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).

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CC -!- FUNCTION: May play a role in the attachment, organization, and/or
CC dynamics of microtubule ends at the spindle pole body.
CC -!- SUBUNIT: Binds to microtubules.
CC -!- SUBCELLULAR LOCATION: LOCALIZES PRIMARILY TO THE SPINDLE POLE BODY
CC (SPB) AND TO A LESSER EXTENT ALONG SPINDLE MICROTUBULES.
CC -!- MISCELLANEOUS: Mutations in STU2 suppress a cold-sensitive
CC mutation in TUB2.
CC -!- SIMILARITY: Belongs to the TOG/XMAP215 family.
CC -!- SIMILARITY: Contains 2 HEAT repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U35247; AAA79057.1; -
CC EMBL; X94607; CAA64292.1; -
CC EMBL; Z73217; CAA97574.1; -
CC PIR; S61619; S61619.
CC GerMOnline; 142107; -
CC SGD; S0004035; STU2.
CC GO; GO:0005816; C:spindle pole body; IDA.
CC GO; GO:0008017; F:microtubule binding; IMP.
CC GO; GO:0005200; F:structural constituent of cytoskeleton; IPI.
CC GO; GO:0007020; P:microtubule nucleation; IPI.
CC GO; GO:0000071; P:mitotic spindle assembly (sensu Saccharomycetes); IGI.
CC InterPro; IPR008938; ARM.
CC InterPro; IPR000357; HEAT.
CC PROSITE; PS50077; HEAT_REPEAT; 1.
CC Repeat; Microtubule.
CC REPEAT 453 490 HEAT 1.
CC REPEAT 498 535 HEAT 2.
CC FT REPEAT 498 535
CC SQ SEQUENCE 888 AA; 100918 MW; 7A49C3702E21C7BF CRC64;

Query Match 87.1%; Score 27; DB 1; Length 888;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSSRAT 7
DB 113 TSSRAT 118

RESULT 11
ID TERT SCHPO STANDARD; PRT; 988 AA.
AC O13339; O13338;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
DE subunit).
GN TERT OR SPBC29A3.14C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=97400623; PubMed=9252327;
RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H.,
RA Lingner J., Harley C.B., Cech T.R.;
RT "Telomerase catalytic subunit homologs from fission yeast and human.";
RL Science 277:955-959(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;

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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leach S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weijens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel K., Fuchs M., Fritz C., Holzer C., Leinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Leinhardt R., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds
CC single sequence repeats to chromosome ends by copying a template
CC sequence within the RNA component of the enzyme.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O13339-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O13339-2; Sequence=VSP_006395;
CC -!- MISCELLANEOUS: DELETION CAUSES TELOMERASE SHORTENING AND SENESENCE.
CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
CC Telomerase subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF015783; AAC49802.1; -
CC EMBL; AF015783; AAC49803.1; -
CC EMBL; AL022299; CAA18391.1; -
CC PIR; T03838; T03838.
CC GeneDB SPombe; SPBC29A3.14C; -.
CC InterPro; IPR000477; RVTse.
CC InterPro; IPR003545; Telomerase_RT.
CC Pfam; PF00078; rvt; 2.
CC PRINTS; PR01365; TELOMERASERT.
CC Transferrase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
CC DNA-binding; Alternative splicing.
CC FT VARSPPLIC 524 524 K -> KQ (in isoform 2).
CC /FTID=VSP_006395.
CC SQ SEQUENCE 988 AA; 116328 MW; AB2DC7030228F443 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 988;
Best Local Similarity 85.7%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
DB 626 ATSDRAT 632

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| | |
|--|-------------------------|
| RESULT 12 | |
| ID NS2A HUMAN | STANDARD; PRT; 1153 AA. |
| AC P35228; O60757; O94994; Q16263; Q16692; | |
| DT 01-FEB-1994 (Rel. 28, Created) | |
| DT 01-FEB-1996 (Rel. 33, Last sequence update) | |
| DT 10-OCT-2003 (Rel. 42, Last annotation update) | |
| DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II) | |
| DE (Inducible NOS) (iNOS) (Hepatocyte NOS) (HEP-NOS). | |
| GN NOS2A OR NOS2. | |
| OS Homo sapiens (Human). | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | |
| OX NCBI_TaxID=9606; | |
| RN [1] | |
| RP SEQUENCE FROM N.A. | |
| RC TISSUE=Liver; | |
| RX MEDLINE=93234523; PubMed=7682706; | |
| RA Geller D.A., Lowenstein C.J., Shapiro R.A., Nussler A.K., | |
| RA di Silvio M., Wang S.C., Nakayama D.K., Simmons R.L., Snyder S.H., | |
| RA Billiar T.R.; | |
| RT "Molecular cloning and expression of inducible nitric oxide synthase | |
| RT from human hepatocytes."; | |
| RL Proc. Natl. Acad. Sci. U.S.A. 90:3491-3495 (1993). | |
| RN [2] | |
| RP SEQUENCE FROM N.A. | |
| RC TISSUE=Colorectal adenocarcinoma; | |
| RX MEDLINE=94032282; PubMed=7692964; | |
| RA Sherman P.A., Leubach V.E., Reep B.R., Wood E.R.; | |
| RT "Purification and cDNA sequence of an inducible nitric oxide synthase | |
| RT from a human tumor cell line."; | |
| RL Biochemistry 32:11600-11605 (1993). | |
| RN [3] | |
| RP SEQUENCE FROM N.A. | |
| RC TISSUE=Chondrocytes; | |
| RX MEDLINE=94068614; PubMed=7504305; | |
| RA Charles I.G., Palmer R.M.J., Hickery M.S., Bayliss M.T., | |
| RA Chubb A.P., Hall V.S., Moss D.W., Moncada S.; | |
| RT "Cloning, characterization, and expression of a cDNA encoding an | |
| RT inducible nitric oxide synthase from the human chondrocyte."; | |
| RL Proc. Natl. Acad. Sci. U.S.A. 90:11419-11423 (1993). | |
| RN [4] | |
| RP SEQUENCE FROM N.A. | |
| RC TISSUE=Articular chondrocytes; | |
| RX MEDLINE=94368816; PubMed=7522054; | |
| RA Maier R., Bilbe G., Rediske J., Lotz M.; | |
| RT "Inducible nitric oxide synthase from human articular chondrocytes: | |
| RT cDNA cloning and analysis of mRNA expression."; | |
| RL Biochim. Biophys. Acta 1208:145-150 (1994). | |
| RN [5] | |
| RP SEQUENCE FROM N.A. | |
| RC TISSUE=Retina; | |
| RX MEDLINE=95091827; PubMed=7528017; | |
| RA Park C.S., Parthasaradhi K., Gianotti C., Villegas E., Krishna G.; | |
| RT "Human retina expresses both constitutive and inducible isoforms of | |
| RT nitric oxide synthase mRNA."; | |
| RL Biochem. Biophys. Res. Commun. 205:85-91 (1994). | |
| RN [6] | |
| RP SEQUENCE FROM N.A. | |
| RC TISSUE=Glioblastoma; | |
| RX MEDLINE=95155267; PubMed=7531687; | |
| RA Hokari A., Zeniya M., Esumi H.; | |
| RT "Cloning and functional expression of human inducible nitric oxide | |
| RT synthase (NOS) cDNA from a glioblastoma cell line A-172."; | |
| RL J. Biochem. 116:575-581 (1994). | |
| RN [7] | |
| RP SEQUENCE FROM N.A. | |
| RC TISSUE=Airway epithelium; | |
| RX MEDLINE=95372368; PubMed=7544004; | |
| RA Guo F.H., de Raave R.H., Rice T.W., Stuehr D.J., Thunnissen F.B.J.M., | |
| RA Erzurum S.C.; | |
| RT "Continuous nitric oxide synthesis by inducible nitric oxide synthase | |

| | |
|---|--|
| in normal human airway epithelium in vivo."; | |
| Proc. Natl. Acad. Sci. U.S.A. 92:7809-7813 (1995). | |
| RN [8] | |
| RP SEQUENCE FROM N.A. | |
| RC TISSUE=Cardiac myocytes; | |
| RX MEDLINE=97304504; PubMed=9160867; | |
| RA Luss H., Li R.-K., Shapiro R.A., Tzeng E., McGowan F.X., Yoneyama T., | |
| RA Hatakayama K., Geller D.A., Mickie D.A.G., Simmons R.L., | |
| RA Billiar T.R.; | |
| RT "Differentiated human ventricular cardiac myocytes express | |
| RT inducible nitric oxide synthase mRNA but not protein in response to | |
| RT IL-1, TNF, IFN-gamma, and LPS."; | |
| RL J. Mol. Cell. Cardiol. 29:1153-1165 (1997). | |
| RN [9] | |
| RP SEQUENCE FROM N.A. (ISOFORM 2). | |
| RC Ogawa Y., Nishijima S., Goto M., Ida M.; | |
| RT "Cloning and characterization of a novel splice variant of human | |
| RT inducible nitric oxide synthase."; | |
| RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases. | |
| RN [10] | |
| RP SEQUENCE OF 380-473 FROM N.A. | |
| RC TISSUE=Kidney; | |
| RX MEDLINE=95165725; PubMed=7532448; | |
| RA McVay J.S., Chatterjee P., Nicolson A.G., Jardine A.G., McKay N.G., | |
| RA Ralston S.H., Grabowski P., Hailes N.E., Macleod A.M., | |
| RA Hawksworth G.M.; | |
| RT "Nitric oxide production by human proximal tubular cells: a novel | |
| RT immunomodulatory mechanism"; | |
| RL Kidney Int. 46:1043-1049 (1994). | |
| RN [11] | |
| RP CHARACTERIZATION. | |
| RC MEDLINE=96047340; PubMed=7558036; | |
| RA Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G., | |
| RA Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.; | |
| RT "Three members of the nitric oxide synthase II gene family (NOS2A, | |
| RT NOS2B, and NOS2C) colocalize to human chromosome 17."; | |
| RL Genomics 27:526-530 (1995). | |
| RN [12] | |
| RP CHARACTERIZATION. | |
| RC MEDLINE=98398965; PubMed=9721329; | |
| RA Taylor B.S., Alarcon L.H., Billiar T.R.; | |
| RT "Inducible nitric oxide synthase in the liver: regulation and | |
| RT function."; | |
| RL Biochimica 63:766-781 (1998). | |
| RN [13] | |
| RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 74-504. | |
| RC MEDLINE=99340057; PubMed=10409685; | |
| RA Li H., Raman C.S., Glaser C.B., Blasko E., Young T.A., Parkinson J.F., | |
| RA Whitlow M., Poulos T.L.; | |
| RT "Crystal structures of zinc-free and -bound heme domain of human | |
| RT inducible nitric-oxide synthase. Implications for dimer stability and | |
| RT comparison with endothelial nitric-oxide synthase."; | |
| RL J. Biol. Chem. 274:21276-21284 (1999). | |
| RN [14] | |
| RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 82-528. | |
| RC MEDLINE=99173237; PubMed=10074942; | |
| RA Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A., | |
| RA Dolphin B., Prongay A.J., Reichert P., Lundell D.J., Narula S.K., | |
| RA Weber P.C.; | |
| RT "Structural characterization of nitric oxide synthase isoforms | |
| RT reveals striking active-site conservation."; | |
| RL Nat. Struct. Biol. 6:233-242 (1999). | |
| CC -I- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule | |
| CC with diverse functions throughout the body. In macrophages, NO | |
| CC mediates tumoricidal and bactericidal actions. | |
| CC -I- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline + | |
| CC nitric oxide + N NADP(+). | |
| CC -I- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires | |
| CC tetrahydrobiopterin (BH4) which may stabilize the dimeric form of | |
| CC the enzyme (By similarity). | |
| CC -I- ENZYME REGULATION: Regulated by calcium/calmodulin (in contrast | |
| CC with mouse NOS2). Aspirin inhibits expression and function of this | |
| CC enzyme and effects may be exerted at the level of | |

translational/posttranslational modification and directly on the
catalytic activity (By similarity).
-!- SUBUNIT: Homodimer.
-!- ALTERNATIVE PRODUCTS:
Name=1;
isoId=P35228-1; Sequence=Displayed;
Name=2;
isoId=P35228-2; Sequence=VSP_003582, VSP_003583;
TISSUE SPECIFICITY: Expressed in the liver, retina, bone cells and
airway epithelial cells of the lung. Not expressed in the
platelets.
-!- INDUCTION: By endotoxins and cytokines.
-!- SIMILARITY: Belongs to the NOS family.
-!- SIMILARITY: Contains 1 flavodoxin-like domain.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
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EMBL; L09210; AAA59171.1; -;
EMBL; L24553; AAA36375.1; -;
EMBL; X73029; CAA51512.1; -;
EMBL; U05810; AAA56666.1; -;
EMBL; U31511; AAB49041.1; -;
EMBL; D26525; BAA05531.1; -;
EMBL; U20141; AAB60366.1; -;
EMBL; AF068236; AAC19133.1; -;
EMBL; AB022318; BAA37123.1; -;
EMBL; S75615; AAD14179.1; -;
PIR; A49676; A49676.
PDB; 1NSI; 07-JAN-00.
PDB; 2NSI; 07-JAN-00.
PDB; 4NOS; 04-FEB-00.
Gene; HGNC:7873; NOS2A.
MIM; 163730; -;
GO; GO:0005737; C.cytosolasm; TAS.
GO; GO:0004517; F.nitric-oxide synthase activity; TAS.
InterPro; IPR003097; FAD_Binding.
InterPro; IPR008254; Flav_nitox_synth.
InterPro; IPR001094; Flavodoxin-like.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR004030; NO_synthase.
InterPro; IPR001433; OxRed_FAD/NAD(P).
Pfam; PF00657; FAD_binding_1; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding_1; 1.
Pfam; PF02898; NO_synthase; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
PROSITE; PS50902; FLAVODOXIN-LIKE; 1.
PROSITE; PS50001; NOS; 1.
Oxidoreductase; NADP; FAD; FPN; Calcium-binding; Calmodulin-binding;
KW
Query Match 87.1%; Score 27; DB 1; Length 1153;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TSSRAT 7
Db 747 TSSRAT 752
RESULT 13
NM1_MOUSE
ID NM1_MOUSE STANDARD; PRT; 1464 AA.
AC P35436; 1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)
Glutamate [NMDA] receptor subunit epsilon 1 precursor (N-methyl
D-aspartate receptor subtype 2A) (NR2A) (NMDAR2A).
GRIN2A.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=92244361; PubMed=13741634;
Meguro H., Mori H., Araki K., Kushiya E., Kutsuwada T.,
Yamazaki M., Kumamishi T., Arakawa M., Sakimura K., Mishina M.;
"Functional characterization of a heteromeric NMDA receptor channel
expressed from cloned cDNAs.";
Nature 357:70-74 (1992).
-!- FUNCTION: NMDA receptor subtype of glutamate-gated ion channels
possesses high calcium permeability and voltage-dependent
sensitivity to magnesium and is mediated by glycine.
-!- SUBUNIT: Heterodimer of an epsilon subunit and a zeta subunit.
Interacts with AIP1 (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.

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EMBL; D10217; BAA01069.1; -;
PIR; S29159; S29159.
HSP; P19491; IGR2.
MGD; MGI:195820; Grin2a.
GO; GO:0045211; C.postsynaptic membrane; IDA.
InterPro; IPR001320; Ion_glu_receptor.
InterPro; IPR001508; NMDA_receptor.
InterPro; IPR001311; SBP_glu_receptor.
Pfam; PF00060; lig_chan; 1.
PRINTS; PR00177; NMDARECEPTOR.
SMART; SM00079; PBPe; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Calcium; Magnesium.
SIGNAL 1 22 POTENTIAL.
CHAIN 23 1464
GLUTAMATE [NMDA] RECEPTOR SUBUNIT
EPSILON 1.
EXTRACELLULAR (POTENTIAL).
DOMAIN 23 555
TRANSMEM 556 576 1 (POTENTIAL).
TRANSMEM 593 613 2 (POTENTIAL).
TRANSMEM 634 654 3 (POTENTIAL).
TRANSMEM 817 837 4 (POTENTIAL).
SITE 614 614
FUNCTIONAL DETERMINANT OF NMDA
RECEPTORS (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE 1464 AA; 165490 MW; 422CD68C56379047 CRC64;
Query Match 87.1%; Score 27; DB 1; Length 1464;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TSSRAT 7
Db 1064 TSSRAT 1069
RESULT 14

NMEL RAT
ID NMEL RAT STANDARD; PRT; 1464 AA.
AC Q0059;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glutamate [NMDA] receptor subunit epsilon 1 precursor (N-methyl
D-aspartate receptor subtype 2A) (NR2A) (NMDAR2A).
GN GRIN2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN RN
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92271257; PubMed=1350383;
RA Monyer H., Sprengel R., Schoeffer R., Herb A., Higuchi M., Lomeli H.,
Burnashev N., Sakmann B., Seeburg P.H.;
RT "Heteromeric NMDA receptors: molecular and functional distinction of
subtypes.";
RL Science 256:1217-1221(1992).
RN [2]
RN REVISIONS TO 595 AND 597-598.
RA Monyer H., Sprengel R., Schoeffer R., Herb A., Higuchi M., Lomeli H.,
Burnashev N., Sakmann B., Seeburg P.H.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RN INTERACTION WITH AIPI.
RX MEDLINE=98361985; PubMed=9694864;
RA Hirao K., Hata Y., Ide N., Takeuchi M., Irie M., Yao I., Deguchi M.,
Toyoda A., Sudhof T.C., Takai Y.;
RT "A novel multiple PDZ domain-containing molecule interacting with
N-methyl-D-aspartate receptors and neuronal cell adhesion proteins.";
RL J. Biol. Chem. 273:21105-21110(1998).
CC -!- FUNCTION: NMDA receptor subtype of glutamate-gated ion channels
possesses high calcium permeability and voltage-dependent
sensitivity to magnesium and is mediated by glycine.
CC -!- SUBUNIT: Heterodimer of an epsilon subunit and a zeta subunit.
CC interacts with AIPI.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.

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DR EMBL; M91561; AAC03565.1; -;
DR PIR; A43274; A43274.
DR HSP; P19491; IGR2.
DR InterPro; IPR001320; Ion_glu_receptor.
DR InterPro; IPR001508; NMDA_receptor.
DR InterPro; IPR001311; SBP/glu_receptor.
DR Pfam; PF00060; lig_chan; 1.
DR PRINTS; PR00177; NMDARECEPTOR.
DR SMART; SM00079; PBPE; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Calcium; Magnesium.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 1464
FT CHAIN 23 1464
FT DOMAIN 23 555
FT TRANSMEM 556 576
FT TRANSMEM 593 613
FT TRANSMEM 634 654
FT TRANSMEM 817 837
FT SITE 614 614
FT SITE 614 614
FT CARBOHYD 75 75
N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT

FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 541 541 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1464 AA; 165468 MW; DC1528E189DECA4 CRC64;
Query Match 87.1%; Score 27; DB 1; Length 1464;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TSSRAT 7
Db 1064 TSSRAT 1069
RESULT 15
RP30 HUMAN STANDARD; PRT; 268 AA.
ID RP30 HUMAN
AC P78316;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ribonuclease P protein subunit p30 (EC 3.1.26.5) (RNaseP protein p30)
DE (RNase P subunit 2).
GN RNaseP2 OR RPP30.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RN
RN SEQUENCE FROM N.A., AND SEQUENCE OF 21-30; 140-148 AND 185-198.
RX MEDLINE=97188428; PubMed=9037013;
RA Eder P.S., Kekuda R., Stolic V., Altman S.;
RT "Characterization of two scleroderma autoimmune antigens that copurify
with human ribonuclease P.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:1101-1106(1997).
RN [2]
RN SEQUENCE FROM N.A.
RA Tracey A.;
RN Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
[3]
RN RN
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.M., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Haieh F.,
Hopkins R.F., Jordan H., Moore T., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Matulis M., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.C., Touchman J.W., Green E.D., Dickinson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Component of ribonuclease P, a protein complex that
generates mature tRNA molecules by cleaving their 5' ends.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
extra-nucleotide from tRNA precursor.
CC -!- SUBUNIT: RNase P consists of a RNA moiety and at least 8 protein
subunits; POP1, RPP14, RPP20/POP7, RPP25, RPP29/POP4, RPP30, RPP38
and RPP40.
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (Potential).
CC -!- DISEASE: SERA FROM SCLERODERMA PATIENTS RECOGNIZE RPP38.

```

CC  -!- SIMILARITY: BELONGS TO THE RPE1/RNASEP2 FAMILY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; U77665; AAC51143.1; -.
CC  EMBL; AL590622; CAC70100.1; -.
CC  EMBL; BC006991; AAH06991.1; -.
CC  GK; F78346; -.
CC  MIM; 606115; -.
CC  GO; GO:0005655; C:nucleolar ribonuclease P complex; TAS.
CC  GO; GO:0005634; C:nucleus; TAS.
CC  GO; GO:0004526; F:ribonuclease P activity; TAS.
CC  InterPro; IPR002738; RNase_P_p30.
CC  Pfam; PF01876; RNase_P_D30; 1
CC  Hydrolase; Nuclear protein; tRNA processing; Antigen.
KW  CONFLICT 189 189 S -> I (IN REF. 1; AA SEQUENCE).
SQ  SEQUENCE 268 AA; 29321 MW; 2AB492D9BACDCBB CRC64;

Query Match      83.9%; Score 26; DB 1; Length 268;
Best Local Similarity 100.0%; Pred.No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ATSSRA 6
DB  92 ATSSRA 97

```

Search completed: April 21, 2004, 17:34:01
Job time : 5.55072 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2004, 17:27:33 ; Search time 6.3913 seconds

(without alignments)
105.353 Million cell updates/sec

Title: SEQ5

Perfect score: 31

Sequence: 1 atssrat 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|-------|--------|--------|----|--------------------|
| 1 | 31 | 100.0 | 497 | 2 | T05065 | | pyruvate kinase (E |
| 2 | 28 | 90.3 | 91 | 2 | S37511 | | Ig kappa chain V r |
| 3 | 28 | 90.3 | 482 | 2 | S77660 | | ribosomal protein |
| 4 | 28 | 90.3 | 543 | 2 | S35047 | | mucin JUL7 - human |
| 5 | 28 | 90.3 | 3570 | 2 | T45025 | | mucin MUC5B, trach |
| 6 | 27 | 87.1 | 93 | 2 | S37501 | | Ig kappa chain V r |
| 7 | 27 | 87.1 | 124 | 2 | S20633 | | Ig kappa chain - h |
| 8 | 27 | 87.1 | 131 | 2 | E72469 | | hypothetical prote |
| 9 | 27 | 87.1 | 227 | 2 | B37473 | | envelope antigen h |
| 10 | 27 | 87.1 | 228 | 2 | T47425 | | NAC domain-like pr |
| 11 | 27 | 87.1 | 410 | 2 | B55223 | | aromatic dioxygena |
| 12 | 27 | 87.1 | 475 | 2 | B29606 | | methylomycin A r |
| 13 | 27 | 87.1 | 490 | 2 | T04004 | | probable cytochrom |
| 14 | 27 | 87.1 | 511 | 2 | AG3470 | | glycerol-3-phospha |
| 15 | 27 | 87.1 | 622 | 2 | AG0001 | | potassium transpor |
| 16 | 27 | 87.1 | 888 | 2 | S61619 | | SRU2 protein - yea |
| 17 | 27 | 87.1 | 989 | 2 | T03838 | | telomerase catalyt |
| 18 | 27 | 87.1 | 1153 | 2 | A49676 | | nitric-oxide synth |
| 19 | 27 | 87.1 | 1464 | 1 | S29159 | | glutamate receptor |
| 20 | 27 | 87.1 | 1464 | 2 | A43274 | | N-methyl D-asparta |
| 21 | 26 | 83.9 | 51 | 2 | E82855 | | hypothetical prote |
| 22 | 26 | 83.9 | 128 | 2 | S20636 | | Ig kappa chain V r |
| 23 | 26 | 83.9 | 167 | 2 | A72626 | | hypothetical prote |
| 24 | 26 | 83.9 | 214 | 2 | A46629 | | mucin 6, gastric (|
| 25 | 26 | 83.9 | 280 | 2 | T48434 | | hypothetical prote |
| 26 | 26 | 83.9 | 314 | 2 | A13041 | | ornithine cyclodea |
| 27 | 26 | 83.9 | 328 | 2 | C98244 | | ornithine cyclodea |
| 28 | 26 | 83.9 | 346 | 2 | T51377 | | hypothetical prote |
| 29 | 26 | 83.9 | 355 | 1 | G69309 | | conserved hypothet |

| | | | | | | |
|----|----|------|------|---|--------|--------------------|
| 30 | 26 | 83.9 | 367 | 2 | C39590 | TPA-induced protei |
| 31 | 26 | 83.9 | 429 | 2 | T40463 | O-acetylhomoserine |
| 32 | 26 | 83.9 | 433 | 2 | S31436 | Ig upsilon chain - |
| 33 | 26 | 83.9 | 459 | 2 | D90211 | argininosuccinate |
| 34 | 26 | 83.9 | 504 | 2 | S75310 | gumB protein - Syn |
| 35 | 26 | 83.9 | 507 | 2 | G70649 | probable DNA ligas |
| 36 | 26 | 83.9 | 719 | 2 | T33170 | hypothetical prote |
| 37 | 26 | 83.9 | 750 | 2 | T04980 | hypothetical prote |
| 38 | 26 | 83.9 | 856 | 2 | T52415 | polycarb protein E |
| 39 | 26 | 83.9 | 898 | 2 | T01503 | hypothetical prote |
| 40 | 26 | 83.9 | 928 | 2 | C37271 | A-alpha Y 4 protei |
| 41 | 26 | 83.9 | 928 | 2 | T16759 | hypothetical prote |
| 42 | 26 | 83.9 | 1966 | 2 | T32552 | hypothetical prote |
| 43 | 26 | 83.9 | 2848 | 2 | T32550 | hypothetical prote |
| 44 | 25 | 80.6 | 94 | 2 | T40691 | ribosomal protein |
| 45 | 25 | 80.6 | 126 | 2 | H72486 | hypothetical prote |

ALIGNMENTS

RESULT 1

T05065
Pyruvate kinase (EC 2.7.1.40) - Arabidopsis thaliana

N;Alternate names: protein M3E9.180

C;Species: Arabidopsis thaliana (mouse-ear cross)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999

C;Accession: T05065

R;Bevan, M.; Vandenbol, M.; Jallet, C.; Portetelle, D.; Hoheisel, J.; Mewes, H.W.; Mayer,

submitted to the Protein Sequence Database, March 1999

A;Reference number: Z15396

A;Accession: T05065

A;Molecule type: DNA

A;Residues: 1-497 <BEV>

A;Cross-references: EMBL:AL022223

A;Experimental source: cultivar Columbia; BAC clone M3E9

C;Genetics:

A;Map position: 4

A;Introns: 7/3; 227/3

A;Note: M3E9.180

C;Superfamily: pyruvate kinase

C;Keywords: glycolysis; phosphotransferase

Query Match 100.0%; Score 31; DB 2; Length 497;

Best Local Similarity 100.0%; Pred. No. 9.5; 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7

Db 377 ATSSRAT 383

RESULT 2

S37511

Ig kappa chain V region (V-kappa 3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37511

R;Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A;Description: Human IgM(+)IGD(+) cells, the major B cell subset in the peripheral blood

A;Reference number: S37501

A;Accession: S37511

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-91 <KLE>

A;Cross-references: EMBL:Z26600; NID:g405664; PIDN:CAA81354.1; PID:g405665

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 90.3%; Score 28; DB 2; Length 91;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

A;Accession: T45025
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-3570 <DES>
 A;Cross-references: EMBL:Z72496; NID:G1834502; PIDN:CAA96577.1; PID:G1834503
 A;Experimental source: Placenta
 C;Genetics:
 A;Gene: MUC5B

Query Match 90.3%; Score 28; DB 2; Length 3570;
 Best Local Similarity 85.7%; Pred. No. 3.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
 |||:|
 Db 1681 ATSSKAT 1687

RESULT 6

S37501
 IG kappa chain V region (V-kappa 3) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C;Accession: S37501
 R;Klein, U.; Kueppers, R.; Rajewsky, K.
 A;Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
 submitted to the EMBL Data Library, September 1993
 A;Reference number: S37501
 A;Accession: S37501
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-93 <KLE>
 A;Cross-references: EMBL:Z26611; NID:G405643; PIDN:CAA81364.1; PID:G405644
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin

Query Match 87.1%; Score 27; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TSSRAT 7
 |||:|
 Db 35 TSSRAT 40

RESULT 7

S20633
 IG kappa chain - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1993 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
 C;Accession: S20633
 R;Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
 A;Description: submitted to the EMBL Data Library, April 1992
 A;Reference number: S20631
 A;Accession: S20633
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-124 <LEE>
 A;Cross-references: EMBL:Z11891; NID:G33185; PIDN:CAA77945.1; PID:G33186
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;32-107/Domain: immunoglobulin homology <IMW>

Query Match 87.1%; Score 27; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TSSRAT 7
 |||:|
 Db 68 TSSRAT 73

RESULT 8

Qy 1 ATSSRAT 7
 |||:|
 Db 33 ATSTRAT 39

RESULT 3
 S77660
 ribosomal protein S1 - Mycobacterium leprae
 C;Species: Mycobacterium leprae
 C;Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 13-Aug-1999
 C;Accession: S77660; S49523
 R;Fsihi, H.; Cole, S.T.
 Mol. Microbiol. 16, 909-919, 1995
 A;Title: The Mycobacterium leprae genome: systematic sequence analysis identifies key ca
 A;Reference number: S77652; MUID:96059637; PMID:7476188
 A;Accession: S77660
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-482 <FSI>
 A;Cross-references: EMBL:Z46257; NID:G559905; PIDN:CAA86365.1; PID:G559914
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
 C;Genetics:
 A;Gene: rpsA
 C;Superfamily: Escherichia coli ribosomal protein S1
 C;Keywords: protein biosynthesis; ribosome

Query Match 90.3%; Score 28; DB 2; Length 482;
 Best Local Similarity 85.7%; Pred. No. 50;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
 |||:|
 Db 384 ATSSRAT 390

RESULT 4

S35047
 mucin JUL7 - human
 C;Species: Homo sapiens (man)
 C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999
 C;Accession: S35047
 R;Bufosse, J.; Porchet, N.; Audie, J.P.; Guyonnet Duperrat, V.; Laine, A.; van-Seuningen,
 Biochem. J. 293, 329-337, 1993
 A;Title: Degenerate 87-base-pair tandem repeats create hydrophilic/hydrophobic alternati
 A;Reference number: S35047; MUID:93343858; PMID:7916618
 A;Accession: S35047
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-543 <DUF>
 A;Cross-references: EMBL:X74370; NID:G407081; PIDN:CAA52408.1; PID:G407082
 A;Note: the authors translated the codon AAA for residue 63 as Gln and CGG for residue 3
 A;Note: the amino acid sequence from Fig. 2 is inconsistent with the nucleotide sequence

Query Match 90.3%; Score 28; DB 2; Length 543;
 Best Local Similarity 85.7%; Pred. No. 57;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
 |||:|
 Db 73 ATSSKAT 79

RESULT 5

T45025
 mucin MUC5B, tracheobronchial [imported] - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C;Accession: T45025
 R;Desseyn, J.L.; Guyonnet-Duperrat, V.; Porchet, N.; Aubert, J.P.; Laine, A.
 J. Biol. Chem. 272, 3168-3178, 1997
 A;Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternat
 A;Reference number: Z22899; MUID:97166151; PMID:9013550

E72469
hypothetical protein APE2398 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: E72469
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: E72469
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-131 <KAW>
A:CROSS-references: DBJ:AP000064; NID:G5105945; PIDN:BAAB1413.1; PID:dl045199; PID:G5105945
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2398

Query Match 87.1%; Score 27; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSSRAT 7
DB 38 TSSRAT 43

RESULT 9
B37473
envelope antigen homolog F3R - Orf virus
C:Species: Orf virus
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000
C:Accession: B37473
R: Fleming, S.B.; Block, J.; Fraser, K.M.; Mercer, A.A.; Robinson, A.J.
Virology 195, 175-184, 1993
A:Title: Conservation of gene structure and arrangement between vaccinia virus and orf virus
A:Reference number: A37473; MUID:93303916; PMID:8317094
A:Accession: B37473
A:Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-227 <FLE>
A:CROSS-references: GB:S62819; NID:G386384; PIDN:AAB27258.1; PID:G386386
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:134136, NCBIP:134138)
A:Note: strain N22
C:Superfamily: vaccinia virus H6 protein

Query Match 87.1%; Score 27; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSSRAT 7
DB 118 TSSRAT 123

RESULT 10
T47425
NAC domain-like protein - Arabidopsis thaliana
N:Alternate names: protein T22K7.30
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47425
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24459
A:Accession: T47425
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-228 <RIE>
A:CROSS-references: EMBL:AL138641
A:Experimental source: cultivar Columbia; BAC clone T22K7

C:Genetics:
A:Map position: 3
A:Introns: 53/1; 147/3
A:Note: T22K7.30

Query Match 87.1%; Score 27; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSSRAT 7
DB 175 TSSRAT 180

RESULT 11
B55523
aromatic dioxygenase (EC 1.14.-.-) ferredoxin reductase component - Pseudomonas sp. (strain B55523)
C:Species: Pseudomonas sp.
C>Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 20-Jun-2000
C:Accession: B55523
R:Kikuchi, Y.; Nagata, Y.; Hinata, M.; Kimbara, K.; Fukuda, M.; Yano, K.; Takagi, M.
J. Bacteriol. 176, 1689-1694, 1994
A:Title: Identification of the bphA4 gene encoding ferredoxin reductase involved in biphenyl degradation
A:Reference number: A55523; MUID:94179104; PMID:8132464
A:Accession: B55523
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-410 <KIK>
A:CROSS-references: GB:D16831; NID:G391830; PIDN:BAAB04112.1; PID:G431770
C:Superfamily: toluene dioxygenase ferredoxin reductase component
C:Keywords: oxidoreductase

Query Match 87.1%; Score 27; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSSRAT 7
DB 194 TSSRAT 199

RESULT 12
B29606
methylenomycin A resistance protein - Streptomyces coelicolor plasmid SCP1
C:Species: Streptomyces coelicolor
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 20-Sep-1999
C:Accession: B29606
R:Neal, R.J.; Chater, K.F.
Gene 58, 229-241, 1987
A:Title: Nucleotide sequence analysis reveals similarities between proteins determining methylenomycin A resistance
A:Reference number: A91580; MUID:88112873; PMID:2828187
A:Accession: B29606
A:Molecule type: DNA
A:Residues: 1-475 <NEA>
C:Genetics:
A:Gene: mmr
A:Genome: plasmid
A:Superfamily: tetracycline resistance protein
C:Keywords: antibiotic resistance; transmembrane protein

Query Match 87.1%; Score 27; DB 2; Length 475;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
DB 204 ATSSRAT 210

RESULT 13
T00404
probable cytochrome P450 At2g44890 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 02-Feb-2001
 C;Accession: T00404; A04884
 R;Rounsley, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masc
 submitted to the EMBL Data Library, July 1997
 A;Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.
 A;Reference number: Z14146
 A;Accession: T00404
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-490 <ROU>
 A;Cross-references: EMBL:AC002388; NID:g3420042; PID:g2344895
 A;Experimental source: Cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: A84884
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-490 <STO>
 A;Cross-references: GB:AE002093; NID:g2344895; PIDN:AAC31835.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2G44890; T13E15.10
 A;Map position: 2
 A;Introns: 33/2; 153/3; 248/3; 361/3; 428/3
 C;Superfamily: Candida cytochrome P450 52A3; cytochrome P450 homology
 P;281-456/Domain: cytochrome P450 homology <P45>
 Query Match 87.1%; Score 27; DB 2; Length 490;
 Best Local Similarity 85.7%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ATSSRAT 7
 Db 196 ATSSRAT 202
 RESULT 14
 AG3470
 A;Title: 3-phosphate dehydrogenase (EC 1.1.1.99.5) [imported] - Brucella melitensis (strain
 C;Species: Brucella melitensis
 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
 C;Accession: AG3470
 R;DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova,
 ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A;Reference number: AD3252; PMID:1175668
 A;Accession: AG3470
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-511 <KUR>
 A;Cross-references: GB:AE008917; PIDN:AAL52930.1; PID:g17983778; GSPDB:GN00190
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BME11749
 A;Map position: 1
 C;Superfamily: glycerol-3-phosphate dehydrogenase (aerobic)
 C;Keywords: oxidoreductase
 Query Match 87.1%; Score 27; DB 2; Length 511;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 TSSRAT 7
 Db 55 TSSRAT 60
 RESULT 15
 AG0001

potassium transport protein kup [imported] - Yersinia pestis (strain CO92)
 C;Species: Yersinia pestis
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C;Accession: AG0001
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, J.
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: AG0001
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-622 <KUR>
 A;Cross-references: GB:AL590842; PIDN:CAC88973.1; PID:g15978121; GSPDB:GN00175
 C;Genetics:
 A;Gene: kup
 Query Match 87.1%; Score 27; DB 2; Length 622;
 Best Local Similarity 100.0%; Pred. No. 11e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 TSSRAT 7
 Db 94 TSSRAT 99
 Search completed: April 21, 2004, 17:38:30
 Job time : 8.3913 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:26:23 ; Search time 18.6667 Seconds
(without alignments)
118.319 Million cell updates/sec

Title: SEQ5

Perfect score: 31

Sequence: 1 atserat 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 28 | 90.3 | 281 | 16 Q87CT2 | Q87ct2 xylella fas |
| 2 | 28 | 90.3 | 350 | 2 Q48277 | Q48277 haemophilus |
| 3 | 28 | 90.3 | 440 | 13 Q7R298 | Q7c298 brachydanio |
| 4 | 28 | 90.3 | 543 | 4 Q14879 | Q14879 homo sapien |
| 5 | 28 | 90.3 | 693 | 2 Q50471 | Q50471 mycobacteri |
| 6 | 28 | 90.3 | 716 | 4 Q9NVE4 | Q9nye4 homo sapien |
| 7 | 28 | 90.3 | 798 | 5 Q9U225 | Q9u225 caenorhabdi |
| 8 | 28 | 90.3 | 833 | 5 Q9U016 | Q9u016 plasmodium |
| 9 | 28 | 90.3 | 1205 | 5 Q9V8B7 | Q9v8b7 drosophila |
| 10 | 27 | 87.1 | 109 | 4 Q9UL86 | Q9ul86 homo sapien |
| 11 | 27 | 87.1 | 131 | 17 Q9Y987 | Q9y987 aeropyrum p |
| 12 | 27 | 87.1 | 165 | 4 Q9UD42 | Q9ud42 homo sapien |
| 13 | 27 | 87.1 | 201 | 16 Q8P3G0 | Q8p3g0 xanthomonas |
| 14 | 27 | 87.1 | 227 | 12 Q86620 | Q86620 orf virus (|
| 15 | 27 | 87.1 | 228 | 10 Q9m290 | Q9m290 arabidopsis |
| 16 | 27 | 87.1 | 359 | 10 Q8LPA9 | Q8lpa9 hordeum vul |

| | | | | | |
|----|----|------|------|-----------|---------------------|
| 17 | 27 | 87.1 | 379 | 12 Q8JS35 | Q8js35 phthorimaea |
| 18 | 27 | 87.1 | 391 | 11 Q31ZV1 | Q31zvl rattus norv |
| 19 | 27 | 87.1 | 391 | 16 Q8EC86 | Q8ec86 shewanella |
| 20 | 27 | 87.1 | 401 | 5 Q95TH7 | Q95th7 drosophila |
| 21 | 27 | 87.1 | 430 | 5 Q7YUZ9 | Q7yuz9 trypanosoma |
| 22 | 27 | 87.1 | 490 | 10 Q22162 | Q22162 arabidopsis |
| 23 | 27 | 87.1 | 493 | 5 Q8SWC5 | Q8swc5 encephalito |
| 24 | 27 | 87.1 | 503 | 12 Q99FW7 | Q99fw7 human papil |
| 25 | 27 | 87.1 | 503 | 16 Q8G2W1 | Q8g2w1 bruceella su |
| 26 | 27 | 87.1 | 511 | 16 Q8YEX8 | Q8yex8 bruceella me |
| 27 | 27 | 87.1 | 554 | 6 Q95L89 | Q95l89 bos taurus |
| 28 | 27 | 87.1 | 580 | 6 Q8WML4 | Q8wml4 bos taurus |
| 29 | 27 | 87.1 | 598 | 4 Q75268 | Q75268 homo sapien |
| 30 | 27 | 87.1 | 602 | 10 Q94DS1 | Q94ds1 oryza sativ |
| 31 | 27 | 87.1 | 622 | 16 Q8ZJTO | Q8zjt0 versinia pe |
| 32 | 27 | 87.1 | 622 | 11 Q8Z327 | Q8z327 rattus norv |
| 33 | 27 | 87.1 | 725 | 12 Q8QRW1 | Q8qrw1 chimpanzee |
| 34 | 27 | 87.1 | 753 | 2 Q933S4 | Q933s4 escherichia |
| 35 | 27 | 87.1 | 753 | 2 Q93Q52 | Q93q52 shigella fl |
| 36 | 27 | 87.1 | 852 | 10 Q7Y097 | Q7y097 oryza sativ |
| 37 | 27 | 87.1 | 863 | 4 Q8YF21 | Q8yft21 homo sapien |
| 38 | 27 | 87.1 | 880 | 5 Q7YU85 | Q7yu85 drosophila |
| 39 | 27 | 87.1 | 882 | 5 Q9VA36 | Q9va36 drosophila |
| 40 | 27 | 87.1 | 927 | 16 Q861W9 | Q861w9 pseudomonas |
| 41 | 27 | 87.1 | 1127 | 13 Q9PU92 | Q9pu92 cyprinus ca |
| 42 | 27 | 87.1 | 1171 | 5 Q9VTW8 | Q9vtw8 drosophila |
| 43 | 27 | 87.1 | 1464 | 11 Q63728 | Q63728 rattus norv |
| 44 | 27 | 87.1 | 1464 | 11 Q08948 | Q08948 rattus norv |
| 45 | 27 | 87.1 | 2012 | 10 Q8GSW6 | Q8gsW6 oryza sativ |

ALIGNMENTS

RESULT 1
Q87CT2 PRELIMINARY; PRT; 281 AA.
ID Q87CT2
AC Q87CT2; (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Plasmid-related protein.
GN TRAN OR PD0981.
OS Xylella fastidiosa (strain Temecula / ATCC 700964).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=183190;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22421331; PubMed=12533478;
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H.,
Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Silva F.R.,
Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Teal S.M.,
Carer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
RA Marino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Baia G.S., Bianco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
da Cunha A.F., Penille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA Kitajima J.P.;
RT "Comparative analyses of the complete genome sequences of Pierce's
disease and citrus variegated chlorosis strains of Xylella
fastidiosa." 185:1018-1026(2003).
RT J. Bacteriol. 185:1018-1026(2003).
RL EMBL; AB012556; AA028843.1; -
DR Interpro; IPR006528; PhagesPPI_gp7.
DR Pfam; PF04233; Phage_Mu_F; 1.
KW Complete proteome.
SQ SEQUENCE 281 AA; 31303 MW; 6B7E5544FAEC6A42 CRC64;


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Query Match          90.3%; Score 28; DB 16; Length 281;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 196 ATASRAT 202

RESULT 2
Q48277 PRELIMINARY; PRT; 350 AA.
AC Q48277;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Putative major capsid protein.
OS Haemophilus somnus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=731;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HS25;
RA Pontarollo R.A.; Rioux C.R.; Potter A.A.;
DR EMBL; U28154; AAC45158.1; -
DR InterPro; IPR006441; Major capsid_p2.
DR Pfam; PF05125; Phage_cap_P2; 1.
DR TIGRFAMs; TIGR01551; major_capsid_p2; 1.
SQ SEQUENCE 350 AA; 38973 MW; 07B47EC8F2C86116 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 350;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 155 ATSNRAT 161

RESULT 3
Q7T298 PRELIMINARY; PRT; 440 AA.
AC Q7T298;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Scapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Uedin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

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RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalon D.K.; Musny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahay J.; Helton E.; Kettman M.; Madan A.; Rodrigues S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
RA Krzywinski M.I.; Skalska U.; Smailus D.E.; Scherch A.; Schein J.E.;
RA Jones S.J.; Mairra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054634; AAH54634.1; -
KW Hypothetical protein.
SQ SEQUENCE 440 AA; 49158 MW; 2480B79309437752 CRC64;

Query Match          90.3%; Score 28; DB 13; Length 440;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 370 ATSSRST 376

RESULT 4
Q14879 PRELIMINARY; PRT; 543 AA.
AC Q14879;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Mucin (Fragment).
GN MUC5B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tracheobronchial mucosa;
RX MEDLINE=93343858; PubMed=7916618;
RA Dufosse J.; Porchet N.; Audie J.P.; Guyonnet Duperrat V.; Laine A.;
RA Van-Seuningen I.; Marrakchi S.; Degand P.; Aubert J.P.;
RT "Degenerate 87-base-pair tandem repeats create hydrophilic/hydrophobic
RT alternating domains in human mucin peptides mapped to 1p15."
RL Biochem. J. 293:329-337 (1993).
DR EMBL; X74370; CAA52408.1; -
DR FIR; S35047; S35047.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
DR InterPro; IPR002965; P:rich extensin.
DR PRINTS; PR01217; PRICEXTENS.
FT NON_TER 1 543
FT NON_TER 543 543
SQ SEQUENCE 543 AA; 55197 MW; 6767A5E3518B287B CRC64;

Query Match          90.3%; Score 28; DB 4; Length 543;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 73 ATSSKAT 79

RESULT 5

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Q50471 ID Q50471 PRELIMINARY; PRT; 693 AA.
AC Q50471;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Orf 5, of katG (species-specific fragment) (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteriales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1173;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95131752; PubMed=7830574;
RA Zhang Y., Young D.;
RT "Strain variation in the katG region of Mycobacterium tuberculosis."
RL Mol. Microbiol. 14:301-308(1994).
DR EMBL; S77045; AAC60492.1; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR InterPro; IPR000183; Decarboxylase2.
DR InterPro; IPR002989; Mycobact_pentapep.
DR Pfam; PF01469; Pentapeptide 2; 8.
DR PROSITE; PS00879; ODR DC 2.2; 3.
FT NON TER
FT TER
SQ SEQUENCE 693 AA; 68111 MW; B614BC8B251B24B CRC64;

Query Match 90.3%; Score 28; DB 2; Length 693;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
DB 693 ATSSRAT 689

RESULT 6
Q9NYE4 ID Q9NYE4 PRELIMINARY; PRT; 716 AA.
AC Q9NYE4;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Cervical mucin MUC5B (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Ho S.B., Toribara N.W., Anway R.E., Spurr-Michaud S.J., Shekels L.L.,
RA Keutmann H.T., Hill J.A., Gipson I.K.;
RT "Expression cloning of human cervical proteins using an antibody to
RT cervical mucus."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF253321; AAF64523.1; -.
FT NON TER
FT NON TER
SQ SEQUENCE 716 AA; 71194 MW; 6F3F20E7512289F3 CRC64;

Query Match 90.3%; Score 28; DB 4; Length 716;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
DB 382 ATSSRAT 388

RESULT 7
Q9U225 ID Q9U225 PRELIMINARY; PRT; 798 AA.
AC Q9U225;
DT 01-MAY-2000 (Tremblrel. 13, Created)

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DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Y56A3A.6 protein.
GN Y56A3A.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Telodermata; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AL132860; CAB60515.1; -.
DR WormRep; Y56A3A.6; CR22577;
SQ SEQUENCE 798 AA; 85950 MW; 172FEB04895A9EEB CRC64;

Query Match 90.3%; Score 28; DB 5; Length 798;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
DB 659 ATSSRAT 665

RESULT 8
Q9U016 ID Q9U016 PRELIMINARY; PRT; 833 AA.
AC Q9U016;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
GN MALP2.35
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=3D7;
RA Devlin K., Bowman S., Churcher C., Harris B., Harris D., Lawson D.,
RA Quail M., Barrell B.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035475; CAB62877.2; -.
KW Hypothetical protein.
SQ SEQUENCE 833 AA; 100542 MW; DD231B04831DFD74 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 833;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
DB 57 ATSSRAT 63

RESULT 9
Q9V8B7 ID Q9V8B7 PRELIMINARY; PRT; 1205 AA.
AC Q9V8B7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE CG5756 protein.
GN CG5756.
OS Drosophila melanogaster (Fruit fly).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abail J.F., Abayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chertys J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003800; AAF57754.1; -.
DR FlyBase; FBgn0034301; CG5756.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; P:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_perA.
DR Pfam; PF01607; CBM_14; 1.
DR SMART; SM00494; ChtBD2; 1.
SQ SEQUENCE 1205 AA; 132314 MW; C18E2F0E0491AF62 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 1205;
Best Local Similarity 85.7%; Pred.No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 725 ATSSRAT 731

RESULT 10
Q9UL86
AC Q9UL86 PRELIMINARY; PRT; 109 AA.
ID Q9UL86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region

```

```

DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1; -.
DR PIR; B30607; B30607.
DR HSR; I30601; I30601.
DR HSR; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 87.1%; Score 27; DB 4; Length 109;
Best Local Similarity 100.0%; Pred.No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSSRAT 7
Db 52 TSSRAT 57

RESULT 11
Q9Y987 PRELIMINARY; PRT; 131 AA.
ID Q9Y987;
AC Q9Y987;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein APE2398.
GN APE2398.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KJ.
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankaï A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999).
DR EMBL; AF000064; BAA81413.1; -.
DR PIR; E72469; E72469.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 131 AA; 13019 MW; 0DA7559BA655BAA1 CRC64;

Query Match 87.1%; Score 27; DB 17; Length 131;
Best Local Similarity 100.0%; Pred.No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSSRAT 7
Db 38 TSSRAT 43

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DR EMBL; AE012535; AAM43332.1; -.
KW Complete proteome. 21267 MW; 08239FA3067863A2 CRC64;
SQ SEQUENCE 201 AA; 21267 MW; 08239FA3067863A2 CRC64;

Query Match 87.1%; Score 27; DB 16; Length 201;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 108 ATSKRAT 114

RESULT 14
Q86620 PRELIMINARY; PRT; 227 AA.
AC Q86620;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope antigen homolog.
GN F1R.
OS Orf virus (strain NZ2) (OV NZ-2).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Parapoxvirus.
OC NCBI_TaxID=10259;
OX NCBI_TaxID=10259;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NZ2;
RX MEDLINE=3303916; PubMed=8317094;
RA Fleming S.B., Siock J., Fraser K.M., Mercer A.A., Robinson A.J.;
RT "Conservation of gene structure and arrangement between vaccinia virus
and orf virus.";
RL Virology 195:175-184(1993).
DR EMBL; S62819; AAB27258.2; -.
DR PIR; B37473; B37473.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR InterPro; IPR004966; Pox_AG35.
DR Pfam; PF03286; Pox_AG35; 1.
DR SEQUENCE 227 AA; 24613 MW; 539DD35C3478316F CRC64;

Query Match 87.1%; Score 27; DB 12; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSSRAT 7
Db 118 TSSRAT 123

RESULT 15
Q9M290 PRELIMINARY; PRT; 228 AA.
AC Q9M290;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NAC domain-like protein.
GN T2X7_30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Meves H.W., Rudd S.;
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP EU Arabidopsis sequencing project;
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AL138641; CAB86913.1; -.
 DR PIR; T47425; T47425. NAM.
 DR InterPro; IPR003441; NAM.
 DR Pfam; PF02365; NAM; 1.
 SQ SEQUENCE 228 AA; 25304 MW; BSD67E70E96D2F44 CRC64;

Query Match 87.1%; Score 27; DB 10; Length 228;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TSSRAT 7
 |||||
 Db 175 TSSRAT 180

Search completed: April 21, 2004, 17:37:21
 Job time : 21.6667 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:18 ; Search time 28 Seconds
(without alignments)
70.637 Million cell updates/sec

Title: SEQ5

Perfect score: 31
Sequence: 1 atsrat 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 31 | 100.0 | 88 | AAU41616 | AAU41616 Propionib |
| 2 | 31 | 100.0 | 88 | ABM38135 | ABM38135 Propionib |
| 3 | 31 | 100.0 | 474 | 3 AAG30724 | AAG30724 Arabidops |
| 4 | 31 | 100.0 | 495 | 3 AAG30723 | AAG30723 Arabidops |
| 5 | 31 | 100.0 | 497 | 3 AAG30722 | AAG30722 Arabidops |
| 6 | 31 | 100.0 | 501 | 7 ADB70174 | ADB70174 C. neofor |
| 7 | 28 | 90.3 | 59 | 4 AAU41209 | AAU41209 Propionib |
| 8 | 28 | 90.3 | 59 | 6 ABM37728 | ABM37728 Propionib |
| 9 | 28 | 90.3 | 70 | 4 AAU66145 | AAU66145 Propionib |
| 10 | 28 | 90.3 | 70 | 4 AAU50420 | AAU50420 Propionib |
| 11 | 28 | 90.3 | 70 | 5 ABP03196 | ABP03196 Human ORF |
| 12 | 28 | 90.3 | 70 | 6 ABM46939 | ABM46939 Propionib |
| 13 | 28 | 90.3 | 70 | 6 ABM62664 | ABM62664 Propionib |
| 14 | 28 | 90.3 | 82 | 6 ABP75831 | ABP75831 Human sec |
| 15 | 28 | 90.3 | 104 | 4 AAU56589 | AAU56589 Propionib |
| 16 | 28 | 90.3 | 104 | 6 ABM64894 | ABM64894 Propionib |
| 17 | 28 | 90.3 | 104 | 6 ABM53108 | ABM53108 Propionib |
| 18 | 28 | 90.3 | 163 | 4 AAU54597 | AAU54597 Propionib |
| 19 | 28 | 90.3 | 163 | 6 ABM51116 | ABM51116 Propionib |
| 20 | 28 | 90.3 | 173 | 3 AAY74998 | AAY74998 Neisseria |
| 21 | 28 | 90.3 | 173 | 3 AAY74997 | AAY74997 Neisseria |
| 22 | 28 | 90.3 | 197 | 3 AAY74994 | AAY74994 Neisseria |
| 23 | 28 | 90.3 | 197 | 3 AAY74995 | AAY74995 Neisseria |
| 24 | 28 | 90.3 | 251 | 3 AAU67887 | AAU67887 Propionib |
| 25 | 28 | 90.3 | 251 | 6 ABM64406 | ABM64406 Propionib |

| | | | | | |
|----|----|------|------|------------|--------------------|
| 26 | 28 | 90.3 | 363 | 6 ABM66094 | ABM66094 Propionib |
| 27 | 28 | 90.3 | 842 | 5 ABP73474 | ABP73474 Candida a |
| 28 | 28 | 90.3 | 1205 | 4 ABM61778 | ABM61778 Drosophil |
| 29 | 28 | 90.3 | 4315 | 5 ABP43908 | ABP43908 MUC5B par |
| 30 | 27 | 87.1 | 7 | 5 ABP62365 | ABP62365 Human imm |
| 31 | 27 | 87.1 | 10 | 4 AAG87027 | AAG87027 Saccharom |
| 32 | 27 | 87.1 | 10 | 4 AAG87029 | AAG87029 Saccharom |
| 33 | 27 | 87.1 | 61 | 4 AAU54148 | AAU54148 Propionib |
| 34 | 27 | 87.1 | 61 | 6 ABM50667 | ABM50667 Propionib |
| 35 | 27 | 87.1 | 102 | 4 AAU89514 | AAU89514 Human imm |
| 36 | 27 | 87.1 | 102 | 6 AAU38332 | AAU38332 Human ant |
| 37 | 27 | 87.1 | 109 | 4 AAB62768 | AAB62768 Human HIV |
| 38 | 27 | 87.1 | 109 | 5 ABG92885 | ABG92885 Human imm |
| 39 | 27 | 87.1 | 109 | 6 AAO29549 | AAO29549 Human 7.1 |
| 40 | 27 | 87.1 | 109 | 6 ABG71911 | ABG71911 Human ant |
| 41 | 27 | 87.1 | 109 | 6 ADA89184 | ADA89184 Human ant |
| 42 | 27 | 87.1 | 120 | 5 ABP62191 | ABP62191 Human imm |
| 43 | 27 | 87.1 | 178 | 4 AAU33249 | AAU33249 Novel hum |
| 44 | 27 | 87.1 | 183 | 2 AAY29862 | AAY29862 Human sec |
| 45 | 27 | 87.1 | 203 | 2 AAR47336 | AAR47336 Peptide f |

ALIGNMENTS

RESULT 1
AAU41616
ID AAU41616 standard; protein; 88 AA.
XX
AC AAU41616;
XX
DT 13-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #2512.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US012865.

XX 21-APR-2000; 2000US-0199047P.

XX 02-JUN-2000; 2000US-0208941P.

XX 07-JUL-2000; 2000US-0216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-6156774/71.

XX N-PSDB; AAS59515.

XX Propionibacterium acnes polypeptides and nucleic acids useful for

XX vaccinating against and diagnosing infections, especially useful for

XX treating acne vulgaris.

XX Example 1; SEQ ID NO 2811; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

XX polypeptides. The proteins and their associated DNA sequences are used in

XX the treatment, prevention and diagnosis of medical conditions caused by

XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

XX pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

XX P. acnes is also involved in infections of bone, joints and the central

XX nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 88 AA;

Query Match 100.0%; Score 31; DB 4; Length 88;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
 Db 75 ATSSRAT 81
 |||||

RESULT 2
 ID ABM38135 standard; protein; 88 AA.
 XX ABM38135;
 DT 20-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #2811.
 XX
 KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 OS
 XX Propionibacterium acnes.
 XX
 PN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032727.
 XX
 PR 15-OCT-2001; 2001US-00978825.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MU, Benson DR, Jones R, Carter D;
 PI Barth B, Valliave-Douglas J;
 XX
 DR WPI; 2003-381789/36.
 DR N-PSDB; ACF64444.
 XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 PS Example 1; SEQ ID NO 2811; 1481pp; English.
 XX
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,

CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 88 AA;

Query Match 100.0%; Score 31; DB 6; Length 88;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
 Db 75 ATSSRAT 81
 |||||

RESULT 3
 AAG30724
 ID AAG30724 standard; protein; 474 AA.
 XX AAG30724;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 36783.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-00301439.
 XX
 PR 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.
 PR 16-APR-1999; 99US-0129845P.
 PR 19-APR-1999; 99US-0130077P.
 PR 21-APR-1999; 99US-0130449P.
 PR 23-APR-1999; 99US-0130510P.
 PR 28-APR-1999; 99US-0130891P.
 PR 30-APR-1999; 99US-0131449P.
 PR 30-APR-1999; 99US-0132048P.
 PR 04-MAY-1999; 99US-0132407P.
 PR 05-MAY-1999; 99US-0132484P.
 PR 06-MAY-1999; 99US-0132485P.
 PR 06-MAY-1999; 99US-0132486P.
 PR 07-MAY-1999; 99US-0132487P.
 PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 28-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 01-JUN-1999; 99US-0137528P.
PR 03-JUN-1999; 99US-0137502P.
PR 04-JUN-1999; 99US-0137724P.
PR 07-JUN-1999; 99US-0138094P.
PR 08-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 10-JUN-1999; 99US-0139119P.
PR 14-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139753P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140931P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
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| PR | 19-JUL-1999; | 99US-0144332P. | PR | 14-OCT-1999; | 99US-0159330P. |
| PR | 19-JUL-1999; | 99US-0144333P. | PR | 14-OCT-1999; | 99US-0159331P. |
| PR | 19-JUL-1999; | 99US-0144334P. | PR | 14-OCT-1999; | 99US-0159637P. |
| PR | 19-JUL-1999; | 99US-0144335P. | PR | 14-OCT-1999; | 99US-0159638P. |
| PR | 20-JUL-1999; | 99US-0144352P. | PR | 18-OCT-1999; | 99US-0159584P. |
| PR | 20-JUL-1999; | 99US-0144632P. | PR | 21-OCT-1999; | 99US-0160741P. |
| PR | 20-JUL-1999; | 99US-0144884P. | PR | 21-OCT-1999; | 99US-0160767P. |
| PR | 21-JUL-1999; | 99US-0144814P. | PR | 21-OCT-1999; | 99US-0160768P. |
| PR | 21-JUL-1999; | 99US-0145086P. | PR | 21-OCT-1999; | 99US-0160770P. |
| PR | 21-JUL-1999; | 99US-0145088P. | PR | 21-OCT-1999; | 99US-0160814P. |
| PR | 22-JUL-1999; | 99US-0145087P. | PR | 21-OCT-1999; | 99US-0160815P. |
| PR | 22-JUL-1999; | 99US-0145089P. | PR | 22-OCT-1999; | 99US-0160980P. |
| PR | 22-JUL-1999; | 99US-0145192P. | PR | 22-OCT-1999; | 99US-0160981P. |
| PR | 23-JUL-1999; | 99US-0145145P. | PR | 22-OCT-1999; | 99US-0160989P. |
| PR | 23-JUL-1999; | 99US-0145218P. | PR | 25-OCT-1999; | 99US-0161404P. |
| PR | 23-JUL-1999; | 99US-0145224P. | PR | 25-OCT-1999; | 99US-0161405P. |
| PR | 26-JUL-1999; | 99US-0145276P. | PR | 25-OCT-1999; | 99US-0161406P. |
| PR | 27-JUL-1999; | 99US-0145913P. | PR | 26-OCT-1999; | 99US-0161359P. |
| PR | 27-JUL-1999; | 99US-0145918P. | PR | 26-OCT-1999; | 99US-0161360P. |
| PR | 27-JUL-1999; | 99US-0145919P. | PR | 26-OCT-1999; | 99US-0161361P. |
| PR | 28-JUL-1999; | 99US-0145951P. | PR | 28-OCT-1999; | 99US-0161920P. |
| PR | 02-AUG-1999; | 99US-0146386P. | PR | 28-OCT-1999; | 99US-0161922P. |
| PR | 02-AUG-1999; | 99US-0146388P. | PR | 28-OCT-1999; | 99US-0161993P. |
| PR | 03-AUG-1999; | 99US-0147038P. | PR | 29-OCT-1999; | 99US-0162142P. |
| PR | 04-AUG-1999; | 99US-0147204P. | | | |
| PR | 04-AUG-1999; | 99US-0147302P. | | | |
| PR | 05-AUG-1999; | 99US-0147192P. | | | |

Query Match 100.0%; Score 31; DB 3; Length 497;

```

Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 377 ATSSRAT 383

RESULT 6
ADB70174
ID ADB70174 standard; protein; 501 AA.
AC ADB70174;
XX
XX 04-DEC-2003 (first entry)
XX
XX C. neoformans amino acid sequence SEQ ID NO:3218.
XX
XX fungicide; gene therapy; infection.
XX
XX Cryptococcus neoformans.
XX
XX WO2003052076-A2.
XX
XX 26-JUN-2003.
XX
XX 17-DEC-2002; 2002WO-US040225.
XX
XX 17-DEC-2001; 2001US-0341261P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Zamudio C, Eroshkin AM;
XX
XX WPI; 2003-533017/50.
XX
XX N-PSDB; ADB69091.
XX
XX New nucleic acid, useful for preparing a composition for treating an
XX infection caused by Cryptococcus neoformans.
XX
XX Claim 9; SEQ ID NO 3218; 136pp; English.
XX
XX The invention relates to a novel purified or isolated Cryptococcus
XX neoformans nucleic acid molecule comprising a sequence encoding a
XX polypeptide comprising a sequence not given in the specification. A
XX polynucleotide of the invention has fungicide activity, and may have a
XX use in gene therapy. The nucleic acid is useful for preparing a
XX composition for treating an infection caused by Cryptococcus neoformans.
XX The present sequence represents a C. neoformans sequence of the
XX invention. Note: The sequence data for this patent is not represented in
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
XX Sequence 501 AA;

Query Match 100.0%; Score 31; DB 7; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 47 ATSSRAT 53

RESULT 7
AAU41209
ID AAU41209 standard; protein; 59 AA.
XX
XX AAU41209;
XX
XX 13-FEB-2002 (first entry)
XX
XX Propionibacterium acnes immunogenic protein #2105.
XX
XX

Best Local Similarity 90.3%; Score 28; DB 4; Length 59;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 27 ATASRAT 33

RESULT 8
ABM37728
ID ABM37728 standard; protein; 59 AA.
XX
XX ABM37728;
XX
XX 20-OCT-2003 (first entry)
XX
XX Propionibacterium acnes predicted ORF-encoded polypeptide #2404.
XX
XX

```

```

XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
XX
XX WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX
XX 02-JUN-2000; 2000US-0208841P.
XX
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI; 2001-616774/71.
XX
XX N-PSDB; AAS59514.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX vaccinating against and diagnosing infections, especially useful for
XX treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 2404; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX polypeptides. The proteins and their associated DNA sequences are used in
XX the treatment, prevention and diagnosis of medical conditions caused by
XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX P. acnes is also involved in infections of bone, joints and the central
XX nervous system, however it is particularly involved in the inflammatory
XX lesions associated with acne vulgaris. A method for detecting the
XX presence or absence of P. acnes in a patient comprises contacting a
XX sample with a binding agent that binds to the proteins of the invention
XX and determining the amount of bound protein in the sample. The
XX polypeptides may be used as antigens in the production of antibodies
XX specific for P. acnes proteins. These antibodies can be used to
XX downregulate expression and activity of P. acnes polypeptides and
XX therefore treat P. acnes infections. The antibodies may also be used as
XX diagnostic agents for determining P. acnes presence, for example, by
XX enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pat_sequences
XX
XX Sequence 59 AA;

Query Match 90.3%; Score 28; DB 4; Length 59;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 27 ATASRAT 33

RESULT 8
ABM37728
ID ABM37728 standard; protein; 59 AA.
XX
XX ABM37728;
XX
XX 20-OCT-2003 (first entry)
XX
XX Propionibacterium acnes predicted ORF-encoded polypeptide #2404.
XX
XX

```

XX Acne vulgaris; antisborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 XX Propionibacterium acnes.
 XX WO2003033515-A1.
 XX 24-APR-2003.
 XX 11-OCT-2002; 2002WO-US032727.
 XX 15-OCT-2001; 2001US-00978825.
 XX (CORI-) CORIXA CORP.
 XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes WJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieue-Douglas J;
 XX WPI; 2003-381789/36.
 DR N-PSDB; ACF64443.
 XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX Example 1; SEQ ID NO 2404; 1481pp; English.
 XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 59 AA;
 SQ
 Query Match 90.3%; Score 28; DB 6; Length 59;
 Best Local Similarity 85.7%; Pred. No. 59;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSRAT 7
 Db 27 ATASRAT 33
 RESULT 9
 AAU66145
 ID AAU66145 standard; protein; 70 AA.
 XX
 AC AAU66145;

XX 27-FEB-2002 (first entry)
 DT Propionibacterium acnes immunogenic protein #27041.
 XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX Propionibacterium acnes.
 XX WO200181581-A2.
 XX 01-NOV-2001.
 XX 20-APR-2001; 2001WO-US012865.
 XX 21-APR-2000; 2000US-0199047P.
 XX 02-JUN-2000; 2000US-0208841P.
 XX 07-JUL-2000; 2000US-0216747P.
 XX (CORI-) CORIXA CORP.
 XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'Maisonneuve J, Zhang Y, Jen S, Carter D;
 XX WPI; 2001-616774/71.
 DR N-PSDB; AAS59715.
 XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX Example 1; SEQ ID NO 27340; 1069pp; English.
 XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis,
 CC hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 70 AA;
 SQ
 Query Match 90.3%; Score 28; DB 4; Length 70;
 Best Local Similarity 85.7%; Pred. No. 72;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSRAT 7
 Db 3 ATSSRAT 9
 RESULT 10
 AAU50420
 ID AAU50420 standard; protein; 70 AA.
 XX
 AC AAU50420;

XX DT 27-FEB-2002 (first entry)
 XX DE Propionibacterium acnes immunogenic protein #11316.
 XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX OS Propionibacterium acnes.
 XX PN WO200181581-A2.
 XX PD 01-NOV-2001.
 XX PF 20-APR-2001; 2001WO-US012865.
 XX PR 21-APR-2000; 2000US-0199047P.
 XX PR 02-JUN-2000; 2000US-0208841P.
 XX PR 07-JUL-2000; 2000US-0216747P.
 XX PA (CORI-) CORIXA CORP.
 XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX DR WPI; 2001-616774/71.
 XX DR N-PSDB; AAS59548.
 XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX PS Example 1; SEQ ID NO 11615; 1069pp; English.
 XX CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: the sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 70 AA;
 Query Match 90.3%; Score 28; DB 4; Length 70;
 Best Local Similarity 85.7%; Pred. No. 72;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSSRAT 7
 Db 3 ATSSSRST 9
 RESULT 11
 ABP03196
 ID ABP03196 standard; protein; 70 AA.
 XX
 AC ABP03196;

XX DT 24-JUN-2002 (first entry)
 XX DE Human ORFX protein sequence SEQ ID NO:6374.
 XX KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.
 XX OS Homo sapiens.
 XX PN WO200192523-A2.
 XX PD 06-DEC-2001.
 XX PF 29-MAY-2001; 2001WO-US010836.
 XX PR 30-MAY-2000; 2000US-0206132P.
 XX PR 29-AUG-2000; 2000US-0228716P.
 XX PA (CURA-) CURAGEN CORP.
 XX PI Shimkets RA, Leach MD;
 XX PI WPI; 2002-106308/14.
 XX DR N-PSDB; ABN18948.
 XX PT Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders.
 XX PS Disclosure; SEQ ID NO 6374; 1037pp; English.
 XX CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN27452 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 70 AA;
 Query Match 90.3%; Score 28; DB 5; Length 70;
 Best Local Similarity 85.7%; Pred. No. 72;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSSRAT 7
 Db 3 ATSSSRST 9

```
Query Match          90.3%; Score 28; DB 6; Length 70;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Query Match 90.3%; Score 28; DB 6; Length 70;
 Best Local Similarity 85.7%; Pred. No. 72;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
 3 ATSSRST 9

Db
 RESULT 14
 ABP75831
 ID ABP75831 standard; protein; 82 AA.
 AC ABP75831;
 XX
 DT 10-FEB-2003 (first entry)
 XX
 DE Human secretory polypeptide SPTM SEQ ID NO 1015.
 XX
 KW Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;
 KW asthma; Crohn's disease; neurological disorder; epilepsy; cancer;
 KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
 KW multiple sclerosis; Parkinson's disease; cell proliferative disorder;
 KW anti-inflammatory; immunosuppressive; neuroprotective; neoplastic;
 KW neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;
 KW antipsychotic; antianemic; anti-HIV; human immunodeficiency virus;
 KW secretory polynucleotide; secretory protein.
 XX
 OS Homo sapiens.
 XX
 FN WO200283876-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 27-MAR-2002; 2002WO-US009921.
 XX
 PR 29-MAR-2001; 2001US-0280067P.
 PR 29-MAR-2001; 2001US-0280068P.
 PR 16-MAY-2001; 2001US-0291280P.
 PR 17-MAY-2001; 2001US-0291829P.
 PR 17-MAY-2001; 2001US-0291849P.
 PR 19-JUN-2001; 2001US-0293428P.
 PR 20-JUN-2001; 2001US-0293778P.
 PR 20-JUN-2001; 2001US-0300001P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Ameshey SR;
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstein EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 XX
 WPI; 2003-075543/07.
 DR N-PSDB; AB236273.
 XX
 XX New human secretory proteins and polynucleotides, useful for diagnosing,
 PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),
 PT neurological disorders (e.g. Alzheimer's), or cell proliferations or
 PT cancers.
 XX
 PS Claim 27; SEQ ID NO 1015; 458pp + Sequence Listing; English.
 XX
 CC The invention relates to a secretory polynucleotide (designated sptm)
 CC comprising any of 567 polynucleotide sequences (AB235837-AB236403), a
 CC naturally occurring polynucleotide sequence at least 90 % identical to
 CC the polynucleotide sequence, a polynucleotide complementary to them or an
 CC RNA equivalent of them. The polypeptide or polynucleotide are useful for
 CC treating, preventing or diagnosing a disease or condition associated with
 CC the expression of functional SPTM. These are particularly useful for
 CC diagnosing, treating or preventing autoimmune/inflammatory disorders
 CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
 CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,

CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
 CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
 CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
 CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
 CC breast, cervix or prostate). The present sequence is one of the SPTM
 CC proteins of the invention (ABP75831-ABP75962). Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 82 AA;
 Query Match 90.3%; Score 28; DB 6; Length 82;
 Best Local Similarity 85.7%; Pred. No. 85;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
 74 ATSSKAT 80

Db
 RESULT 15
 AAU56589
 ID AAU56589 standard; protein; 104 AA.
 XX
 AC AAU56589;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #17485.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 FN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US012865.
 XX
 PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 WPI; 2001-616774/71.
 DR N-PSDB; AAS59577.
 XX
 XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX
 PS Example 1; SEQ ID NO 17784; 1069pp; English.
 XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention

CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 104 AA;
Query Match 90.3%; Score 28; DB 4; Length 104;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSRAT 7
Db 45 ATSSKAT 51
Search completed: April 21, 2004, 17:33:15
Job time : 31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2004, 17:37:29 ; Search time 21.1014 Seconds
(without alignments)
91.715 Million cell updates/sec

Title: SEQ5
Perfect score: 31
Sequence: 1 atssrat 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 31 | 100.0 | 96 | 14 | US-10-041-860-377 |
| 2 | 31 | 100.0 | 108 | 14 | US-10-041-860-49 |
| 3 | 31 | 100.0 | 108 | 14 | US-10-041-860-225 |
| 4 | 31 | 100.0 | 108 | 14 | US-10-041-860-259 |
| 5 | 31 | 100.0 | 108 | 14 | US-10-041-860-375 |
| 6 | 31 | 100.0 | 140 | 12 | US-10-424-599-176884 |
| 7 | 31 | 100.0 | 497 | 16 | US-10-389-566-2341 |
| 8 | 31 | 100.0 | 501 | 15 | US-10-320-797-3218 |
| 9 | 28 | 90.3 | 842 | 12 | US-10-425-114-41459 |
| 10 | 28 | 90.3 | 842 | 12 | US-10-032-588-7311 |
| 11 | 27 | 87.1 | 79 | 12 | US-10-424-599-148739 |
| 12 | 27 | 87.1 | 96 | 14 | US-10-041-860-376 |
| 13 | 27 | 87.1 | 109 | 12 | US-10-371-942-28 |
| 14 | 27 | 87.1 | 109 | 14 | US-10-067-800-62 |
| 15 | 27 | 87.1 | 109 | 15 | US-10-292-486-47 |

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| 16 | 27 | 87.1 | 212 | 14 | US-10-006-593-118 | Sequence 118, App |
| 17 | 27 | 87.1 | 212 | 15 | US-10-307-724-118 | Sequence 118, App |
| 18 | 27 | 87.1 | 245 | 14 | US-10-128-714-3428 | Sequence 3428, App |
| 19 | 27 | 87.1 | 245 | 15 | US-10-369-493-3216 | Sequence 3216, App |
| 20 | 27 | 87.1 | 263 | 15 | US-10-422-628-14 | Sequence 14, Appl |
| 21 | 27 | 87.1 | 269 | 12 | US-10-425-114-50879 | Sequence 50879, A |
| 22 | 27 | 87.1 | 331 | 15 | US-10-327-413-2 | Sequence 2, Appl |
| 23 | 27 | 87.1 | 345 | 14 | US-10-128-714-8428 | Sequence 8428, App |
| 24 | 27 | 87.1 | 501 | 12 | US-10-424-599-192945 | Sequence 192945, A |
| 25 | 27 | 87.1 | 622 | 12 | US-10-282-122A-77710 | Sequence 77710, A |
| 26 | 27 | 87.1 | 752 | 15 | US-10-104-047-1975 | Sequence 1975, App |
| 27 | 27 | 87.1 | 753 | 14 | US-10-238-075-1277 | Sequence 1277, App |
| 28 | 27 | 87.1 | 777 | 14 | US-10-208-219-93 | Sequence 93, Appl |
| 29 | 27 | 87.1 | 988 | 9 | US-09-843-676-69 | Sequence 69, Appl |
| 30 | 27 | 87.1 | 988 | 9 | US-09-766-253-69 | Sequence 69, Appl |
| 31 | 27 | 87.1 | 988 | 10 | US-09-438-486-69 | Sequence 69, Appl |
| 32 | 27 | 87.1 | 988 | 12 | US-10-325-810-112 | Sequence 112, App |
| 33 | 27 | 87.1 | 988 | 14 | US-10-053-758-69 | Sequence 69, Appl |
| 34 | 27 | 87.1 | 988 | 14 | US-10-054-295-69 | Sequence 69, Appl |
| 35 | 27 | 87.1 | 988 | 14 | US-10-054-611-69 | Sequence 69, Appl |
| 36 | 27 | 87.1 | 988 | 14 | US-10-044-692-112 | Sequence 112, App |
| 37 | 27 | 87.1 | 988 | 14 | US-10-044-539-112 | Sequence 112, App |
| 38 | 27 | 87.1 | 1153 | 9 | US-09-992-056-2 | Sequence 2, Appl |
| 39 | 27 | 87.1 | 1153 | 12 | US-10-220-282A-2 | Sequence 2, Appl |
| 40 | 27 | 87.1 | 1153 | 14 | US-10-224-249-13 | Sequence 13, Appl |
| 41 | 27 | 87.1 | 1464 | 10 | US-09-934-070-15 | Sequence 15, Appl |
| 42 | 27 | 87.1 | 1464 | 10 | US-09-922-011-1 | Sequence 1, Appl |
| 43 | 27 | 87.1 | 1464 | 12 | US-10-222-772-15 | Sequence 15, Appl |
| 44 | 26 | 83.9 | 34 | 14 | US-10-218-103-255 | Sequence 255, App |
| 45 | 26 | 83.9 | 65 | 12 | US-10-424-599-158367 | Sequence 158367, A |

ALIGNMENTS

RESULT 1
US-10-041-860-377
; Sequence 377, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezaheh, Binayam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 377
; LENGTH: 96
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-377

Query Match 100.0%; Score 31; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 51 ATSSRAT 57

RESULT 2
US-10-041-860-49
; Sequence 49, Application US/10041860

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; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-49

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Query Match      100.0%; Score 31; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATSSRAT 7
Db 51 ATSSRAT 57

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RESULT 3
US-10-041-860-225
; Sequence 225, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-225

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Query Match      100.0%; Score 31; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATSSRAT 7
Db 51 ATSSRAT 57

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RESULT 4
US-10-041-860-259
; Sequence 259, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.

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; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-259

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Query Match      100.0%; Score 31; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATSSRAT 7
Db 51 ATSSRAT 57

```

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RESULT 5
US-10-041-860-375
; Sequence 375, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-375

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```

Query Match      100.0%; Score 31; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 ATSSRAT 7
Db 51 ATSSRAT 57

```

```

RESULT 6
US-10-424-599-176884
; Sequence 176884, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

```

```
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; ORGANISM: Cryptococcus neoformans
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 176884
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_130743C.1.pep
US-10-424-599-176884

Query Match          100.0%; Score 31; DB 12; Length 140;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
Db 21 ATSSRAT 27

RESULT 7
US-10-389-566-2341
; Sequence 2341, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2341
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-389-566-2341

Query Match          100.0%; Score 31; DB 16; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
Db 377 ATSSRAT 383

RESULT 8
US-10-320-797-3218
; Sequence 3218, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Eroskin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 3218
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (435)..(435)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (437)..(438)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (429)..(429)
; OTHER INFORMATION: Xaa = any amino acid
US-10-320-797-3218

Query Match          100.0%; Score 31; DB 15; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
Db 47 ATSSRAT 53

RESULT 9
US-10-425-114-41459
; Sequence 41459, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 41459
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3075-022-A3_FLI.pep
US-10-425-114-41459

Query Match          90.3%; Score 28; DB 12; Length 340;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
Db 254 ATSSRAT 260

RESULT 10
US-10-032-585-7311
; Sequence 7311, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
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; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7311
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7311

Query Match      90.3%; Score 28; DB 14; Length 842;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATSSRAT 7
DB      482 STSSRAT 488

RESULT 11
US-10-424-599-148739
; Sequence 148739, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yinhua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 148739
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_1053333C.1.pcp
US-10-424-599-148739

Query Match      87.1%; Score 27; DB 12; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.8e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
DB      17 TSSRAT 22

RESULT 12
US-10-041-860-376
; Sequence 376, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvatan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376
; LENGTH: 96
; TYPE: PRT
US-10-041-860-376

Query Match      87.1%; Score 27; DB 14; Length 842;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
DB      52 TSSRAT 57

RESULT 13
US-10-371-942-28
; Sequence 28, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-28

Query Match      87.1%; Score 27; DB 12; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
DB      52 TSSRAT 57

RESULT 14
US-10-067-800-62
; Sequence 62, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-62

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Query Match      87.1%; Score 27; DB 14; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
Db      52 TSSRAT 57

RESULT 15
US-10-292-486-47
; Sequence 47, Application US/10292486
; Publication No. US20030228309A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors
; FILE REFERENCE: PFS32PI
; CURRENT APPLICATION NUMBER: US/10/292,486
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/403,376
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/377,973
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/331,309
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/986,149
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,359
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/295,018
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/252,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/248,847
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/246,612
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 47
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-486-47

Query Match      87.1%; Score 27; DB 15; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
Db      52 TSSRAT 57
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Search completed: April 21, 2004, 18:02:07
Job time : 22.1014 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:37:29 ; Search time 27.1304 Seconds
(without alignments)
91.715 Million cell updates/sec

Title: SEQ6
Perfect score: 51
Sequence: 1 qygspscs 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues 1133595

Total number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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ALIGNMENTS

RESULT 1
US-10-041-860-49
; Sequence 49, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; NUMBER FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-49

Query Match 100.0%; Score 51; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.25; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QYGSPPCS 9
Db 90 QYGSPPCS 98
RESULT 2
US-10-041-860-225
; Sequence 225, Application US/10041860

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 51 | 100.0 | 108 | 14 | US-10-041-860-225 |
| 3 | 51 | 100.0 | 108 | 14 | US-10-041-860-239 |
| 4 | 51 | 100.0 | 108 | 14 | US-10-041-860-375 |
| 5 | 39 | 76.5 | 412 | 15 | US-10-104-047-3475 |
| 6 | 39 | 76.5 | 695 | 13 | US-10-013-310-3 |
| 7 | 39 | 76.5 | 1242 | 9 | US-09-903-248-5 |
| 8 | 39 | 76.5 | 1242 | 9 | US-09-859-604-5 |
| 9 | 39 | 76.5 | 1242 | 9 | US-09-903-063-5 |
| 10 | 39 | 76.5 | 1242 | 9 | US-09-903-216-5 |
| 11 | 39 | 76.5 | 1242 | 9 | US-09-903-199-5 |
| 12 | 39 | 76.5 | 1242 | 9 | US-09-903-023-5 |
| 13 | 39 | 76.5 | 1242 | 10 | US-09-436-184-5 |
| 14 | 39 | 76.5 | 1242 | 13 | US-10-085-027-1 |
| 15 | 39 | 76.5 | 1316 | 15 | US-10-334-143-10 |

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; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-225

Query Match      100.0%; Score 51; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QYGGSSPCS 9
DB      90 QYGGSSPCS 98

RESULT 3
US-10-041-860-259
; Sequence 259, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-259

Query Match      100.0%; Score 51; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QYGGSSPCS 9
DB      90 QYGGSSPCS 98

RESULT 4
US-10-041-860-375
; Sequence 375, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-375

Query Match      100.0%; Score 51; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QYGGSSPCS 9
DB      90 QYGGSSPCS 98

RESULT 5
US-10-104-047-3475
; Sequence 3475, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: H1-A0105
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3475
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3475

Query Match      76.5%; Score 39; DB 15; Length 412;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYGGSSPCS 9
DB      93 RYGTSPCS 100

RESULT 6
US-10-013-310-3
; Sequence 3, Application US/10013310
; Publication No. US20020192216A1
; GENERAL INFORMATION:
; APPLICANT: Lamb, Jonathon Robert
; APPLICANT: Hoyne, Gerard Francis
; APPLICANT: Dallman, Margaret Jane
; APPLICANT: Therapeutic Use
; TITLE OF INVENTION: Therapeutic Use
; FILE REFERENCE: 674525-2003
; CURRENT APPLICATION NUMBER: US/10/013,310
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/GB00/02191
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: UK 9913350.6

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; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: UK 9921953.7
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 695
; TYPE: PRT
; ORGANISM: House Mouse
US-10-013-310-3

Query Match      76.5%; Score 39; DB 13; Length 695;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPCS 9
Db 376 RYGTSPCS 383

RESULT 7
US-09-903-248-5
; Sequence 5, Application US/09903248
; Patent No. US20020102263A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV5
; CURRENT APPLICATION NUMBER: US/09/903,248
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-248-5

Query Match      76.5%; Score 39; DB 9; Length 1242;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
Db 430 EYGSPPC 436

RESULT 8
US-09-859-604-5
; Sequence 5, Application US/09859604
; Patent No. US20020110559A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: Deutch, Alan H
; APPLICANT: Ghanbari, Hossein A
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 CIP
; CURRENT APPLICATION NUMBER: US/09/859,604
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-248-5

Query Match      76.5%; Score 39; DB 9; Length 1242;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
Db 430 EYGSPPC 436

RESULT 8
US-09-859-604-5
; Sequence 5, Application US/09903216
; Patent No. US20020114811A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV2
; CURRENT APPLICATION NUMBER: US/09/903,216
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-216-5

Query Match      76.5%; Score 39; DB 9; Length 1242;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
Db 430 EYGSPPC 436
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; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: R.I. Hosp. - Malignant Neoplasms
; CURRENT APPLICATION NUMBER: US/09/436,184
; CURRENT FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-436-184-5

Query Match 76.5%; Score 39; DB 10; Length 1242;
Best Local Similarity 85.7%; Pred. NO. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSSPC 8
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DB 430 EYGSSPC 436

RESULT 14
US-10-085-027-1
; Sequence 1, Application US/10085027
; Publication NO. US20020132759A1
; GENERAL INFORMATION:
; APPLICANT: YAZAKI, YOSHIO
; APPLICANT: ASANO, TOMOICHIRO
; APPLICANT: KUBO, HIDEO
; APPLICANT: KANDA, AKIRA
; TITLE OF INVENTION: REMEDIES FOR DISEASES CAUSED BY INSULIN RESISTANCE
; FILE REFERENCE: 4895-0019-0PCT
; CURRENT APPLICATION NUMBER: US/10/085,027
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 09/508,691
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PCT/JF98/04293
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: JP9-263719
; PRIOR FILING DATE: 1997-09-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-027-1

Query Match 76.5%; Score 39; DB 13; Length 1242;
Best Local Similarity 85.7%; Pred. NO. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSSPC 8
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DB 430 EYGSSPC 436

RESULT 15
US-10-334-143-10
; Sequence 10, Application US/10334143
; Publication NO. US20040009549A1
; GENERAL INFORMATION:
; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; FILE REFERENCE: 038602/1543
; CURRENT APPLICATION NUMBER: US/10/334,143
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: 60/343,169
; PRIOR FILING DATE: 2001-12-31

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; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-334-143-10
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Query Match      76.5%; Score 39; DB 15; Length 1316;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db      504 EYGSSPC 510
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Job time : 27.1304 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Perfect score: 31

Sequence: 1 atssrat 7

Scoring table: BLOSUM62

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pdp:*
- 6: /cgn2_6/ptodata/2/iaa/Backfiles.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 28 | 90.3 | 138 | 4 | US-09-252-991A-17444 |
| 3 | 28 | 90.3 | 141 | 4 | US-09-252-991A-18631 |
| 4 | 28 | 90.3 | 155 | 4 | US-09-252-991A-31910 |
| 5 | 28 | 90.3 | 262 | 4 | US-09-252-991A-17126 |
| 6 | 28 | 90.3 | 270 | 4 | US-09-252-991A-22477 |
| 7 | 28 | 90.3 | 427 | 4 | US-09-252-991A-19612 |
| 8 | 27 | 87.1 | 203 | 1 | PCT-US93-05704-6 |
| 9 | 27 | 87.1 | 203 | 5 | PCT-US93-05704-6 |
| 10 | 27 | 87.1 | 219 | 4 | US-09-621-976-4221 |
| 11 | 27 | 87.1 | 497 | 4 | US-09-252-991A-30856 |
| 12 | 27 | 87.1 | 988 | 3 | US-08-851-843A-69 |
| 13 | 27 | 87.1 | 988 | 3 | US-08-974-549A-112 |
| 14 | 27 | 87.1 | 988 | 3 | US-08-854-050-69 |
| 15 | 27 | 87.1 | 988 | 4 | US-09-430-323-69 |
| 16 | 27 | 87.1 | 988 | 4 | US-08-912-951-112 |
| 17 | 27 | 87.1 | 988 | 4 | US-09-402-181B-112 |
| 18 | 27 | 87.1 | 988 | 4 | US-09-721-458-112 |
| 19 | 27 | 87.1 | 1146 | 3 | US-09-126-109-12 |
| 20 | 27 | 87.1 | 1153 | 1 | US-08-314-917-2 |
| 21 | 27 | 87.1 | 1153 | 1 | US-08-265-046-2 |
| 22 | 27 | 87.1 | 1153 | 2 | US-08-465-523-2 |
| 23 | 27 | 87.1 | 1153 | 4 | US-09-661-258-4 |
| 24 | 27 | 87.1 | 1153 | 5 | PCT-US93-11401-2 |
| 25 | 27 | 87.1 | 1153 | 5 | PCT-US95-07849-2 |
| 26 | 27 | 87.1 | 1464 | 1 | US-08-026-138E-1 |
| 27 | 26 | 83.9 | 141 | 4 | US-09-252-991A-25325 |

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|----|----|------|-----|---|----------------------|--------------------|
| 28 | 26 | 83.9 | 148 | 4 | US-09-252-991A-16783 | Sequence 16783, A |
| 29 | 26 | 83.9 | 150 | 4 | US-09-252-991A-31728 | Sequence 31728, A |
| 30 | 26 | 83.9 | 169 | 4 | US-09-252-991A-24301 | Sequence 24301, A |
| 31 | 26 | 83.9 | 189 | 4 | US-09-252-991A-23376 | Sequence 23376, A |
| 32 | 26 | 83.9 | 262 | 4 | US-09-252-991A-28282 | Sequence 28282, A |
| 33 | 26 | 83.9 | 277 | 4 | US-09-252-991A-28460 | Sequence 28460, A |
| 34 | 26 | 83.9 | 426 | 4 | US-09-252-991A-18298 | Sequence 18298, A |
| 35 | 26 | 83.9 | 536 | 4 | US-09-252-991A-20771 | Sequence 20771, A |
| 36 | 26 | 83.9 | 611 | 4 | US-09-252-991A-32402 | Sequence 32402, A |
| 37 | 26 | 83.9 | 635 | 4 | US-09-252-991A-33100 | Sequence 33100, A |
| 38 | 26 | 83.9 | 856 | 4 | US-09-699-266A-13 | Sequence 13, Appl |
| 39 | 25 | 80.6 | 52 | 1 | US-08-361-920-17 | Sequence 17, Appl |
| 40 | 25 | 80.6 | 52 | 1 | US-08-479-939-17 | Sequence 17, Appl |
| 41 | 25 | 80.6 | 52 | 1 | US-08-483-432-17 | Sequence 17, Appl |
| 42 | 25 | 80.6 | 75 | 4 | US-09-345-238B-101 | Sequence 101, Appl |
| 43 | 25 | 80.6 | 85 | 4 | US-09-732-210-42 | Sequence 42, Appl |
| 44 | 25 | 80.6 | 111 | 4 | US-09-252-991A-17821 | Sequence 17821, A |
| 45 | 25 | 80.6 | 138 | 4 | US-09-252-991A-30362 | Sequence 30362, A |

ALIGNMENTS

RESULT 1
US-09-252-991A-28404
; Sequence 28404, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28404
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28404

Query Match 90.3%; Score 28; DB 4; Length 115;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
Db 99 ATSRAT 105

RESULT 2
US-09-252-991A-17444
; Sequence 17444, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17444
; LENGTH: 138
; TYPE: PRT

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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17444

Query Match      90.3%; Score 28; DB 4; Length 138;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 80 ATASRAT 86

RESULT 3
US-09-252-991A-18631
; Sequence 18631, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18631
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18631

Query Match      90.3%; Score 28; DB 4; Length 141;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 41 STSSRAT 47

RESULT 4
US-09-252-991A-31910
; Sequence 31910, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31910
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31910

Query Match      90.3%; Score 28; DB 4; Length 155;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 101 ATSSRAT 107

RESULT 5
US-09-252-991A-17126
; Sequence 17126, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17126
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17126

Query Match      90.3%; Score 28; DB 4; Length 262;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 37 ATASRAT 43

RESULT 6
US-09-252-991A-22477
; Sequence 22477, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22477
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22477

Query Match      90.3%; Score 28; DB 4; Length 270;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 1 ATSSRAT 7

RESULT 7
US-09-252-991A-19612
; Sequence 19612, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

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; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19612
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19612

Query Match 90.3%; Score 28; DB 4; Length 427;
Best Local Similarity 85.7%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
Db 420 STSSRAT 426

RESULT 8
US-08-063-552-6
; Sequence 6, Application US/08063552
; Patent No. 568936
; GENERAL INFORMATION:
; APPLICANT: Edwards, Robert H
; TITLE OF INVENTION: Vesicle Membrane Transport Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, Ninth Floor
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/063,552
FILING DATE: 19930514
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9067-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Streptomyces plasmid
US-08-063-552-6

Query Match 87.1%; Score 27; DB 1; Length 203;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
Db 194 ATSSRAT 200

RESULT 9

PCT-US93-05704-6
; Sequence 6, Application PC/TUS9305704
; GENERAL INFORMATION:
; APPLICANT: Edwards, Robert H
; TITLE OF INVENTION: Vesicle Membrane Transport Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, Ninth Floor
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05704
FILING DATE: 19930611
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9067-1PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Streptomyces plasmid
PCT-US93-05704-6

Query Match 87.1%; Score 27; DB 5; Length 203;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
Db 194 ATSSRAT 200

RESULT 10

US-09-621-976-4221
; Sequence 4221, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4221
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -16..-1
; NAME/KEY: UNSURE

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; LOCATION: 57
; OTHER INFORMATION: Xaa = Asp.Gly
; NAME/KEY: UNSURE
; LOCATION: 58
; OTHER INFORMATION: Xaa = Cys.Ser
US-09-621-976-4221

Query Match      87.1%; Score 27; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  TSSRAT 7
      |||||
Db      196  TSSRAT 201

RESULT 11
US-09-252-991A-30856
; Sequence 30856, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30856
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30856

Query Match      87.1%; Score 27; DB 4; Length 497;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATSSRAT 7
      |||||
Db      457  ATSSRAS 463

RESULT 12
US-08-851-843A-69
; Sequence 69, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; LOCATION: 57
; OTHER INFORMATION: Xaa = Asp.Gly
; NAME/KEY: UNSURE
; LOCATION: 58
; OTHER INFORMATION: Xaa = Cys.Ser
US-09-621-976-4221

Query Match      87.1%; Score 27; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  TSSRAT 7
      |||||
Db      196  TSSRAT 201

RESULT 11
US-09-252-991A-30856
; Sequence 30856, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30856
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30856

Query Match      87.1%; Score 27; DB 4; Length 497;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATSSRAT 7
      |||||
Db      457  ATSSRAS 463

RESULT 12
US-08-851-843A-69
; Sequence 69, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 988 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-851-843A-69

Query Match      87.1%; Score 27; DB 3; Length 988;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATSSRAT 7
      |||||
Db      626  ATSDRAT 632

RESULT 13
US-08-974-549A-112
; Sequence 112, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 988 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-549A-112

```

```

Query Match      87.1%; Score 27; DB 3; Length 988;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 ATSSRAT 7
Db      626 ATSDRAT 632

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RESULT 14
US-08-854-050-69
; Sequence 69, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 988 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-854-050-69

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Query Match      87.1%; Score 27; DB 3; Length 988;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 ATSSRAT 7
Db      626 ATSDRAT 632

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RESULT 15
US-09-430-323-69
; Sequence 69, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:

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; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-C02930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 988 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-430-323-69
Query Match 87.1%; Score 27; DB 4; Length 988;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATSSRAT 7
Db 626 ATSDRAT 632
Search completed: April 21, 2004, 17:40:05
Job time : 9.42029 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:48 ; Search time 4.56522 Seconds

(without alignments)
102.653 Million cell updates/sec

Title: SEQ6

Perfect score: 51

Sequence: 1 QYGSPPCS 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|---------------|--------------------|
| 1 | 39 | 76.5 | 109 | 1 KV3G HUMAN | P04206 homo sapien |
| 2 | 39 | 76.5 | 695 | 1 DVL1 MOUSE | P51141 mus musculu |
| 3 | 39 | 76.5 | 695 | 1 DVL1 RAT | Q9WV69 rattus norv |
| 4 | 39 | 76.5 | 1235 | 1 IRS1 MOUSE | P35569 mus musculu |
| 5 | 39 | 76.5 | 1235 | 1 IRS1 RAT | P35570 rattus norv |
| 6 | 39 | 76.5 | 1242 | 1 IRS1 HUMAN | P35568 homo sapien |
| 7 | 39 | 76.5 | 4543 | 1 LRPI CHICK | P98157 gallus gall |
| 8 | 38 | 74.5 | 108 | 1 KV3A HUMAN | P01619 homo sapien |
| 9 | 38 | 74.5 | 109 | 1 KV3B HUMAN | P01620 homo sapien |
| 10 | 38 | 74.5 | 109 | 1 KV3D HUMAN | P01622 homo sapien |
| 11 | 38 | 74.5 | 129 | 1 KV3M HUMAN | P18136 homo sapien |
| 12 | 35 | 68.6 | 100 | 1 SI07 HUMAN | P31151 homo sapien |
| 13 | 35 | 68.6 | 100 | 1 SI15 HUMAN | Q86895 homo sapien |
| 14 | 35 | 68.6 | 129 | 1 KV3L HUMAN | P18135 homo sapien |
| 15 | 35 | 68.6 | 595 | 1 Z440 HUMAN | O81Y18 homo sapien |
| 16 | 35 | 68.6 | 899 | 1 ZCH2 HUMAN | Q9C0B9 homo sapien |
| 17 | 34 | 66.7 | 214 | 1 ENH2 CHLPPN | Q9Z962 chlamydia p |
| 18 | 34 | 66.7 | 276 | 1 MYO1 ONCMY | Q91205 oncorhynch |
| 19 | 34 | 66.7 | 410 | 1 TDG HUMAN | Q13569 homo sapien |
| 20 | 34 | 66.7 | 514 | 1 PHLD MYCTU | Q3XB13 mycobacteri |
| 21 | 34 | 66.7 | 517 | 1 PHLC MYCTU | P95245 mycobacteri |
| 22 | 34 | 66.7 | 722 | 1 DLI1 MOUSE | Q8WY33 mus musculu |
| 23 | 34 | 66.7 | 722 | 1 DLI1 MOUSE | Q61483 mus musculu |
| 24 | 34 | 66.7 | 843 | 1 CO7 HUMAN | P10643 homo sapien |
| 25 | 34 | 66.7 | 901 | 1 RAC3 HUMAN | Q08043 homo sapien |
| 26 | 34 | 66.7 | 1129 | 1 AKI1 RAT | O62924 rattus norv |
| 27 | 34 | 66.7 | 1178 | 1 TSP2 CHICK | P35440 gallus gall |
| 28 | 33 | 64.7 | 140 | 1 CO8B RAT | P55314 rattus norv |
| 29 | 33 | 64.7 | 224 | 1 T257 STRAU | P14506 staphylococ |
| 30 | 33 | 64.7 | 224 | 1 T431 STRAU | P19380 staphylococ |
| 31 | 33 | 64.7 | 271 | 1 PD5 DROME | P32029 drosophila |
| 32 | 33 | 64.7 | 298 | 1 SVGA HELPU | Q9ZKPI helicobacte |
| 33 | 33 | 64.7 | 486 | 1 ENV_HTLV2 | P03383 human t-cel |

ALIGNMENTS

RESULT 1

KV3G_HUMAN
ID KV3G_HUMAN STANDARD; PRT; 109 AA.
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region GOL (Rheumatoid factor).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
EX MEDLINE=86230578; PubMed=3086710;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the Wa idiotype group, in part predicted by its
RT reactivity with anti-peptide antibodies.";
RL Mol. Immunol. 23:239-244(1986).
DR PIR; A01893; K3HUGO.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;

Query Match 76.5%; Score 39; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.95;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYGSPPCS 9
DB 90 QYGSPPCS 98

RESULT 2

DVL1_MOUSE
ID DVL1_MOUSE STANDARD; PRT; 695 AA.
AC P51141; Q60868;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)
DE (DSH homolog 1).
OS Mus musculus (Mouse).
GN DVL1 OR DVL.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=95046919; PubMed=7958461;
RA Sussman D.J., Klingensmith J., Salinas P., Adams P.S., Nusse R.,
RA Perrimon N.;
RT "Isolation and characterization of a mouse homolog of the Drosophila
RT segment polarity gene dishevelled.";
RL Dev. Biol. 166:73-86(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=96232916; PubMed=9132266;
RA Lijam N., Sussman D.J.;
RT "Organization and promoter analysis of the mouse dishevelled-1 gene.";
RL Genome Res. 5:116-124(1995).
RN [3]
RP KNOCK-OUT.
RX MEDLINE=97442352; PubMed=9298901;
RA Lijam N., Paylor R., McDonald M.P., Crawley J.N., Deng C.-X.,
RA Herrup K., Stevens K.B., Maccaferri G., McBain C.J., Sussman D.J.,
RA Wynshaw-Boris A.;
RT "Social interaction and sensorimotor gating abnormalities in mice
RT lacking Dvl1.";
RL Cell 90:895-905(1997).
CC -!- FUNCTION: May play a role in the signal transduction pathway
CC mediated by multiple Wnt genes. Dvl1 deficient mice display
CC abnormalities in social behaviors and sensorimotor gating.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- TISSUE SPECIFICITY: High levels are seen in the brain, testis and
CC kidney, lower levels in the ovary, breast, muscle, liver and small
CC intestine, and very low levels are seen in the spleen and thymus.
CC A moderate level expression is seen in the heart.
CC -!- DEVELOPMENTAL STAGE: Is expressed throughout the embryonic central
CC nervous system from presomite stages and in neuron-rich areas of
CC the brain throughout postnatal development, as well as in many
CC other tissues.
CC -!- SIMILARITY: Contains 1 DEP domain.
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -!- SIMILARITY: Belongs to the DSH family.
CC -!- SIMILARITY: Contains 1 DIX domain.
CC -----
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CC -----
CC EMBL; U10115; AAA82175.1; -;
CC EMBL; U28138; AAA74049.1; -;
CC FDB; 1F5H; 31-DEC-02.
CC MGD; MGI:94941; Dvl1.
CC GO; GO:0016023; C:cytoplasmic vesicle; IDA.
CC InterPro; IPR000591; DEP.
CC InterPro; IPR008339; Dishevelled.
CC InterPro; IPR003351; Dishevelled.
CC InterPro; IPR008340; Dishevelled_1.
CC InterPro; IPR001158; DIX.
CC InterPro; IPR001478; PDZ.
CC Pfam; PF00610; DEP; 1.
CC Pfam; PF02377; Dishevelled; 1.
CC Pfam; PF00778; DIX; 1.
CC Pfam; PF00595; PDZ; 1.
CC PRINTS; PR01760; DISHEVELLED.
CC PRINTS; PR01761; DISHEVELLED1.
CC PRODOM; PD003639; DIX; 1.
CC SMART; SMO0021; DAX; 1.
CC SMART; SMO0049; DEP; 1.
CC SMART; SMO0228; PDZ; 1.

DR PROSITE; PS50186; DEP; 1.
DR PROSITE; PS50841; DIX; 1.
DR PROSITE; PS50106; PDZ; 1.
KW Wnt signaling pathway; Developmental protein; 3D-structure.
FT DOMAIN 1 85 DIX.
FT DOMAIN 251 323 PDZ.
FT DOMAIN 425 499 DEP.
FT DOMAIN 390 393 POLY-SER.
FT CONFLICT 122 125 MISSING (IN REF. 2).
FT CONFLICT 211 211 T -> N (IN REF. 2).
SQ SEQUENCE 695 AA; 75350 MW; A9FA449F5CF75F2 CRC64;
Query Match 76.5%; Score 39; DB 1; Length 695;
Best Local Similarity 75.0%; Pred. No. 6.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 QYGSSPCS 9
DB 376 RYGTSPCS 383
RESULT 3
ID DVL1 RAT STANDARD; PRT; 695 AA.
AC Q9WVB9; OSQUG5; Q9WVB8;
CT 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)
DE (DSH homolog 1).
GN DVL1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar Kyoto;
RX MEDLINE=21254118; PubMed=11354832;
RA de Lange R.P.J., Burr K., Clark J.S., Negrin C.D., Broshan M.J.,
RA St Clair D.M., Dominiczak A.F., Shaw D.J.;
RT "Mapping and sequencing rat dishevelled-1: a candidate gene for
RT cerebral ischaemic insult in a rat model of stroke.";
RL Neurogenetics 3:99-106(2001).
CC -!- FUNCTION: May play a role in the signal transduction pathway
CC mediated by multiple Wnt genes.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the DSH family.
CC -!- SIMILARITY: Contains 1 DEP domain.
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -!- SIMILARITY: Contains 1 DIX domain.
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CC -----
CC EMBL; AF143545; AAD33896.2; -;
CC EMBL; AF143545; AAD33897.2; -;
CC EMBL; AF143548; AAD41492.2; -;
CC EMBL; AF143547; AAD41492.2; JOINED.
CC EMBL; AF143550; AAD41493.1; -;
CC EMBL; AF143549; AAD41493.1; JOINED.
CC InterPro; IPR000591; DEP.
CC InterPro; IPR008339; Dishevelled.
CC InterPro; IPR003351; Dishevelled.
CC InterPro; IPR008340; Dishevelled_1.
CC InterPro; IPR001158; DIX.
CC InterPro; IPR001478; PDZ.
CC Pfam; PF00610; DEP; 1.


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RA Sun X.J., Crimmins D.L., Myers M.G., Miralpeix M., White M.F.;
RT "Pleiotropic insulin signals are engaged by multisite phosphorylation
RL of IRS-1."
RL Mol. Cell. Biol. 13:7418-7428(1993).
RN [3]
RP PHOSPHORYLATION SITES
RX MEDLINE=93352637; PubMed=8349691;
RA Tanasijevic M.J., Myers M.G., Thoma R.S., Crimmins D.L., White M.F.,
RA Sacks D.B.;
RT "Phosphorylation of the insulin receptor substrate IRS-1 by casein
RT kinase II."
RL J. Biol. Chem. 268:18157-18166(1993).
CC -!- FUNCTION: May mediate the control of various cellular processes by
CC insulin. When phosphorylated by the insulin receptor binds
CC specifically to various cellular proteins containing SH2 domains
CC such as phosphatidylinositol 3-kinase p85 subunit or GRB2.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 1 PTP domain.
CC -----
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CC -----
CC EMBL; X58375; CAA41264.1; --
CC HSP; S16948; S16948.
CC DR PIR; P35568; IIRS.
CC DR InterPro; IPR002404; Insln_receptorS1.
CC DR InterPro; IPR001849; PH.
CC DR Pfam; PF021174; IRS; 1.
CC DR Pfam; PF00169; PH; 1.
CC DR PRINTS; PR00628; INSULNRS1.
CC DR SMART; SM00233; PH; 1.
CC DR SMART; SM00310; PTH1; 1.
CC DR PROSITE; PSS0003; PH_DOMAIN; 1.
CC KW Phosphorylation.
FT DOMAIN 12 115 PH.
FT DOMAIN 152 262 PTH.
FT DOMAIN 872 881 POLY-GLN.
FT DOMAIN 1196 1200 POLY-PRO.
FT MOD_RES 99 99 PHOSPHORYLATION (BY CK2).
FT MOD_RES 460 460 PHOSPHORYLATION (BY INSR).
FT MOD_RES 502 502 PHOSPHORYLATION (BY CK2).
FT MOD_RES 608 608 PHOSPHORYLATION (BY INSR).
FT MOD_RES 628 628 PHOSPHORYLATION (BY INSR).
FT MOD_RES 895 895 PHOSPHORYLATION (BY INSR).
FT MOD_RES 939 939 PHOSPHORYLATION (BY INSR).
FT MOD_RES 987 987 PHOSPHORYLATION (BY INSR).
FT MOD_RES 1172 1172 PHOSPHORYLATION (BY INSR).
FT MOD_RES 1222 1222 PHOSPHORYLATION (BY INSR).
SQ SEQUENCE 1235 AA; 131178 MW; A274BC7540CA85C5 CRC64;

Query Match 76.5%; Score 39; DB 1; Length 1235;
Best Local Similarity 85.7%; Pred.No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYSSPC 8
Db 425 EYSSPC 431
:|||||
:|||||

RESULT 6
ID IRS1_HUMAN STANDARD; PRT; 1242 AA.
AC P35568;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Insulin receptor substrate-1 (IRS-1).
GN IRS1.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=93292739; PubMed=8513971;
RA Araki E., Sun X.J., Haag B.L. III, Chuang L.M., Zhang Y.,
RA Yang-Feng T.L., White M.F., Kahn C.R.;
RT "Human skeletal muscle insulin receptor substrate-1. Characterization
RT of the cDNA, gene, and chromosomal localization."
RL Diabetes 42:1041-1054(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92181456; PubMed=13111924;
RA Nishiyama M., Wands J.R.;
RT "Cloning and increased expression of an insulin receptor substrate-1
RT like gene in human hepatocellular carcinoma."
RL Biochem. Biophys. Res. Commun. 183:280-285(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye; PubMed=12477932;
RX MEDLINE=92388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP VARIANTS PRO-512 AND ARG-971.
RX MEDLINE=93390176; PubMed=8104271;
RA Almind K., Bjoerbaek C., Vestergaard H., Hansen T., Schwald S.,
RA Pedersen O.;
RT "Aminoacid polymorphisms of insulin receptor substrate-1 in
RT non-insulin-dependent diabetes mellitus."
RL Lancet 342:828-832(1993).
RN [5]
RP VARIANT NIDDM GLY-723 DEL.
RX MEDLINE=96303710; PubMed=8723689;
RA Esposito D.L., Mammarella S., Ranieri A., della Loggia F., Capani F.,
RA Consoli A., Mariani-Costantini R., Caramia F.G., Cama A., Battista P.;
RT "Deletion of Gly723 in the insulin receptor substrate-1 of a patient
RT with noninsulin-dependent diabetes mellitus."
RL Hum. Mutat. 7:364-366(1996).
RN [6]
RP VARIANTS NIDDM TYR-1043 AND TYR-1095.
RA Mammarella S., Creati B., Esposito D.L., Arcuri P., della Loggia F.,
RA Capani F., Mariani-Costantini R., Caramia F.G., Battista P., Cama A.;
RT "Novel allele of the insulin receptor substrate-1 bearing two
RT non-conservative amino acid substitutions in a patient with
RT noninsulin-dependent diabetes mellitus."
RL Hum. Mutat. 11:411-411(1998).
RN [7]
RP STRUCTURE BY NMR OF 157-267.
RX MEDLINE=96185451; PubMed=8599766;
RA Zhou M.-M., Huang B., Olejniczak E.T., Meadows R.P., Shuker S.B.,
RA Miyazaki M., Trueb T., Shoelson S.E., Feelik S.W.;

```

RT "Structural basis for IL-4 receptor phosphopeptide recognition by the
 RL Ins-1 PTB domain.";
 CC Nat. Struct. Biol. 3:388-393(1996).
 CC !- FUNCTION: May mediate the control of various cellular processes by
 CC insulin. When phosphorylated by the insulin receptor binds
 CC specifically to various cellular proteins containing SH2
 CC domains such as phosphatidylinositol 3-kinase p85 subunit or GRB2.
 CC !- DISEASE: POLYMORPHISMS IN IRS1 MAY BE INVOLVED IN THE ETIOLOGY OF
 CC A SUBSET OF LATE-ONSET NON-INSULIN-DEPENDENT DIABETES MELLITUS
 CC (NIDDM).
 CC !- SIMILARITY: Contains 1 PH domain.
 CC !- SIMILARITY: Contains 1 PTB domain.
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 CC EMBL; S95963; AAB21608.1; -;
 CC EMBL; S62539; AAB27175.1; -;
 CC EMBL; BC053895; AAH53895.1; -;
 CC PIR; I31160; JS0670.
 CC PDB; 1JRS; 15-MAY-97.
 CC PDB; 1K3A; 05-DEC-01.
 CC PDB; 1QQG; 10-NOV-99.
 CC Genew; HGNC:6125; IRS1.
 CC MIM; 147545; -;
 CC GO; GO:0005737; Cytoplasm; TAS.
 CC GO; GO:0005515; R:protein binding; IPI.
 CC GO; GO:0004871; F:signal transducer activity; TAS.
 CC GO; GO:0005065; F:transmembrane receptor protein tyrosine kin. . . ; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR002404; Insln_receptorS1.
 CC InterPro; IPR001849; PH.
 CC Pfam; PF02174; IRS; 1.
 CC Pfam; PF00169; PH; 1.
 CC PRINTS; PR00628; INSLINRS1.
 CC SMART; SM00233; PH; 1.
 CC SMART; SM00310; PTB; 1.
 CC PROSITE; PS00003; PH_DOMAIN; 1.
 CC Phosphorylation; Polymorphism; Diabetes mellitus; Disease mutation;
 KW 3D-structure.
 FT DOMAIN 12 115 PH.
 FT DOMAIN 157 267 PTB.
 FT DOMAIN 128 134 POLY-GLY.
 FT DOMAIN 331 338 POLY-SER.
 FT DOMAIN 680 686 POLY-SER.
 FT DOMAIN 807 815 POLY-SER.
 FT DOMAIN 877 882 POLY-GLN.
 FT DOMAIN 1035 1038 POLY-SER.
 FT DOMAIN 1126 1130 POLY-GLY.
 FT DOMAIN 1131 1135 POLY-SER.
 FT DOMAIN 1197 1207 POLY-PRO.
 FT MOD_RES 99 99 PHOSPHORYLATION (BY CK2)
 FT (BY SIMILARITY).
 FT MOD_RES 465 465 PHOSPHORYLATION (BY INSR)
 FT (BY SIMILARITY).
 FT MOD_RES 612 612 PHOSPHORYLATION (BY INSR)
 FT (BY SIMILARITY).
 FT MOD_RES 632 632 PHOSPHORYLATION (BY INSR)
 FT (BY SIMILARITY).
 FT MOD_RES 896 896 PHOSPHORYLATION (BY INSR)
 FT (BY SIMILARITY).
 FT MOD_RES 941 941 PHOSPHORYLATION (BY INSR)
 FT (BY SIMILARITY).
 FT MOD_RES 989 989 PHOSPHORYLATION (BY INSR)
 FT (BY SIMILARITY).
 FT MOD_RES 1179 1179 PHOSPHORYLATION (BY INSR)
 FT (BY SIMILARITY).
 FT MOD_RES 1229 1229 PHOSPHORYLATION (BY INSR)

FT VARIANT 158 158 (BY SIMILARITY).
 FT P -> R (in dbSNP:1801108).
 FT /FTID=VAR 014853.
 FT VARIANT 209 209 M -> T (in dbSNP:1801118).
 FT /FTID=VAR 014854.
 FT VARIANT 512 512 A -> P (in dbSNP:1801276).
 FT /FTID=VAR 005299.
 FT VARIANT 723 723 MISSING (IN NIDDM).
 FT /FTID=VAR 005301.
 FT VARIANT 809 809 S -> F (in dbSNP:1801120).
 FT /FTID=VAR 014855.
 FT VARIANT 892 892 S -> G (in dbSNP:1801277).
 FT /FTID=VAR 014856.
 FT VARIANT 971 971 G -> R (in dbSNP:1801278).
 FT /FTID=VAR 005300.
 FT VARIANT 1043 1043 S -> Y (IN NIDDM).
 FT /FTID=VAR 005302.
 FT VARIANT 1095 1095 C -> Y (IN NIDDM).
 FT /FTID=VAR 005303.
 FT CONFLICT 134 134 G -> GG (IN REF. 2).
 FT CONFLICT 362 362 S -> R (IN REF. 2).
 FT CONFLICT 384 384 P -> R (IN REF. 2).
 FT STRAND 162 168
 FT HELIX 173 176
 FT STRAND 182 188
 FT STRAND 189 190
 FT STRAND 191 196
 FT TURN 197 198
 FT STRAND 204 207
 FT TURN 208 210
 FT STRAND 211 217
 FT TURN 218 219
 FT STRAND 220 225
 FT TURN 227 228
 FT STRAND 234 236
 FT STRAND 238 239
 FT TURN 243 244
 FT HELIX 245 262
 FT TURN 263 264
 SQ SEQUENCE 1242 AA; 131590 MW; 3C0EFD9E32B3E64A CRC64;
 Query Match 76.5%; Score 39; DB 1; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 QYGSPPC 8
 Db 430 EYGSPPC 436
 :|||||
 ID_LRPI_CHICK STANDARD; PRT; 4543 AA.
 AC P98157;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Low-density lipoprotein receptor-related protein 1 precursor (LRP)
 DE (Alpha-2-macroglobulin receptor) (A2MR).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OK NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=white leghorn; TISSUE=Liver, and Ovary;
 RX MEDLINE=9410312; PubMed=7506255;
 RA Nimpf J., Stifani S., Bilous P.T., Schneider W.J.;
 RT "The somatic cell-specific low density lipoprotein receptor-related
 RT protein of the chicken. Close kinship to mammalian low density
 RT lipoprotein receptor gene family members.";
 RL J. Biol. Chem. 269:212-219 (1994).

Query Match 76.5%; Score 39; DB 1; Length 4543;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOYGSPCS 9
DB 1839 QOAGSNPCS 1847

RESULT 8
KV3A_HUMAN
ID KV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

Query Match 74.5%; Score 38; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSP 7
DB 90 QOYGSSP 96

RESULT 9
KV3B_HUMAN
ID KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

Query Match 74.5%; Score 38; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSP 7
DB 90 QOYGSSP 96

RESULT 10
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

Query Match 74.5%; Score 38; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSP 7
DB 90 QOYGSSP 96

RESULT 9
KV3B_HUMAN
ID KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

Query Match 74.5%; Score 38; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSP 7
DB 90 QOYGSSP 96

RESULT 10
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

FT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
 RT Ti). IV. The complete amino acid sequence and its significance for
 RT the mechanism of antibody production.";
 CC Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
 RL -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01895; K3HUT1.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON TER 109 109
 SQ SEQUENCE 109 AA; 11788 MW; 8C35058DCD7749BC CRC64;
 Query Match 74.5%; Score 38; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. NO. 1.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQYGSSP 7
 DB 90 QQYGSSP 96
 RESULT 11
 KV3M HUMAN
 ID KV3M HUMAN STANDARD; PRT; 129 AA.
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region HIC precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -!- DISEASE: The protein is one of the surface immunoglobulin M
 CC autoantibodies expressed in patients with chronic lymphocytic
 CC leukemia.
 DR PIR; P18021; K3HUT1.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 103 FRAMEWORK-3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 129 JK1 SEGMENT.

FT DISULFID 43 109 BY SIMILARITY.
 FT NON TER 129 129
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 Query Match 74.5%; Score 38; DB 1; Length 129;
 Best Local Similarity 100.0%; Pred. NO. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQYGSSP 7
 DB 110 QQYGSSP 116
 RESULT 12
 S107 HUMAN
 ID S107 HUMAN STANDARD; PRT; 100 AA.
 AC P31151; O9HUE2;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE S100 calcium-binding protein A7 (Psoriasis).
 GN S100A7 OR PSORI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Keratinocytes;
 RX MEDLINE=92043866; PubMed=1940442;
 RA Madsen P., Rasmussen H.H., Leffers H., Honore B., Dejgaard K.,
 RA Olsen E., Kii J., Walbum E., Andersen A.H., Basse B., Lauridsen J.B.,
 RA Ratz G.P., Celis A., Vandeckerckhove J., Celis J.E.;
 RT "Molecular cloning, occurrence, and expression of a novel partially
 RT secreted protein 'psoriasis' that is highly up-regulated in psoriatic
 RT skin.";
 RL J. Invest. Dermatol. 97:701-712(1991).
 RN [2]
 RP SEQUENCE, AND ACETYLATION.
 RC TISSUE=Psoriatic skin;
 RX MEDLINE=96095666; PubMed=8526920;
 RA Burgisser D.M., Siegenthaler G., Kuster T., Heilmann U., Hunziker P.,
 RA Birchler N., Heizmann C.W.;
 RT "Amino acid sequence analysis of human S100A7 (psoriasis) by tandem
 RT mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 217:257-263(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Maman A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 1-88 FROM N.A.
 RA Glaeser R., Harder J., Christophers E., Schroeder J.M.;

RT "Genomic organization of human psoriasis (S100A7) gene.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 8-18; 37-47; 49-60; 68-86 AND 88-100.
 RC TISSUE=Keratinocytes;
 RA Rasmussen H.H., van Damme J., Puyte M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RA "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 RN [6]
 RP TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
 RX MEDLINE=96212542; PubMed=8618345;
 RA Celis J.E., Rasmussen H.H., Vorum H., Madsen P., Honore B., Wolf H.,
 RA Orntoft T.F.;
 RA "Bladder squamous cell carcinomas express psoriasis and externalize it
 RT to the urine.";
 RL J. Urol. 155:2105-2112(1996).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.05 ANGSTROMS).
 RX MEDLINE=98230746; PubMed=9562557;
 RA Brodersen D.E., Rzerodt M., Madsen P., Celis J.E., Thøgersen H.C.,
 RA Nyborg J., Kjeldgaard M.;
 RA "EF-hands at atomic resolution: the structure of human psoriasis
 RT (S100A7) solved by MAD phasing.";
 RL Structure 6:477-489(1998).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
 RX MEDLINE=99152356; PubMed=10026247;
 RA Brodersen D.E., Nyborg J., Kjeldgaard M.;
 RA "Zinc-binding site of an S100 protein revealed. Two crystal
 RT structures of Ca2+-bound human psoriasis (S100A7) in the Zn2+-loaded
 RT and Zn2+-free states.";
 RL Biochemistry 38:1695-1704(1999).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Also secreted by a non-
 CC classical secretory pathway.
 CC -!- TISSUE SPECIFICITY: Fetal ear, skin, and tongue and human cell
 CC lines. Highly up-regulated in psoriatic epidermis. Also highly
 CC expressed in the urine of bladder squamous cell carcinoma (SCC)
 CC bearing patients.
 CC -!- MASS SPECTROMETRY: MW=11365; MW ERR=0.7; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
 CC -----
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 CC -----
 CC EMBL; M86757; AAA60210.1; -;
 CC EMBL; BC034687; AAH34687.1; -;
 CC EMBL; AJ012825; CAC20409.1; -;
 CC PIR; A54327; A54327.
 CC PDB; 1PSR; 13-JAN-99.
 CC PDB; 2PSR; 15-JUN-99.
 CC PDB; 3PSR; 15-JUN-99.
 CC Aarhus/Ghent-2DPAGE; 3002; IEF.
 CC Genew; HGNC:10497; S100A7.
 CC MIM; 600353; -;
 CC GO; GO:0005509; F:calcium ion binding; TAS.
 CC GO; GO:0008544; P:epidermal differentiation; TAS.
 CC InterPro; IPR001751; CaBP S100.
 CC InterPro; IPR002048; EF-hand.
 CC Pfam; PF000036; ehand; 1.
 CC Pfam; PF01023; S_100; 1.
 CC ProDom; PD003407; CaBP S100; 1.
 CC PROSITE; PS00018; EF HAND; 1.
 CC PROSITE; PS00303; S100 CBP; 1.
 CC Calcium-binding; Zinc; Metal-binding; Acetylation; 3D-structure.

FT INIT MET 0 0
 FT MOD RES 1 1
 FT CA BIND 62 73
 FT DISULFID 46 95
 FT METAL 17 17
 FT METAL 24 24
 FT METAL 86 86
 FT METAL 90 90
 FT HELIX 4 18
 FT TURN 19 19
 FT TURN 22 23
 FT TURN 26 26
 FT STRAND 28 38
 FT HELIX 40 48
 FT TURN 49 50
 FT HELIX 53 55
 FT TURN 56 56
 FT HELIX 57 61
 FT TURN 63 64
 FT STRAND 69 69
 FT TURN 71 88
 FT TURN 89 91
 SQ SEQUENCE 100 AA; 11326 MW; 0E361FD5DEA9DCE8 CRC64;
 Query Match 68.6%; Score 35; DB 1; Length 100;
 Best Local Similarity 55.6%; Pred. No. 5.2;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QYQSSPCS 9
 Db 88 QSHGAPCS 96
 RESULT 13
 S115_HUMAN STANDARD; PRT; 100 AA.
 AC Q86SG5;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE S100 calcium-binding protein A15.
 GN S100A15.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Epidermis;
 RX MEDLINE=22881852; PubMed=12923069;
 RA Wolf R., Mirzohamadsadeh A., Waiz M., Lyse B., Tartler U., Remus R.,
 RA Hengge U., Michel G., Ruzicka T.;
 RA "Molecular cloning and characterization of alternatively spliced mRNA
 RT isoforms from psoriatic skin encoding a novel member of the S100
 RL family";
 RL FASEB J. 17:1969-1971(2003).
 CC -!- FUNCTION: May be involved in epidermal differentiation and
 CC inflammation and might therefore be important for the pathogenesis
 CC of psoriasis and other diseases.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- TISSUE SPECIFICITY: Overexpressed in psoriasis.
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
 CC -----
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 CC or send an email to license@isb-sib.ch.
 CC -----
 CC EMBL; AY189117; AAO400032.1; -;

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DR EMBL; AY189118; AAC040033.1; -
DR EMBL; AY189119; AAC040034.1; -
DR Genbank; HGNC:21657; S100A15.
DR InterPro; IPR001751; CAPP_S100.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CAPP_S100; 1.
DR ProSITE; PS00018; EF_HAND; 1.
DR ProSITE; PS00303; S100_CAPP; 1.
KW Calcium-binding; Zinc; Metal-binding; Acetylation.
FT INIT MET 0
FT MOD_RES 1
FT CA_BIND 62 73
FT METAL 17 17
FT METAL 86 86
FT METAL 90 90
SQ SEQUENCE 100 AA; 11174 MW; AFE23C8821B507AB CRC64;
Query Match 68.6%; Score 35; DB 1; Length 100;
Best Local Similarity 55.6%; Pred. No. 5.2; Mismatches 3; Indels 1; Gaps 0;
Matches 5; Conservative 3;

QY 1 QYGSPPCS 9
Db 88 QSHGAPCS 96

RESULT 14
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID KV3L_HUMAN STANDARD; PRT; 595 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT Antibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy."
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR; P18022; K3HUHA.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129
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SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;
Query Match 68.6%; Score 35; DB 1; Length 129;
Best Local Similarity 85.7%; Pred. No. 6.8; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1;

QY 1 QYGSPP 7
Db 110 QYGTSP 116

RESULT 15
Z440_HUMAN STANDARD; PRT; 595 AA.
ID Z440_HUMAN STANDARD; PRT; 595 AA.
AC Q8YI18; Q8NLR9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Zinc finger protein 440.
DE ZNF440.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Tongue;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otakuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuna M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Naganari K., Masuho Y., Negai K.,
RA Isogai T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Uterus;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: May be involved in transcriptional regulation.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.
CC -1- SIMILARITY: Contains 1 KRAB domain.
CC -1- SIMILARITY: Contains 12 C2H2-type zinc fingers.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; BC035760; AAH35760.1; -;
DR EMBL; AK095252; BAC04510.1; -;
DR Genew; HGNC:20874; ZNF440.
DR InterPro; IPR001909; KRAB.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF01352; KRAB; 1; _C2H2.
DR Pfam; PF00096; Zf-C2H2; 11.
DR SMART; SM00349; KRAB; 1.
DR SMART; SM00355; Znf_C2H2; 11.
DR PROSITE; PS00805; KRAB; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 10.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 12.
KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
KW Nuclear protein; Repeat.
FT DOMAIN 4 86
FT ZN_FING 144 166
FT ZN_FING 172 194
FT ZN_FING 200 222
FT ZN_FING 228 250
FT ZN_FING 256 278
FT ZN_FING 284 306
FT ZN_FING 312 334
FT ZN_FING 340 362
FT ZN_FING 368 390
FT ZN_FING 396 418
FT ZN_FING 424 448
FT ZN_FING 458 480
FT CONFLICT 40 40 L -> M (IN REF. 1).
FT CONFLICT 569 569 S -> N (IN REF. 1).
SQ SEQUENCE 595 AA; 69105 MW; 7DCDFB698E40661 CRC64;
C2H2-TYPE 1 (DEGENERATE).
C2H2-TYPE 2.
C2H2-TYPE 3.
C2H2-TYPE 4.
C2H2-TYPE 5 (DEGENERATE).
C2H2-TYPE 6.
C2H2-TYPE 7.
C2H2-TYPE 8.
C2H2-TYPE 9.
C2H2-TYPE 10.
C2H2-TYPE 11.
C2H2-TYPE 12.

Query Match 68.6%; Score 35; DB 1; Length 595;
Best Local Similarity 62.5%; Pred. NO. 33;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QYGSPPC 8
DB 137 QYGPKEC 144

Search completed: April 21, 2004, 17:34:02
Job time : 5.56522 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:26:23 ; Search time 24 Seconds
(without alignments)
118.319 Million cell updates/sec

Title: SEQ6

Perfect score: 51
Sequence: 1 gqygspsc 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_prodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 39 | 76.5 | 412 | 4 Q8NA39 | Q8NA39 homo sapien |
| 2 | 39 | 76.5 | 885 | 13 Q91615 | Q91615 xenopus lae |
| 3 | 39 | 76.5 | 1240 | 13 P79773 | P79773 gallus gall |
| 4 | 39 | 76.5 | 1251 | 6 Q28224 | Q28224 cercopithec |
| 5 | 38 | 74.5 | 109 | 4 Q9UL78 | Q9UL78 homo sapien |
| 6 | 36 | 70.6 | 517 | 16 Q7UFH0 | Q7UFH0 rhodospirill |
| 7 | 36 | 70.6 | 524 | 10 Q9LGX9 | Q9LGX9 oryza sativ |
| 8 | 36 | 70.6 | 591 | 16 Q8RD12 | Q8RD12 thermocoaer |
| 9 | 35 | 68.6 | 151 | 11 Q8CB29 | Q8CB29 mus musculu |
| 10 | 35 | 68.6 | 174 | 2 Q9AFD0 | Q9AFD0 rhizobium m |
| 11 | 35 | 68.6 | 174 | 16 Q92TG3 | Q92TG3 rhizobium m |
| 12 | 35 | 68.6 | 267 | 13 Q9PUA5 | Q9PUA5 xenopus lae |
| 13 | 35 | 68.6 | 298 | 4 Q9NRF6 | Q9NRF6 homo sapien |
| 14 | 35 | 68.6 | 347 | 11 Q8K340 | Q8K340 mus musculu |
| 15 | 35 | 68.6 | 362 | 11 Q8COD3 | Q8COD3 mus musculu |
| 16 | 35 | 68.6 | 584 | 11 Q8BL43 | Q8BL43 mus musculu |

ALIGNMENTS

RESULT 1

Q8NA39 ID Q8NA39 PRELIMINARY; PET; 412 AA.
AC Q8NA39;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ35870.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Chiba Y.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Ohshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuno Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK093189; BAC04089.1; -
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0007222; P:fertilized signaling pathway; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR000591; DEP.
DR InterPro; IPR008339; Dishevelled_1.
DR InterPro; IPR008340; Dishevelled_1.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF00610; DEP; 1.
DR Pfam; PF00595; PDZ; 1.
DR PRINTS; PR01760; DISHEVELLED.
DR PRINTS; PR01761; DISHEVELLED1.
DR SMART; SM00049; DEP; 1.

Q93xr7 bruguiera g
Q7zy80 xenopus lae
Q84w49 arabidopsis
Q9s7t0 arabidopsis
Q95q02 caenorhabdi
Q93j21 fugu rubrip
Q85n8 oryza sativ
Q9acx8 streptomyce
Q9qz5 mus musculu
Q96nx9 homo sapien
Q7zzn1 salmo salar
Q7y8w0 portunus tr
Q84al bifidobacte
Q8nab9 homo sapien
P96397 mycobacteri
Q86ja7 dictyosteli
Q9gyv5 drosophila
Q9w105 drosophila
Q7u2j8 mycobacteri
O13963 schizosacch
Q8a529 bacteroides
Q81zm3 homo sapien
Q81uz6 homo sapien
Q8bh27 mus musculu
Q81fw9 ciona intes
Q81ni4 oryza sativ
Q87ld0 neurospora
Q7t0s1 xenopus lae
Q9ems7 amaecta moo

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DR PROSITE; PSS0186; DEP; 1.
DR PROSITE; PSS0106; PDZ; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 412 AA; 43743 MW; 93C3ABB1BF01C207 CRC64;

Query Match
Best Local Similarity 76.5%; Score 39; DB 4; Length 412;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPS 9
Db 93 RYGTSPS 100

RESULT 2
ID Q91615 PRELIMINARY; PRT; 885 AA.
AC Q91615;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Insulin receptor substrate-1-like protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1];
RP SEQUENCE FROM N.A.
RA Liu J.X., Sorisky A., Zhu L., Pawson T.;
RT "Molecular cloning of an Amphibian Insulin Receptor Substrate-1-like
RT cDNA and involvement of Phosphatidylinositol 3-kinase in insulin-
RT induced Xenopus oocyte maturation."
RL Mol. Cell. Biol. 15:0-0(1995).
DR EMBL; U27842; AAA73572.1; -.
DR HSP; P35568; IIRS.
DR GO; GO:0005158; F:insulin receptor binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002404; Insln_receptorS1.
DR Pfam; PF02174; IRS; 1.
DR PRINTS; PR00628; INSULINRSI.
DR SMART; SM00310; PTBI; 1.
KW Receptor.
SQ SEQUENCE 885 AA; 96146 MW; 9F1B96C64949CA7D CRC64;

Query Match
Best Local Similarity 76.5%; Score 39; DB 13; Length 885;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPS 8
Db 223 EYGSPPS 229

RESULT 3
ID P79773 PRELIMINARY; PRT; 1240 AA.
AC P79773;
DT 01-MAY-1997 (TREMELrel. 03, Created)
DT 01-MAY-1997 (TREMELrel. 03, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Insulin receptor substrate 1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1];
RP SEQUENCE FROM N.A.
RA STRAIN=Leghorn;
RX MEDLINE=97080546; PubMed=8921891;
RA Taouis M., Taylor S.I., Reitman M.;

```

```

RT "Cloning of the chicken insulin receptor substrate 1 gene."
RL Gene 178:51-55(1996).
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; U43502; AAC60050.1; -.
DR PIR; JC5209; JC5209.
DR HSP; P35568; IIRS.
DR GO; GO:0005158; F:insulin receptor binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002404; Insln_receptorS1.
DR InterPro; IPR001849; PH.
DR Pfam; PF02174; IRS; 1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PR00628; INSULINRSI.
DR SMART; SM00233; PH; 1.
DR SMART; SM00310; PTBI; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
KW Receptor.
SQ SEQUENCE 1240 AA; 131813 MW; 7FDEB2CEADECA7B6 CRC64;

Query Match
Best Local Similarity 76.5%; Score 39; DB 13; Length 1240;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPS 8
Db 428 EYGSPPS 434

RESULT 4
ID Q28224 PRELIMINARY; PRT; 1251 AA.
AC Q28224;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE IRS-1(COS).
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1];
RP SEQUENCE FROM N.A.
RA Wang L., Hayashi H., Mitani Y., Ishii K., Ohnishi T., Niwa Y.;
RT "Cloning of a cDNA encoding a 190-kDa insulin receptor substrate-1-
RT like protein of simian COS cells."
RL Biochem. Biophys. Res. Commun. 216:321-328(1995).
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; D64157; BAA11026.1; -.
DR HSP; P35568; IIRS.
DR GO; GO:0005158; F:insulin receptor binding; IEA.
DR InterPro; IPR002404; Insln_receptorS1.
DR InterPro; IPR001849; PH.
DR Pfam; PF02174; IRS; 1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PR00628; INSULINRSI.
DR SMART; SM00233; PH; 1.
DR SMART; SM00310; PTBI; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
SQ SEQUENCE 1251 AA; 133054 MW; 924CCAC3B8E8EB98 CRC64;

Query Match
Best Local Similarity 76.5%; Score 39; DB 6; Length 1251;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPS 8
Db 430 EYGSPPS 436

RESULT 5

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Q9UL78 Q9UL78 PRELIMINARY; PRT; 109 AA.
 AC Q9UL78;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M., Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035036; AAD56272.1; -;
 DR PIR; A30601; A30601.
 DR PIR; A30608; A30608.
 DR PIR; B30601; B30601.
 DR PIR; B30607; B30607.
 DR PIR; C30601; C30601.
 DR PIR; C30607; C30607.
 DR PIR; C30608; C30608.
 DR PIR; D30601; D30601.
 DR PIR; D30607; D30607.
 DR PIR; D30608; D30608.
 DR PIR; F30607; F30607.
 DR PIR; F30608; F30608.
 DR PIR; G30601; G30601.
 DR PIR; G30608; G30608.
 DR PIR; H30607; H30607.
 DR PIR; H30608; H30608.
 DR PIR; I30601; I30601.
 DR PIR; PH0963; PH0963.
 DR PIR; PH0965; PH0965.
 DR PIR; S34096; S34096.
 DR HSP; P80362; IWL1.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
 Query Match 74.5%; Score 38; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QYGGSP 7
 Db 90 QYGGSP 96
 RESULT 6
 Q7UFHO Q7UFHO PRELIMINARY; PRT; 517 AA.
 AC Q7UFHO;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN RB557.
 OS Rhodospirillum rubrum.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;

[1]
 RN RP SEQUENCE FROM N.A.
 RX STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.;
 RA "Complete genome sequence of the marine planctomycete Pirellula sp. strain 1";
 RT Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 RL EMBL; BX294147; CAD78712.1; -;
 DR Hypothetical protein; Complete proteome.
 KW SEQUENCE 517 AA; 58112 MW; 8F8A047FBC7133D8 CRC64;
 SQ SEQUENCE 517 AA; 58112 MW; 8F8A047FBC7133D8 CRC64;
 Query Match 70.6%; Score 36; DB 16; Length 517;
 Best Local Similarity 87.5%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QYGGSPCS 9
 Db 273 QYGGSPIS 280
 RESULT 7
 Q9LGX9 Q9LGX9 PRELIMINARY; PRT; 524 AA.
 AC Q9LGX9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC clone: P0702F03";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP002481; BAA96595.1; -;
 DR Gramene; Q9LGX9; -;
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003340; TF_B3.
 DR Pfam; PF02362; B3; 1.
 DR Hypothetical protein.
 KW SEQUENCE 524 AA; 58677 MW; 9F75AC5DC94C3E95 CRC64;
 SQ SEQUENCE 524 AA; 58677 MW; 9F75AC5DC94C3E95 CRC64;
 Query Match 70.6%; Score 36; DB 10; Length 524;
 Best Local Similarity 75.0%; Pred. No. 66;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QYGGSPCS 9
 Db 97 RYSSSPCS 104
 RESULT 8
 Q8RD12 Q8RD12 PRELIMINARY; PRT; 591 AA.
 AC Q8RD12;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-glucosidase-related glycosidases.
 GN BGLX2 OR TTE0241.
 OS Thermoanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.

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OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RA Del Papa M.P., Balague L.J., Legares A.;
RT "Putative Sinorhizobium meliloti gene cluster for phenylacetic acid
degradation.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF350436; AAK29442.1; -.
DR InterPro: IPR002744; DUF59.
DR Pfam: PF01883; DUF59; 1.
DR ProDom: PD005595; DUF59; 1.
SQ SEQUENCE 174 AA; 18973 MW; 349FF670182ADF2E CRC64;

Query Match 68.6%; Score 35; DB 2; Length 174;
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYGSPPC 8
Db 149 QFGSTPC 155

RESULT 11
Q92TG3 PRELIMINARY; PRT; 174 AA.
ID Q92TG3
AC Q92TG3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative phenylacetic acid degradation protein.
GN PAAD OR RB1557 OR SMB21637.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymB (megaplasmid 2).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RA Finan T.M., Weidner S., Wong K., Buhrmaster J., Chain P., Gouzy J.,
RA Vorholter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puehler A.;
RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
fixing endosymbiont Sinorhizobium meliloti.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
DR EMBL: AL803647; CAC49956.1; -.
DR PIR: D86036; D96036.
DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro: IPR002744; DUF59.
DR Pfam: PF01883; DUF59; 1.
DR ProDom: PD005595; DUF59; 1.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 174 AA; 19029 MW; ABE64850182DD83C CRC64;

Query Match 68.6%; Score 35; DB 16; Length 174;
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYGSPPC 8
Db 149 QFGSTPC 155

RESULT 12
Q9PUA5 PRELIMINARY; PRT; 267 AA.
ID Q9PUA5
AC Q9PUA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
GN PAAD.

```

```

OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=MB4 / JCM 11007;
RA MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700 (2002).
DR EMBL: AF012996; AAM23537.1; -.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR002772; Glyco_hydro_3C.
DR InterPro: IPR001764; Glyco_hydro_3N.
DR Pfam: PF00933; Glyco_hydro_3; 1.
DR Pfam: PF01915; Glyco_hydro_3_C; 1.
DR PRINTS: PR00133; GLHDLRASE3.
KW Glycosidase; Complete proteome.
SQ SEQUENCE 591 AA; 64817 MW; EBF5A938DEA54101 CRC64;

Query Match 70.6%; Score 36; DB 16; Length 591;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYGSPPC 9
Db 550 QYGMNPS 557

RESULT 9
Q8CB29 PRELIMINARY; PRT; 151 AA.
ID Q8CB29
AC Q8CB29;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Vagina;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL: AK036917; BAC29638.1; -.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 151 AA; 16328 MW; C54CBC212D283BAF CRC64;

Query Match 68.6%; Score 35; DB 11; Length 151;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YGSPPC 9
Db 58 YGVSPCS 64

RESULT 10
Q9AFD0 PRELIMINARY; PRT; 174 AA.
ID Q9AFD0
AC Q9AFD0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Paad.
GN PAAD.

```


DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE bzip transcription factor L-Maf.
 CN MAF.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 CC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21152895; PubMed=11231068;
 RA Ishibashi S., Yasuda K.;
 RL "Distinct roles of maf genes during Xenopus lens development."; Mech. Dev. 101:155-166(2001).
 RL EMBL; AF202059; AAF08317.2; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006355; R:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008917; Euk.transcr_DNA.
 DR InterPro; IPR004827; TF_Maf.
 DR Pfam; PF03131; bzip_Maf; 1.
 DR SMART; SM00338; BRLZ; 1.
 DR PROSITE; PS50217; BZIP; 1.
 SQ SEQUENCE 267 AA; 29637 MW; 2F48837AD0675232 CRC64;

Query Match 68.6%; Score 35; DB 13; Length 267;
 Best Local Similarity 66.7%; Pred. No. 53;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOYGSPPCS 9
 DB 42 QSLGTPCS 50

RESULT 13
 Q9NKF6 PRELIMINARY; PRT; 298 AA.
 AC Q9NKF6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ20281.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isegai T., Sugano S.;
 RT "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK000288; BA91057.1; -.
 DR GO; GO:000288; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf-CCHC; 1.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; ZNF_C2HC; 1.
 DR PROSITE; PS50158; ZF_CCHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 298 AA; 30699 MW; C2195F66A7E861B CRC64;

Query Match 68.6%; Score 35; DB 4; Length 298;
 Best Local Similarity 75.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOYGSPPC 8
 DB 125 QQMGSGPC 132

RESULT 14
 Q8K340 PRELIMINARY; PRT; 347 AA.
 AC Q8K340;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC028854; AAH28854.1; -.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 DR InterPro; IPR000159; RA_domain.
 DR PROSITE; PS50200; RA; 1.
 DR Hypothetical protein.
 KW NON_TER
 FT NON_TER 1
 SQ SEQUENCE 347 AA; 39160 MW; 306E40D38A14B3DE CRC64;

Query Match 68.6%; Score 35; DB 11; Length 347;
 Best Local Similarity 77.8%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOYGSPPCS 9
 DB 128 QOQFSSPCS 136

RESULT 15
 Q8COD3 PRELIMINARY; PRT; 362 AA.
 AC Q8COD3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical serine-rich region/aminocyl-transfer RNA synthetases class-II containing protein.
 GN 4632411J06RIK.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK011660; BAC27498.1; -.
 DR MGD; MGI:1925998; 4632411J06RIK.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 DR InterPro; IPR000159; RA_domain.
 DR PROSITE; PS50200; RA; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 362 AA; 40933 MW; 32B1047ACC07B987 CRC64;

Query Match 68.6%; Score 35; DB 11; Length 362;
 Best Local Similarity 77.8%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOYGSPPCS 9
 DB 192 QOQFSSPCS 200

Search completed: April 21, 2004, 17:37:23
Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:18 ; Search time 36 Seconds
(without alignments)
70.637 Million cell updates/sec

Title: SEQ6

Perfect score: 51

Sequence: 1 qyygsspc 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

- Database : A Geneseq 29Jan04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 40 | 78.4 | 87 | 4 | Aau43833 Propionib |
| 2 | 40 | 78.4 | 87 | 6 | Abm40352 Propionib |
| 3 | 39 | 76.5 | 412 | 7 | Adb65321 Human pro |
| 4 | 39 | 76.5 | 695 | 4 | Aay97560 Mouse Dis |
| 5 | 39 | 76.5 | 695 | 6 | Abg71359 Mouse dis |
| 6 | 39 | 76.5 | 1155 | 2 | Aar28047 IRS-1 pro |
| 7 | 39 | 76.5 | 1235 | 6 | Aao16354 Rat IRSAL |
| 8 | 39 | 76.5 | 1242 | 2 | Aay13461 Amino aci |
| 9 | 39 | 76.5 | 1242 | 2 | Aaw93972 Human IRS |
| 10 | 39 | 76.5 | 1242 | 4 | Aab83921 Amino aci |
| 11 | 39 | 76.5 | 1242 | 6 | Abb99797 Amino aci |
| 12 | 39 | 76.5 | 1242 | 6 | Abg72369 Human Ins |
| 13 | 39 | 76.5 | 1242 | 6 | Abg72372 Human Ins |
| 14 | 39 | 76.5 | 1242 | 6 | Abg72370 Human Ins |
| 15 | 39 | 76.5 | 1242 | 6 | Abg72371 Human Ins |
| 16 | 39 | 76.5 | 1242 | 6 | Abg72368 Human Ins |
| 17 | 39 | 76.5 | 1242 | 6 | Ada00642 Human IRS |
| 18 | 39 | 76.5 | 1243 | 2 | Aar67708 Insulin r |
| 19 | 38 | 74.5 | 8 | 5 | Abp62398 Human inm |
| 20 | 38 | 74.5 | 9 | 2 | Aaw24773 Human inm |
| 21 | 38 | 74.5 | 9 | 2 | Aay80140 Light cha |
| 22 | 38 | 74.5 | 9 | 2 | Aay40425 Amino aci |
| 23 | 38 | 74.5 | 9 | 4 | Aab67495 Human lfg |
| 24 | 38 | 74.5 | 9 | 5 | Abg78316 Human Fv |
| 25 | 38 | 74.5 | 9 | 5 | Abp62421 Human inm |

| | | | | | |
|----|----|------|---|---|--------------------|
| 26 | 38 | 74.5 | 9 | 5 | ABP62407 Human inm |
| 27 | 38 | 74.5 | 9 | 5 | ABP62414 Human inm |
| 28 | 38 | 74.5 | 9 | 5 | ABP62458 Human inm |
| 29 | 38 | 74.5 | 9 | 5 | ABP62408 Human inm |
| 30 | 38 | 74.5 | 9 | 5 | ABP62423 Human inm |
| 31 | 38 | 74.5 | 9 | 5 | ABP62460 Human inm |
| 32 | 38 | 74.5 | 9 | 5 | ABP62395 Human inm |
| 33 | 38 | 74.5 | 9 | 5 | ABP62406 Human inm |
| 34 | 38 | 74.5 | 9 | 5 | ABP62419 Human inm |
| 35 | 38 | 74.5 | 9 | 5 | ABP62402 Human inm |
| 36 | 38 | 74.5 | 9 | 5 | ABP62422 Human inm |
| 37 | 38 | 74.5 | 9 | 5 | ABP62426 Human inm |
| 38 | 38 | 74.5 | 9 | 5 | ABP62420 Human inm |
| 39 | 38 | 74.5 | 9 | 5 | ABP62457 Human inm |
| 40 | 38 | 74.5 | 9 | 5 | ABP62401 Human inm |
| 41 | 38 | 74.5 | 9 | 5 | ABP62404 Human inm |
| 42 | 38 | 74.5 | 9 | 5 | ABP62416 Human inm |
| 43 | 38 | 74.5 | 9 | 5 | ABP62461 Human inm |
| 44 | 38 | 74.5 | 9 | 5 | ABP62409 Human inm |
| 45 | 38 | 74.5 | 9 | 5 | ABP62413 Human inm |

ALIGNMENTS

RESULT 1
AAU43833
ID AAU43833 standard; protein; 87 AA.

XX AC AAU43833;
XX DT 13-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #4729.

XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

XX PN WO200181581-A2.

XX PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US012865.

XX PR 21-APR-2000; 2000US-0199047P.

XX PR 02-JUN-2000; 2000US-0208841P.

XX XX 07-JUL-2000; 2000US-0216747P.

XX PA (CORI-) CORIXA CORP.

XX PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX PI WPI; 2001-616774/71.

XX DR N-PSDB; AAS59521.

XX XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX PT vaccinating against and diagnosing infections, especially useful for
XX PT treating acne vulgaris.

XX PS Example 1; SEQ ID NO 5028; 1069pp; English.

XX CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX CC polypeptides. The proteins and their associated DNA sequences are used in
XX CC the treatment, prevention and diagnosis of medical conditions caused by
XX CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX CC P. acnes is also involved in infections of bone, joints and the central
XX CC nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: the sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 87 AA;
 SQ

Query Match 78.4%; Score 40; DB 4; Length 87;
 Best Local Similarity 87.5%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOYGSPPC 8
 Db 55 QOYGSPPC 62

RESULT 2
 ID ABM40352 standard; protein; 87 AA.
 AC ABM40352;
 XX
 XX 20-OCT-2003 (first entry)
 DT
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #5028.
 XX
 XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 XX
 XX Propionibacterium acnes.
 OS
 XX WO2003033515-A1.
 PN
 XX 24-APR-2003.
 PD
 XX 11-OCT-2002; 2002WO-US032727.
 PF
 XX 15-OCT-2001; 2001US-00978825.
 PR
 XX (CORI-) CORIXA CORP.
 PA
 XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes WJ, Benson DR, Jones R, Carter D;
 PI Barth B, Valliave-Douglas J;
 XX WPI; 2003-381789/36.
 DR N-PSDB; ACF64450.
 DR

XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide useful for diagnosing preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 XX Example 1; SEQ ID NO 5028; 1481pp; English.
 PS
 XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC

CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 87 AA;
 SQ

Query Match 78.4%; Score 40; DB 6; Length 87;
 Best Local Similarity 87.5%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOYGSPPC 8
 Db 55 QOYGSPPC 62

RESULT 3
 ID ADB65321 standard; protein; 412 AA.
 AC ADB65321;
 XX
 XX 04-DEC-2003 (first entry)
 DT
 DE Human protein encoded by clone TESTI20079980.
 XX

XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
 KW cell regeneration; membrane protein; signal transduction-related protein;
 KW transcription-related protein; osteoporosis; neurological disease;
 KW cancer; tumour.
 XX
 XX Homo sapiens.
 OS
 XX EPI308459-A2.
 FN
 XX 07-MAY-2003.
 PD
 XX 28-MAR-2002; 2002EP-00007401.
 PF
 XX 05-NOV-2001; 2001JP-00379298.
 PR
 XX 25-JAN-2002; 2002US-00350978.
 PR

XX (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 XX Isoqai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX WPI; 2003-450961/43.
 DR N-PSDB; ADB63351.
 DR

XX New polynucleotides and polypeptides, useful for developing a diagnostic
 PT marker or medicines for regulation of their expression and activity, or
 PT as targets of gene therapy.
 XX
 XX Claim 1; Page; 222pp; English.
 PS
 XX The invention discloses a polynucleotide comprising a sequence selected
 CC from 1970 fully defined nucleotide sequences which encode novel
 CC

XX Lamb JR, Hoyne GF, Dallman MJ, Champion BR;
 XX WPI: 2003-058470/05.
 XX N-PSDB; ABS55984.
 XX Use of a modulator of Hedgehog signaling pathways for treating T-cell
 PT mediated disease or infection and diseases associated with increased or
 PT decreased T-cell apoptosis and T-cell proliferation.
 XX Disclosure; Page 150; 154pp; English.
 XX The invention relates to use of a modulator of a Hedgehog signalling
 CC pathway or a modulator of a target of the pathway in the preparation of a
 CC medicament for treating T-cell mediated disease or infection or a disease
 CC or disorder associated with increased or decreased T-cell apoptosis and
 CC for modification of (peripheral) T-cell activation or proliferation or T-
 CC cell apoptosis, and for modulation of the Notch signalling pathway in
 CC immune cells. The modulator is useful for treating cancer of the breast,
 CC prostate or ovary, lymphomas and carcinomas, autoimmune diseases such as
 CC systemic lupus erythematosus, multiple sclerosis and diabetes,
 CC inflammatory diseases such as osteoarthritis and Crohn's disease,
 CC proliferative disorders such as atherosclerosis and psoriasis, viral
 CC infections such as AIDS and herpesviruses, genetic immunodeficiencies,
 CC neurodegenerative diseases such as Alzheimer's disease and Parkinson's
 CC disease, myelodysplastic syndromes such as aplastic anaemia, ischaemic
 CC injuries such as myocardial infarction, toxin-induced diseases such as
 CC cirrhosis and wasting diseases such as cachexia. This sequence represents
 CC the mouse disvelled-1 (Dvl-1) protein
 XX Sequence 695 AA;
 Query Match 76.5%; Score 39; DB 6; Length 695;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYGS3PCS 9
 Db 376 RYGTSPCS 383
 RESULT 6
 AAR28047
 ID AAR28047 standard; protein; 1155 AA.
 XX
 AC AAR28047;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-MAR-1993 (first entry)
 XX
 DE IRS-1 protein.
 XX Insulin receptor substrate-1; IRS-1; probe; vector; transform;
 XX IRS-1 metabolism; insulin related disease.
 KW Rattus rattus.
 XX WO9213083-A1.
 XX 06-AUG-1992.
 XX 17-JAN-1992; 92WO-US000437.
 XX 18-JAN-1991; 91US-00643982.
 XX (JOSL-) JOSLIN DIABETES CENT INC.
 XX Kahn CR, White MF, Rothenberg PL;
 PI WPI: 1992-365881/44.
 XX N-PSDB; AAQ29703.
 XX Purified nucleic acid encoding Insulin Receptor Substrate - used to

PT prepare IRS-1, for diagnosis and treatment of insulin related diseases
 PT and abnormal cellular proliferation.
 XX Disclosure; Fig 12; 128pp; English.
 XX The sequence given is the rat insulin receptor substrate-1 (IRS-1). The
 CC IRS-1 gene was isolated using the probe sequences given in AAQ29701-02.
 CC The IRS-1 sequence can be inserted into a vector and used to transform
 CC cells to produce IRS-1. The level of IRS-1 metabolism can then be studied
 CC and abnormal levels may be seen to be indicative of insulin related
 CC disease. (Updated on 25-MAR-2003 to correct FN field.)
 XX Sequence 1155 AA;
 Query Match 76.5%; Score 39; DB 2; Length 1155;
 Best Local Similarity 85.7%; Pred. No. 3.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYGS3PC 8
 Db 385 EYGS3PC 391
 RESULT 7
 AAO16354
 ID AAO16354 standard; protein; 1235 AA.
 XX
 AC AAO16354;
 XX
 DT 03-APR-2003 (first entry)
 XX
 DE Rat IRSAL-related protein.
 XX Rat; IRSAL; insulin activity modification; saccharide intake;
 KW Gene diagnosis; screening; type II diabetes.
 XX Rattus sp.
 OS WO200283730-A1.
 FN 24-OCT-2002.
 PD 10-APR-2002; 2002WO-JP003579.
 PF 10-APR-2001; 2001JP-00111864.
 PR (TAIS) TAISHO PHARM CO LTD.
 XX Takahashi S, Hakuno F, Kurihara S;
 PI WPI: 2003-075521/07.
 DR N-PSDB; AAL51458.
 XX Novel protein IRSAL and encoding gene for modifying insulin physiological
 PT activity and controlling intake of saccharides into cells, applicable in
 PT gene diagnosis and screening e.g. drug candidates for type II diabetes.
 XX Claim 1; Page 40-48; 58pp; Japanese.
 XX The invention comprises the amino acid and coding sequence of the IRSAL
 CC protein which functions to modify insulin physiological activity and
 CC control the intake of saccharides into cells. The DNA and protein
 CC sequences of the invention are useful in gene diagnosis and screening
 CC (e.g. drug candidates for type II diabetes). The present amino acid
 CC sequence represents a rat IRSAL-related protein
 XX Sequence 1235 AA;
 Query Match 76.5%; Score 39; DB 6; Length 1235;
 Best Local Similarity 85.7%; Pred. No. 3.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYGS3PC 8

```

Db      425 EYGSSPC 431
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RESULT 8
AAV13461
ID AAV13461 standard; protein; 1242 AA.
XX AC AAV13461;
XX DT 26-JUL-1999 (first entry)
XX DE Amino acid sequence of human IRS-1 protein.
XX KW Phosphotyrosine interaction domain; PI domain; modulator; APP;
XX KW amyloid precursor protein; cytoplasmic domain; Alzheimer's disease;
XX KW neurodegenerative disease; dementia; IRS-1.
XX OS Homo sapiens.
XX PN WO9921995-A1.
XX PD 06-MAY-1999.
XX PF 23-OCT-1998; 98WO-US022523.
XX PR 24-OCT-1997; 97US-00957660.
XX PR 17-APR-1998; 98US-00062085.
XX PA (UYRQ ) UNIV ROCKEFELLER.
XX PI Sabo S, Buxbaum J, Greengard P;
XX WPI; 1999-326703/27.
XX Cell line for screening agents that inhibit processing of amyloid
XX precursor protein.
XX Claim 4; Fig 16; 86pp; English.
XX The invention relates to modulators that affect the interaction of a
XX polypeptide defining a PI (phosphotyrosine interaction) domain, or its
XX conserved variants or fragments, with APP (amyloid precursor protein).
XX The polypeptide defining a PI domain binds to the cytoplasmic domain of
XX APP, regulating the secretion of APP fragments. By modulating this
XX interaction, the modulator can inhibit or prevent APP processing and
XX trafficking, and thus progress or onset of Alzheimer's disease. The
XX modulators are used to treat and/or prevent neurodegenerative diseases in
XX mammals, particularly Alzheimer's disease and dementia. Sequences
XX AAV13448-461 represent examples of polypeptides defining a PI domain
XX Sequence 1242 AA;

Query Match      76.5%; Score 39; DB 2; Length 1242;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYGSSPC 8
Db      430 EYGSSPC 436
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RESULT 10
AAB83921
ID AAB83921 standard; protein; 1242 AA.
XX AC AAB83921;
XX DT 23-JUL-2001 (first entry)
XX DE Amino acid sequence of a human insulin receptor substrate (IRS).
XX KW Epidermal growth factor-like domain; EGF-like domain; cancer;
XX KW human aspartyl beta-hydroxylase; HAAH; malignant neoplasm; tumour;
XX KW insulin receptor substrate; IRS.
XX OS Homo sapiens.
XX PN WO200135102-A2.
XX PD 17-MAY-2001.
XX PF 08-NOV-2000; 2000WO-US030738.
XX

insulin resistance; 14-3-3 protein; inhibitor; screening; diabetes;
diabetic retinopathy; diabetic neuropathy; glucose tolerance;
diabetic nephropathy; hyperinsulinaemia; hyperlipemia; arteriosclerosis;
hypertension; ischaemic heart disease; ischaemic brain disease;
peripheral embolism.
Homo sapiens.
WO9916462-A1.
08-APR-1999.
25-SEP-1998; 98WO-JP004293.
29-SEP-1997; 97JP-00263719.
(DAUC ) DAIICHI PHARM CO LTD.
Yazaki Y, Asano T, Kubo H, Kanda A;
WPI; 1999-254929/21.
Treatment of insulin resistance using insulin receptor substrate binding
inhibitor.
Disclosure; Page 16-22; 30pp; Japanese.
This invention describes a method for the treatment of diseases involving
insulin resistance using a substance which inhibits the binding of
insulin receptor substrate to 14-3-3 protein, identified by screening
potential inhibitors for their ability to inhibit this binding. The
composition described in the invention for the treatment of diseases
involving insulin resistance contains as active component, an inhibitor
of the binding of all or part of insulin receptor substrate 1 or 2 (IRS-
1, IRS-2) to all or part of 14-3-3 protein. Disorders involving insulin
resistance include diabetes, diabetic retinopathy, diabetic neuropathy,
impaired glucose tolerance, diabetic nephropathy, hyperinsulinaemia,
hyperlipemia, arteriosclerosis, hypertension, obesity, ischaemic heart
disease, ischaemic brain disease and peripheral embolism
Sequence 1242 AA;

Query Match      76.5%; Score 39; DB 2; Length 1242;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYGSSPC 8
Db      430 EYGSSPC 436
      :|||||
RESULT 9
AAW93972
ID AAW93972 standard; protein; 1242 AA.
XX AC AAW93972;
XX DT 30-JUN-1999 (first entry)
XX DE Human IRS-1 and IRS-2 binding inhibitor protein.
XX KW Insulin receptor substrate; IRS-1; IRS-2; inhibitor; disease; obesity;

```

PR 08-NOV-1999; 99US-00436184.
 XX (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER.
 PA
 PI Wanda JR, De La Monte SM, Ince N, Carlson RI;
 XX
 DR WPI; 2001-329171/34.
 DR N-PSDB; AAF89816.
 XX
 PT Diagnosing malignant neoplasm in a mammal, involves contacting mammalian
 PT sample with antibody that binds to human aspartyl beta-hydroxylase
 PT polypeptide to form antigen-antibody complex and detecting the complex.
 PS
 PS Example 7; Page 52; 76pp; English.
 XX
 CC The present sequence represents a human insulin receptor substrate (IRS).
 CC Compounds which inhibit IRS also inhibit growth of tumours which
 CC overexpress human aspartyl (asparaginyl) beta-hydroxylase (HAAH) enzyme.
 CC Epidermal growth factor (EGF)-like domains of polypeptides are
 CC hydroxylated by HAAH enzymes. HAAH is used in the method of the
 CC invention. The specification describes a method for diagnosing a
 CC malignant neoplasm in a mammal. The method comprises contacting a body
 CC fluid with an antibody which binds to HAAH polypeptide under complex
 CC forming conditions, and detecting the antigen-antibody complex. The
 CC method is useful for diagnosing and prognosing a malignant neoplasm in a
 CC bodily fluid e.g. central nervous system (CNS)-derived body fluid, blood,
 CC serum, urine, saliva, sputum, lung effusion, and ascites fluid of mammal,
 CC where the neoplasm is derived from endodermal tissue and is selected from
 CC colon cancer, breast cancer, pancreatic cancer, liver cancer, cancer of
 CC bile ducts, and cancer of the CNS. HAAH antibodies, linked to a cytotoxic
 CC agent, are useful for killing tumour cells
 XX
 SQ Sequence 1242 AA;
 Query Match 76.5%; Score 39; DB 4; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYGSSPC 8
 Db 430 EYGSPPC 436
 RESULT 11
 ABB99797
 ID ABB99797 standard; protein; 1242 AA.
 AC ABB99797;
 DT 07-APR-2003 (first entry)
 XX
 DE Amino acid sequence of human insulin receptor substrate-1.
 XX
 KW IRS-1; insulin receptor substrate-1; angiogenesis; capillary tube;
 KW endothelial cell; retinopathy; rheumatoid arthritis; Crohn's disease;
 KW atherosclerosis; ovarian hyperstimulation; psoriasis; endometriosis;
 KW restenosis; wound healing; peripheral vascular disease; hypertension;
 KW vascular inflammation; Raynaud disease; aneurysm; arterial restenosis;
 KW thrombophlebitis; lymphagitis; lymphodema; ischemia; angina;
 KW myocardial infarction; chronic heart disease; macular degeneration;
 KW osteoporosis; cell multiplication; antitumor.
 XX
 OS Homo sapiens.
 XX
 WO2002103014-A2.
 XX
 PD 27-DEC-2002.
 XX
 FF 14-JUN-2002; 2002WO-FR002067.
 XX
 PR 14-JUN-2001; 2001FR-00007805.
 XX
 PA (ALMA/) AL-MAHMOOD S.

XX
 PI Al-Mahmood S;
 XX
 DR WPI; 2003-167520/16.
 DR N-PSDB; ABZ23324.
 XX
 FT Angiogenesis-modifying composition, useful for treatment or diagnosis of
 FT e.g. retinopathy, comprises inhibitor of expression of the insulin
 FT receptor substrate-1 gene.
 XX
 PS Disclosure; Page 49-52; 52pp; French.
 XX
 CC The present sequence represents IRS-1 (insulin receptor substrate-1)
 CC polypeptide. IRS-1 is used to produce the compositions of the invention.
 CC The specification describes an angiogenesis-modifying composition,
 CC containing at least one a nucleic acid selected from the gene encoding
 CC IRS-1 or a molecule that inhibits expression of that nucleic acid. The
 CC composition inhibits the formation of capillary tubes by endothelial
 CC cells. The composition is used to treat and diagnose diseases associated
 CC with angiogenesis, particularly retinopathy, rheumatoid arthritis,
 CC Crohn's disease, atherosclerosis, ovarian hyperstimulation, psoriasis,
 CC endometriosis, restenosis after balloon angioplasty, overproduction of
 CC tissue during wound healing, peripheral vascular diseases, hypertension,
 CC vascular inflammation, Raynaud disease, aneurysm, arterial restenosis,
 CC thrombophlebitis, lymphagitis, lymphodema, ischemia, angina, myocardial
 CC infarction, chronic heart disease, (congestive) cardiac insufficiency,
 CC age-related macular degeneration and osteoporosis. It is also used to
 CC prevent cell multiplication, especially as antitumor agents, and as
 CC research reagents for in vitro or in vivo studies on signalling pathways
 XX
 SQ Sequence 1242 AA;
 Query Match 76.5%; Score 39; DB 6; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYGSSPC 8
 Db 430 EYGSPPC 436
 RESULT 12
 ABB972369
 ID ABB972369 standard; protein; 1242 AA.
 AC ABB972369;
 DT 06-FEB-2003 (first entry)
 XX
 DE Human Insulin-receptor substrate-1, IRS-1, Y896F mutant.
 XX
 KW Human; aspartyl (asparaginyl) beta-hydroxylase; HAAH; cytostatic;
 KW immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B;
 KW brain tumour; glioma; glioblastoma; astrocytoma; haemangioma;
 KW pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer;
 KW liver cancer; cancer of the bile ducts; primary malignant CNS neoplasm;
 KW metastatic CNS neoplasm; IRS-1; insulin receptor substrate-1; mutant;
 KW mutin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 896 /note= "Wild-type Tyr substituted by Phe"
 FT
 XX
 PN US2002110559-A1.
 XX
 PD 15-AUG-2002.
 XX
 FF 17-MAY-2001; 2001US-00859604.
 XX
 PR 08-NOV-1999; 99US-00436184.

XX (WAND/) WANDS J R.
 PA (DMON/) DE LA MONTE S M.
 PA (DEUT/) DEUTCH A H.
 PA (GHAN/) GHANBARI H A.
 XX
 PI Wands JR, De La Monte SM, Deutch AH, Ghanbari HA;
 XX WPI; 2003-066676/06.
 DR
 XX
 XX Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of
 PT mammal with detectably-labeled antibody which binds to human aspartyl
 PT (asparaginyl) beta-hydroxylase.
 XX
 XX Example 7; Page; 34pp; English.
 PS
 XX The invention relates to diagnosing a neoplasm and inhibiting tumor
 CC growth in a mammal, using an antibody that binds to human aspartyl
 CC (asparaginyl) beta-hydroxylase (HAH). Diagnosing a neoplasm comprises
 CC contacting a tissue with a detectably-labelled antibody where an increase
 CC in level of antibody binding at tissue site compared to the level of
 CC binding to normal non-neoplastic tissue indicates the presence of a
 CC neoplasm at the tissue site. Inhibiting tumor growth in mammal involves
 CC administering the antibody conjugated to a cytotoxic agent to a mammal.
 CC Also included are a method of conferring an immune response to a tumor
 CC cell in a mammal, by administering the antibody, a method of inducing an
 CC HAAH-specific immune response in a mammal, by administering to the mammal
 CC an HAAH polypeptide (or a polynucleotide composition encoding the
 CC polypeptide, or its degenerate variant), a fragment of HAAH comprising an
 CC extracellular domain and lacking a cytoplasmic domain of HAAH, an
 CC antibody or its fragment which binds to HAAH (where the antibody is FB50,
 CC 86A, 5C7 or 19B), a hybridoma cell line chosen from hybridoma FB50,
 CC HA386A, HA15CA and HA219B, and a fragment of HAAH which lacks enzymatic
 CC activity or alpha-ketoglutarate binding domain and epidermal growth
 CC factor (EGF)-like domain. The methods are useful for diagnosing neoplasm
 CC in a mammal, inhibiting tumor growth in a mammal, conferring an immune
 CC response to a brain tumor cell (e.g. glioma, glioblastoma, astrocytoma
 CC or haemangioma) in a mammal, for conferring an immune response to a
 CC pancreatic carcinoma cell and for inducing a HAAH-specific immune
 CC response in a mammal. The method is useful for diagnosing malignant
 CC neoplasms derived from endodermal tissue, e.g. colon cancer, breast
 CC cancer, pancreatic cancer, liver cancer and cancer of the bile ducts. The
 CC method is also useful for diagnosing neoplasms of central nervous system
 CC (CNS) e.g. primary malignant CNS neoplasms of both neuronal and glial
 CC cell origin and metastatic CNS neoplasms, and for diagnosing brain
 CC tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The
 CC present sequence represents a mutant human IRS-1 (insulin receptor
 CC substrate-1). IRS-1 mutants were used to elucidate the upregulation of
 CC HAAH expression when activated by the IRS-1 signal transduction cascade.
 CC Note: The present sequence is not shown in the specification but was
 CC created by the indexer using the IRS-1 sequence appearing as ABG72368 and
 CC the information in Example 7
 XX
 XX Sequence 1242 AA;
 SQ
 Query Match 76.5%; Score 39; DB 6; Length 1242;
 ID Best Local Similarity 85.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYGSPP 8
 Db 430 EYGSPP 436
 :|||||
 RESULT 13
 ABG72372
 ID ABG72372 standard; protein; 1242 AA.
 XX
 AC ABG72372;
 XX
 DT 06-FEB-2003 (first entry)
 XX
 DE Human Insulin-receptor substrate-1, IRS-1, Y612P/Y941P mutant.

XX Human; aspartyl (asparaginyl) beta-hydroxylase; HAAH; cytostatic;
 KW immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B;
 KW brain tumour; glioma; glioblastoma; astrocytoma; haemangioma;
 KW pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer;
 KW liver cancer; cancer of the bile ducts; primary malignant CNS neoplasm;
 KW metastatic CNS neoplasm; IRS-1; insulin receptor substrate-1; mutant;
 KW mutain.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 612 /note= "Wild-type Tyr substituted by Phe"
 FT Misc-difference 941 /note= "Wild-type Tyr substituted by Phe"
 FT
 XX US2002110559-A1.
 XX 15-AUG-2002.
 XX 17-MAY-2001; 2001US-00859604.
 XX 08-NOV-1999; 99US-00436184.
 XX (WAND/) WANDS J R.
 PA (DMON/) DE LA MONTE S M.
 PA (DEUT/) DEUTCH A H.
 PA (GHAN/) GHANBARI H A.
 XX Wands JR, De La Monte SM, Deutch AH, Ghanbari HA;
 WPI; 2003-066676/06.
 XX
 XX Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of
 PT mammal with detectably-labeled antibody which binds to human aspartyl
 PT (asparaginyl) beta-hydroxylase.
 XX
 XX Example 7; Page; 34pp; English.
 XX The invention relates to diagnosing a neoplasm and inhibiting tumor
 CC growth in a mammal, using an antibody that binds to human aspartyl
 CC (asparaginyl) beta-hydroxylase (HAH). Diagnosing a neoplasm comprises
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 CC in level of antibody binding at tissue site compared to the level of
 CC binding to normal non-neoplastic tissue indicates the presence of a
 CC neoplasm at the tissue site. Inhibiting tumor growth in mammal involves
 CC administering the antibody conjugated to a cytotoxic agent to a mammal.
 CC Also included are a method of conferring an immune response to a tumor
 CC cell in a mammal, by administering the antibody, a method of inducing an
 CC HAAH-specific immune response in a mammal, by administering to the mammal
 CC an HAAH polypeptide (or a polynucleotide composition encoding the
 CC polypeptide, or its degenerate variant), a fragment of HAAH comprising an
 CC extracellular domain and lacking a cytoplasmic domain of HAAH, an
 CC antibody or its fragment which binds to HAAH (where the antibody is FB50,
 CC 86A, 5C7 or 19B), a hybridoma cell line chosen from hybridoma FB50,
 CC HA386A, HA15CA and HA219B, and a fragment of HAAH which lacks enzymatic
 CC activity or alpha-ketoglutarate binding domain and epidermal growth
 CC factor (EGF)-like domain. The methods are useful for diagnosing neoplasm
 CC in a mammal, inhibiting tumor growth in a mammal, conferring an immune
 CC response to a brain tumor cell (e.g. glioma, glioblastoma, astrocytoma
 CC or haemangioma) in a mammal, for conferring an immune response to a
 CC pancreatic carcinoma cell and for inducing a HAAH-specific immune
 CC response in a mammal. The method is useful for diagnosing malignant
 CC neoplasms derived from endodermal tissue, e.g. colon cancer, breast
 CC cancer, pancreatic cancer, liver cancer and cancer of the bile ducts. The
 CC method is also useful for diagnosing neoplasms of central nervous system
 CC (CNS) e.g. primary malignant CNS neoplasms of both neuronal and glial
 CC cell origin and metastatic CNS neoplasms, and for diagnosing brain
 CC tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The
 CC present sequence represents a mutant human IRS-1 (insulin receptor
 CC substrate-1). IRS-1 mutants were used to elucidate the upregulation of
 CC HAAH expression when activated by the IRS-1 signal transduction cascade.
 CC Note: The present sequence is not shown in the specification but was
 CC created by the indexer using the IRS-1 sequence appearing as ABG72368 and
 CC the information in Example 7
 XX
 XX Sequence 1242 AA;
 SQ
 Query Match 76.5%; Score 39; DB 6; Length 1242;
 ID Best Local Similarity 85.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYGSPP 8
 Db 430 EYGSPP 436
 :|||||
 RESULT 13
 ABG72372
 ID ABG72372 standard; protein; 1242 AA.
 XX
 AC ABG72372;
 XX
 DT 06-FEB-2003 (first entry)
 XX
 DE Human Insulin-receptor substrate-1, IRS-1, Y612P/Y941P mutant.

XX (WAND/) WANDS J R.
PA (DMON/) DE LA MONTE S M.
PA (DEUT/) DEUTCH A H.
PA (CHAN/) GHANBARI H A.
XX
PI Wands JR, De La Monte SM, Deutch AH, Ghanbari HA;
XX
DR WPI; 2003-066676/06.
XX
PT Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of
PT mammal with detectably-labeled antibody which binds to human aspartyl
PT (asparaginyl) beta-hydroxylase.
XX
PS Example 7; Page; 34pp; English.
XX
CC The invention relates to diagnosing a neoplasm and inhibiting tumour
CC growth in a mammal, using an antibody that binds to human aspartyl
CC (asparaginyl) beta-hydroxylase (HAAH). Diagnosing a neoplasm comprises
CC contacting a tissue with a detectably-labelled antibody where an increase
CC in level of antibody binding at tissue site compared to the level of
CC binding to normal non-neoplastic tissue indicates the presence of a
CC neoplasm at the tissue site. Inhibiting tumour growth in mammal involves
CC administering the antibody conjugated to a cytotoxic agent to a mammal.
CC Also included are a method of conferring an immune response to a tumour
CC cell in a mammal, by administering the antibody, a method of inducing an
CC HAAH-specific immune response in a mammal, by administering to the mammal
CC an HAAH polypeptide (or a polynucleotide composition encoding the
CC polypeptide, or its degenerate variant), a fragment of HAAH comprising an
CC extracellular domain and lacking a cytoplasmic domain of HAAH, an
CC antibody or its fragment which binds to HAAH (where the antibody is FBS0,
CC 86A, 5C7 or 19B), a hybridoma cell line chosen from hybridoma FBS0,
CC HA386A, HA15CA and HA219B, and a fragment of HAAH which lacks enzymatic
CC activity or alpha-ketoglutarate binding domain and epidermal growth
CC factor (EGF)-like domain. The methods are useful for diagnosing neoplasm
CC in a mammal, inhibiting tumour growth in a mammal, conferring an immune
CC response to a brain tumour cell (e.g. glioma, glioblastoma, astrocytoma
CC or haemangioma) in a mammal, for conferring immune response to a
CC pancreatic carcinoma cell and for inducing a HAAH-specific immune
CC response in a mammal. The method is useful for diagnosing malignant
CC neoplasms derived from endodermal tissue, e.g. colon cancer, breast
CC cancer, pancreatic cancer, liver cancer and cancer of the bile ducts. The
CC method is also useful for diagnosing neoplasms of both neuronal and glial
CC (CNS) e.g. primary malignant CNS neoplasms, and for diagnosing brain
CC cell origin and metastatic CNS neoplasms, and for diagnosing brain
CC tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The
CC present sequence represents a mutant human IRS-1 (insulin receptor
CC substrate-1). IRS-1 mutants were used to elucidate the upregulation of
CC HAAH expression when activated by the IRS-1 signal transduction cascade.
CC Note: The present sequence is not shown in the specification but was
CC created by the indexer using the IRS-1 sequence appearing as ABG72368 and
CC the information in Example 7
XX
SQ Sequence 1242 AA;

Query Match 76.5%; Score 39; DB 6; Length 1242;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
:|||||
Db 430 EYGSPPC 436

Search completed: April 21, 2004, 17:33:16
Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:33:24 ; Search time 133.826 Seconds

(without alignments)
65.641 Million cell updates/sec

Title: SEQ6

Perfect score: 51

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Scoring table: BLOSUM62

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Searched: 6019581 seqs, 976033577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 33: /cgn2_6/ptodata/2/paa/US106 COMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
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| 1 | 51 | 100.0 | 108 | 1 | PCT-US03-00398-49 | Sequence 49, Appl |
| 2 | 51 | 100.0 | 108 | 1 | PCT-US03-00398-225 | Sequence 225, App |
| 3 | 51 | 100.0 | 108 | 1 | PCT-US03-00398-259 | Sequence 259, App |
| 4 | 51 | 100.0 | 108 | 1 | PCT-US03-00398-375 | Sequence 375, App |
| 5 | 51 | 100.0 | 108 | 1 | PCT-US03-29414-4 | Sequence 4, Appli |
| 6 | 51 | 100.0 | 108 | 26 | US-10-041-860-49 | Sequence 49, Appl |
| 7 | 51 | 100.0 | 108 | 26 | US-10-041-860-225 | Sequence 225, App |
| 8 | 51 | 100.0 | 108 | 26 | US-10-041-860-259 | Sequence 259, App |
| 9 | 51 | 100.0 | 108 | 26 | US-10-041-860-375 | Sequence 375, App |
| 10 | 51 | 100.0 | 108 | 31 | US-10-665-383-4 | Sequence 4, Appli |
| 11 | 48 | 94.1 | 100 | 22 | US-09-791-537-11779 | Sequence 11779, A |
| 12 | 45 | 88.2 | 106 | 22 | US-09-791-537-82003 | Sequence 82003, A |
| 13 | 45 | 88.2 | 116 | 22 | US-09-791-537-97444 | Sequence 97444, A |
| 14 | 40.5 | 79.4 | 100 | 22 | US-09-791-537-11863 | Sequence 11863, A |
| 15 | 40 | 78.4 | 81 | 22 | US-09-791-537-36703 | Sequence 36703, A |
| 16 | 40 | 78.4 | 87 | 1 | PCT-US02-32727-5028 | Sequence 5028, Ap |
| 17 | 40 | 78.4 | 87 | 25 | US-09-978-825-5028 | Sequence 5028, Ap |
| 18 | 40 | 78.4 | 87 | 26 | US-10-057-498-5028 | Sequence 5028, Ap |
| 19 | 39 | 76.5 | 74 | 33 | US-60-160-209-3594 | Sequence 3594, Ap |
| 20 | 39 | 76.5 | 74 | 33 | US-60-169-868-4772 | Sequence 4772, Ap |
| 21 | 39 | 76.5 | 81 | 22 | US-09-791-537-36707 | Sequence 36707, A |
| 22 | 39 | 76.5 | 86 | 33 | US-60-160-209-4387 | Sequence 4387, Ap |
| 23 | 39 | 76.5 | 86 | 33 | US-60-169-868-6544 | Sequence 6544, Ap |
| 24 | 39 | 76.5 | 89 | 22 | US-09-791-537-127769 | Sequence 127769, A |
| 25 | 39 | 76.5 | 90 | 22 | US-09-791-537-36078 | Sequence 36078, A |
| 26 | 39 | 76.5 | 92 | 33 | US-60-162-245-3568 | Sequence 3568, Ap |
| 27 | 39 | 76.5 | 100 | 22 | US-09-791-537-133434 | Sequence 133434, A |
| 28 | 39 | 76.5 | 102 | 33 | US-60-162-245-2740 | Sequence 2740, Ap |
| 29 | 39 | 76.5 | 102 | 33 | US-60-169-868-5366 | Sequence 5366, Ap |
| 30 | 39 | 76.5 | 142 | 33 | US-60-188-162-5064 | Sequence 5064, Ap |
| 31 | 39 | 76.5 | 212 | 33 | US-60-192-739-2484 | Sequence 2484, Ap |
| 32 | 39 | 76.5 | 212 | 33 | US-60-194-243-1769 | Sequence 1769, Ap |
| 33 | 39 | 76.5 | 212 | 33 | US-60-194-508-1871 | Sequence 1871, Ap |
| 34 | 39 | 76.5 | 234 | 22 | US-09-760-479-604 | Sequence 604, App |
| 35 | 39 | 76.5 | 234 | 28 | US-10-206-008-604 | Sequence 604, App |
| 36 | 39 | 76.5 | 277 | 22 | US-09-760-448A-2273 | Sequence 2273, Ap |
| 37 | 39 | 76.5 | 277 | 28 | US-10-206-664-2273 | Sequence 2273, Ap |
| 38 | 39 | 76.5 | 332 | 22 | US-09-760-446A-1676 | Sequence 1676, Ap |
| 39 | 39 | 76.5 | 392 | 28 | US-10-206-664-1676 | Sequence 1676, Ap |
| 40 | 39 | 76.5 | 412 | 27 | US-10-104-047-3475 | Sequence 3475, Ap |
| 41 | 39 | 76.5 | 530 | 33 | US-60-452-680-19149 | Sequence 19149, A |
| 42 | 39 | 76.5 | 669 | 1 | PCT-US03-28227-3972 | Sequence 3972, Ap |
| 43 | 39 | 76.5 | 691 | 22 | US-09-791-537-885 | Sequence 885, App |
| 44 | 39 | 76.5 | 695 | 1 | PCT-US03-28227-3973 | Sequence 3973, Ap |
| 45 | 39 | 76.5 | 695 | 22 | US-09-791-537-71531 | Sequence 71531, A |

ALIGNMENTS

RESULT 1
PCT-US03-00398-49
; Sequence 49, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ARGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gad
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binayam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens

PCT-US03-00398-49

Query Match 100.0%; Score 51; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSPPCS 9
 |||||
 Db 90 QOYGSPPCS 98

RESULT 2

PCT-US03-00398-225
 ; Sequence 225, Application PC/TUS0300398
 ; GENERAL INFORMATION:
 ; APPLICANT: AGENIX, INC.
 ; APPLICANT: CORVALAN, Jose, R.F.
 ; APPLICANT: JIA, Xiao-Chi
 ; APPLICANT: FENG, Xiao
 ; APPLICANT: YANG, Xiao-Dong
 ; APPLICANT: CHEN, Francine
 ; APPLICANT: GAZIT, Gadi
 ; APPLICANT: WEBER, Richard
 ; APPLICANT: BEZABEH, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
 ; FILE REFERENCE: AGENIX.051VPC
 ; CURRENT APPLICATION NUMBER: PCT/US03/00398
 ; CURRENT FILING DATE: 2003-01-06
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 225
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 PCT-US03-00398-225

Query Match 100.0%; Score 51; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSPPCS 9
 |||||
 Db 90 QOYGSPPCS 98

RESULT 3

PCT-US03-00398-259
 ; Sequence 259, Application PC/TUS0300398
 ; GENERAL INFORMATION:
 ; APPLICANT: AGENIX, INC.
 ; APPLICANT: CORVALAN, Jose, R.F.
 ; APPLICANT: JIA, Xiao-Chi
 ; APPLICANT: FENG, Xiao
 ; APPLICANT: YANG, Xiao-Dong
 ; APPLICANT: CHEN, Francine
 ; APPLICANT: GAZIT, Gadi
 ; APPLICANT: WEBER, Richard
 ; APPLICANT: BEZABEH, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
 ; FILE REFERENCE: AGENIX.051VPC
 ; CURRENT APPLICATION NUMBER: PCT/US03/00398
 ; CURRENT FILING DATE: 2003-01-06
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 259
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 PCT-US03-00398-259

Query Match 100.0%; Score 51; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSPPCS 9
 |||||
 Db 90 QOYGSPPCS 98

RESULT 4

PCT-US03-00398-375
 ; Sequence 375, Application PC/TUS0300398
 ; GENERAL INFORMATION:
 ; APPLICANT: AGENIX, INC.
 ; APPLICANT: CORVALAN, Jose, R.F.
 ; APPLICANT: JIA, Xiao-Chi
 ; APPLICANT: FENG, Xiao
 ; APPLICANT: YANG, Xiao-Dong
 ; APPLICANT: CHEN, Francine
 ; APPLICANT: GAZIT, Gadi
 ; APPLICANT: WEBER, Richard
 ; APPLICANT: BEZABEH, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
 ; FILE REFERENCE: AGENIX.051VPC
 ; CURRENT APPLICATION NUMBER: PCT/US03/00398
 ; CURRENT FILING DATE: 2003-01-06
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 375
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 PCT-US03-00398-375

Query Match 100.0%; Score 51; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSPPCS 9
 |||||
 Db 90 QOYGSPPCS 98

RESULT 5

PCT-US03-29414-4
 ; Sequence 4, Application PC/TUS0329414
 ; GENERAL INFORMATION:
 ; APPLICANT: AGENIX, INC.
 ; APPLICANT: FLOERGE, Juergen
 ; APPLICANT: GAZIT, Gadi
 ; APPLICANT: KEYI, Bruce
 ; APPLICANT: LAROCHE, William, J.
 ; APPLICANT: LICHENSTEIN, Henri
 ; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
 ; FILE REFERENCE: AGENIX.052VPC
 ; CURRENT APPLICATION NUMBER: PCT/US03/29414
 ; CURRENT FILING DATE: 2003-09-16
 ; PRIOR APPLICATION NUMBER: US 60/411,137
 ; PRIOR FILING DATE: 2002-09-16
 ; NUMBER OF SEQ ID NOS: 97
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 PCT-US03-29414-4

Query Match 100.0%; Score 51; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSPPCS 9
 |||||
 Db 90 QOYGSPPCS 98

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RESULT 6
US-10-041-860-49
; Sequence 49, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-49

Query Match      100.0%; Score 51; DB 26; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQYGSPPCS 9
Db      90 QQYGSPPCS 98

RESULT 7
US-10-041-860-225
; Sequence 225, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-225

Query Match      100.0%; Score 51; DB 26; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQYGSPPCS 9
Db      90 QQYGSPPCS 98

RESULT 8
US-10-041-860-259
; Sequence 259, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-259

Query Match      100.0%; Score 51; DB 26; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQYGSPPCS 9
Db      90 QQYGSPPCS 98

RESULT 9
US-10-041-860-375
; Sequence 375, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-375

Query Match      100.0%; Score 51; DB 26; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQYGSPPCS 9
Db      90 QQYGSPPCS 98

RESULT 10
US-10-665-383-4
; Sequence 4, Application US/10665383
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: Laroche, William
; APPLICANT: Lichenstein, Henri

```

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; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-259

Query Match      100.0%; Score 51; DB 26; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQYGSPPCS 9
Db      90 QQYGSPPCS 98

RESULT 9
US-10-041-860-375
; Sequence 375, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-375

Query Match      100.0%; Score 51; DB 26; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQYGSPPCS 9
Db      90 QQYGSPPCS 98

RESULT 10
US-10-665-383-4
; Sequence 4, Application US/10665383
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: Laroche, William
; APPLICANT: Lichenstein, Henri

```

; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
 ; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
 ; FILE REFERENCE: ABGNIX 052A
 ; CURRENT APPLICATION NUMBER: US/10/665,383
 ; CURRENT FILING DATE: 2003-09-16
 ; PRIOR APPLICATION NUMBER: 60/411,137
 ; PRIOR FILING DATE: 2002-09-16
 ; NUMBER OF SEQ ID NOS: 97
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-665-383-4

Query Match 100.0%; Score 51; DB 31; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSPCS 9
 Db 90 QOYGSSPCS 98

RESULT 11
 US-09-791-537-11779
 ; Sequence 11779, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 11779
 ; LENGTH: 100
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-791-537-11779

Query Match 94.1%; Score 48; DB 22; Length 100;
 Best Local Similarity 88.9%; Pred. No. 3.5;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSPCS 9
 Db 82 QOYGSSPCS 90

RESULT 12
 US-09-791-537-82003
 ; Sequence 82003, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 82003
 ; LENGTH: 109
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-791-537-82003

Query Match 88.2%; Score 45; DB 22; Length 109;
 Best Local Similarity 77.8%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSPCS 9
 Db 90 QOYGASPCS 98

RESULT 13
 US-09-791-537-97444
 ; Sequence 97444, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 97444
 ; LENGTH: 116
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-791-537-97444

Query Match 88.2%; Score 45; DB 22; Length 116;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSPCS 9
 Db 90 QOYGASPCS 98

RESULT 14
 US-09-791-537-11863
 ; Sequence 11863, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 11863
 ; LENGTH: 100
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-791-537-11863

Query Match 79.4%; Score 40.5; DB 22; Length 100;
 Best Local Similarity 90.0%; Pred. No. 75;
 Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QOYGSSPCS 9
 Db 81 QOYGSSPMCS 90

RESULT 15
 US-09-791-537-36703
 ; Sequence 36703, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek

```
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36703
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-36703

Query Match      78.4%; Score 40; DB 22; Length 81;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QQYGSSPCS 9
        |||||
DB      71 QQYGSSPYS 79

Search completed: April 21, 2004, 17:57:25
Job time : 134.826 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: April 21, 2004, 17:34:09 ; Search time 6.3913 Seconds
(without alignments)
39.310 Million cell updates/sec

Title: SEQ6
Perfect score: 51
Sequence: 1 qygsppc 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198209 seqs, 27915599 residues
Total number of hits satisfying chosen parameters: 198209

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New:
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3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 39 | 76.5 | 1231 | 1 | PCT-US03-34861-3 |
| 2 | 39 | 76.5 | 1242 | 1 | PCT-US03-34861-1 |
| 3 | 38 | 74.5 | 9 | 6 | US-10-663-244-32 |
| 4 | 38 | 74.5 | 9 | 6 | US-10-630-009-52 |
| 5 | 38 | 74.5 | 9 | 6 | US-10-630-009-56 |
| 6 | 38 | 74.5 | 96 | 6 | US-10-612-497A-87 |
| 7 | 38 | 74.5 | 105 | 6 | US-10-630-009-3 |
| 8 | 38 | 74.5 | 105 | 6 | US-10-630-009-7 |
| 9 | 38 | 74.5 | 108 | 1 | PCT-US03-36894-123 |
| 10 | 38 | 74.5 | 108 | 6 | US-10-663-244-9 |
| 11 | 38 | 74.5 | 109 | 1 | PCT-US03-38384A-27 |
| 12 | 38 | 74.5 | 109 | 1 | PCT-US03-38384A-28 |
| 13 | 38 | 74.5 | 109 | 1 | PCT-US03-38234A-4 |
| 14 | 38 | 74.5 | 109 | 1 | PCT-US03-38234A-6 |
| 15 | 38 | 74.5 | 109 | 1 | PCT-US03-38234A-14 |
| 16 | 38 | 74.5 | 109 | 1 | PCT-US03-38234A-210 |
| 17 | 38 | 74.5 | 109 | 6 | US-10-487-525-64 |
| 18 | 38 | 74.5 | 110 | 1 | PCT-US03-38234A-16 |
| 19 | 38 | 74.5 | 110 | 1 | PCT-US03-38234A-213 |
| 20 | 38 | 74.5 | 130 | 6 | US-10-693-629-46 |
| 21 | 38 | 74.5 | 215 | 1 | PCT-US03-36894-122 |
| 22 | 38 | 74.5 | 384 | 6 | US-10-275-027A-804 |
| 23 | 38 | 74.5 | 384 | 6 | US-10-275-027A-805 |
| 24 | 38 | 74.5 | 384 | 6 | US-10-275-027A-806 |
| 25 | 38 | 74.5 | 384 | 6 | US-10-275-027A-807 |
| 26 | 36.5 | 71.6 | 236 | 6 | US-10-800-250-34 |

| | | | | | | |
|----|------|------|-----|---|---------------------|-------------------|
| 27 | 36.5 | 71.6 | 236 | 6 | US-10-800-250-38 | Sequence 38, Appl |
| 28 | 36 | 70.6 | 209 | 6 | US-10-100-683-7250 | Sequence 7250, Ap |
| 29 | 36 | 70.6 | 591 | 7 | US-60-556-841-4272 | Sequence 4272, Ap |
| 30 | 35 | 68.6 | 8 | 6 | US-10-630-009-55 | Sequence 55, Appl |
| 31 | 35 | 68.6 | 9 | 1 | PCT-US03-38384A-132 | Sequence 132, App |
| 32 | 35 | 68.6 | 13 | 1 | PCT-US04-02881-150 | Sequence 150, App |
| 33 | 35 | 68.6 | 104 | 6 | US-10-630-009-6 | Sequence 6, Appl |
| 34 | 35 | 68.6 | 141 | 6 | US-10-612-497A-88 | Sequence 88, Appl |
| 35 | 35 | 68.6 | 142 | 6 | US-10-612-497A-19 | Sequence 19, Appl |
| 36 | 35 | 68.6 | 142 | 6 | US-10-612-497A-92 | Sequence 92, Appl |
| 37 | 35 | 68.6 | 233 | 6 | US-10-045-674A-485 | Sequence 485, App |
| 38 | 35 | 68.6 | 235 | 6 | US-10-612-497A-14 | Sequence 14, Appl |
| 39 | 35 | 68.6 | 235 | 6 | US-10-612-497A-65 | Sequence 65, Appl |
| 40 | 35 | 68.6 | 595 | 6 | US-10-491-472-11 | Sequence 11, Appl |
| 41 | 34 | 66.7 | 104 | 6 | US-10-793-479-4251 | Sequence 4251, Ap |
| 42 | 34 | 66.7 | 134 | 6 | US-10-768-952-24 | Sequence 24, Appl |
| 43 | 34 | 66.7 | 134 | 6 | US-10-767-701-34251 | Sequence 34251, A |
| 44 | 34 | 66.7 | 147 | 6 | US-10-767-701-32361 | Sequence 32361, A |
| 45 | 34 | 66.7 | 212 | 1 | PCT-US03-36894-118 | Sequence 118, App |

ALIGNMENTS

RESULT 1
PCT-US03-34861-3
; Sequence 3, Application PC/TUS0334861
; GENERAL INFORMATION:
; APPLICANT: CELL SIGNALING TECHNOLOGY, INC.
; APPLICANT: POLAKIEWICZ, Roberto
; APPLICANT: LI, Yu
; APPLICANT: WU, Jiong
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR PHOSPHORYLATED IRS-1/2 (Ser1101/Ser1149)
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CST-209 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/34861
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US 60/422,409
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 1231
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US03-34861-3

Query Match 76.5%; Score 39; DB 1; Length 1231;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QYGSPPC 8
Db 425 EYGSPPC 431
RESULT 2
PCT-US03-34861-1
; Sequence 1, Application PC/TUS0334861
; GENERAL INFORMATION:
; APPLICANT: CELL SIGNALING TECHNOLOGY, INC.
; APPLICANT: POLAKIEWICZ, Roberto
; APPLICANT: LI, Yu
; APPLICANT: WU, Jiong
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR PHOSPHORYLATED IRS-1/2 (Ser1101/Ser1149)
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CST-209 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/34861
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US 60/422,409
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.1

; SEQ ID NO 1
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-34861-1

Query Match 76.5%; Score 39; DB 1; Length 1242;
Best Local Similarity 85.7%; Pred. No. 26; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

QY 2 QYGSPPC 8
Db 430 EYGSPPC 436

RESULT 3

US-10-663-244-32
; Sequence 32, Application US/10663244
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-32

Query Match 74.5%; Score 38; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYGSPP 7
Db 1 QYGSPP 7

RESULT 4

US-10-630-009-52
; Sequence 52, Application US/10630009
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US2
; CURRENT APPLICATION NUMBER: US/10/630,009
; CURRENT FILING DATE: 2003-07-29
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-009-52

Query Match 74.5%; Score 38; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QYGSPP 7
Db 1 QYGSPP 7

RESULT 5

US-10-630-009-56
; Sequence 56, Application US/10630009
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US2
; CURRENT APPLICATION NUMBER: US/10/630,009
; CURRENT FILING DATE: 2003-07-29
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-009-56

Query Match 74.5%; Score 38; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYGSPP 7
Db 1 QYGSPP 7

RESULT 6

US-10-612-497A-87
; Sequence 87, Application US/10612497A
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLLA-4
; FILE REFERENCE: ABX-PE1
; CURRENT APPLICATION NUMBER: US/10/612,497A
; CURRENT FILING DATE: 2003-07-01
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-497A-87

Query Match 74.5%; Score 38; DB 6; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYGSPP 7
Db 90 QYGSPP 96

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RESULT 7
US-10-630-009-3
; Sequence 3, Application US/10630009
; GENERAL INFORMATION:
; APPLICANT: Burton, D.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005US2
; CURRENT APPLICATION NUMBER: US/10/630,009
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-009-3

Query Match          74.5%; Score 38; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSSP 7
Db 83 QOYGSSP 89

RESULT 8
US-10-630-009-7
; Sequence 7, Application US/10630009
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005US2
; CURRENT APPLICATION NUMBER: US/10/630,009
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-009-7

Query Match          74.5%; Score 38; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSSP 7
Db 83 QOYGSSP 89

RESULT 9
PCT-US03-36894-123
; Sequence 123, Application PC/TUS0336894
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 54 CIP PCT (1087-2 CIP PCT)
; CURRENT APPLICATION NUMBER: PCT/US03/36894

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; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 10/307,724
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 108
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antibody light chain variable region
PCT-US03-36894-123

Query Match          74.5%; Score 38; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSSP 7
Db 90 QOYGSSP 96

RESULT 10
US-10-663-244-9
; Sequence 9, Application US/10663244
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-9

Query Match          74.5%; Score 38; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSSP 7
Db 90 QOYGSSP 96

RESULT 11
PCT-US03-38384A-27
; Sequence 27, Application PC/TUS0338384A
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: OWENS, Samuel, M.
; APPLICANT: CAREOL, Frank, I.
; APPLICANT: ABRAHAM, Philip
; APPLICANT: GUNNELLS, Melinda, G.
; APPLICANT: HAAK-FRENSCHO, Mary
; APPLICANT: PENG, Xiao
; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
; FILE REFERENCE: ABGENIX.071VFC

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; CURRENT APPLICATION NUMBER: PCT/US03/38384A
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430717
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US03-38384A-27

Query Match          74.5%; Score 38; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSSP 7
Db 90 QQYGSSP 96

RESULT 12
PCT-US03-38384A-28
; Sequence 28, Application PC/TUS0338384A
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: OWENS, Samuel, M.
; APPLICANT: CARROL, Frank, I.
; APPLICANT: ABRAHAM, Philip
; APPLICANT: GUNNELL, Melinda, G.
; APPLICANT: HAAK-FRENDSCHO, Mary
; APPLICANT: FENG, Xiao
; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
; FILE REFERENCE: ABGENIX.071VPC
; CURRENT APPLICATION NUMBER: PCT/US03/38384A
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430717
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US03-38384A-28

Query Match          74.5%; Score 38; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSSP 7
Db 90 QQYGSSP 96

PCT-US03-38234A-6
; Sequence 6, Application PC/TUS0338234A
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: LEXICON GENETICS INCORPORATED
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 AND USES THEREOF
; FILE REFERENCE: ABGENIX.072VPC
; CURRENT APPLICATION NUMBER: PCT/US03/38234A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US03/38234
; PRIOR FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38234A-6

Query Match          74.5%; Score 38; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSSP 7
Db 90 QQYGSSP 96

PCT-US03-38234A-14
; Sequence 14, Application PC/TUS0338234A
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: LEXICON GENETICS INCORPORATED
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 AND USES THEREOF
; FILE REFERENCE: ABGENIX.072VPC
; CURRENT APPLICATION NUMBER: PCT/US03/38234A
; CURRENT FILING DATE: 2003-02-19

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; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US03/38234
; PRIOR FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38234A-14

Query Match 74.5%; Score 38; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGGSP 7
|||
Db 90 QQYGGSP 96

Search completed: April 21, 2004, 17:58:26
Job time : 6.3913 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:28:28 ; Search time 10.8261 Seconds
(without alignments)
42.918 Million cell updates/sec

Title: SEQ6
Perfect score: 51
Sequence: 1 qygsspc 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
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4: /cgn2_6/prodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCITUS_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 39 | 76.5 | 1155 | 1 | US-08-094-948A-29 |
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| 3 | 39 | 76.5 | 1234 | 2 | US-08-317-310A-15 |
| 4 | 39 | 76.5 | 1234 | 5 | PCT-US95-13041-15 |
| 5 | 39 | 76.5 | 1242 | 4 | US-09-508-691-1 |
| 6 | 39 | 76.5 | 1243 | 2 | US-08-557-139-2 |
| 7 | 38 | 74.5 | 9 | 2 | US-08-350-260A-503 |
| 8 | 38 | 74.5 | 9 | 3 | US-09-042-353-362 |
| 9 | 38 | 74.5 | 9 | 4 | US-08-758-417A-210 |
| 10 | 38 | 74.5 | 9 | 4 | US-09-104-337A-503 |
| 11 | 38 | 74.5 | 96 | 4 | US-09-472-087-87 |
| 12 | 38 | 74.5 | 107 | 1 | US-08-107-669D-14 |
| 13 | 38 | 74.5 | 107 | 1 | US-08-472-788A-14 |
| 14 | 38 | 74.5 | 107 | 2 | US-08-477-531B-14 |
| 15 | 38 | 74.5 | 107 | 2 | US-08-652-558-49 |
| 16 | 38 | 74.5 | 107 | 2 | US-08-082-842A-14 |
| 17 | 38 | 74.5 | 107 | 4 | US-08-635-109-7 |
| 18 | 38 | 74.5 | 108 | 1 | US-08-488-113B-150 |
| 19 | 38 | 74.5 | 108 | 1 | US-08-477-484B-150 |
| 20 | 38 | 74.5 | 108 | 2 | US-08-646-360-150 |
| 21 | 38 | 74.5 | 108 | 2 | US-08-232-081B-42 |
| 22 | 38 | 74.5 | 108 | 3 | US-08-839-765-150 |
| 23 | 38 | 74.5 | 108 | 3 | US-09-136-389-150 |
| 24 | 38 | 74.5 | 108 | 3 | US-09-240-274-178 |
| 25 | 38 | 74.5 | 108 | 4 | US-09-610-838-150 |
| 26 | 38 | 74.5 | 108 | 4 | US-09-711-485-150 |
| 27 | 38 | 74.5 | 112 | 1 | US-08-276-852-151 |

| | | | | | | |
|----|----|------|-----|---|--------------------|--------------------|
| 28 | 38 | 74.5 | 112 | 1 | US-08-899-575-151 | Sequence 151, App |
| 29 | 38 | 74.5 | 112 | 1 | US-08-899-575-151 | Sequence 151, App |
| 30 | 38 | 74.5 | 112 | 5 | PCT-US95-08743-151 | Sequence 151, App |
| 31 | 38 | 74.5 | 116 | 1 | US-08-053-131-183 | Sequence 183, App |
| 32 | 38 | 74.5 | 116 | 2 | US-08-096-762-183 | Sequence 183, App |
| 33 | 38 | 74.5 | 116 | 3 | US-09-042-353-46 | Sequence 46, Appl |
| 34 | 38 | 74.5 | 116 | 4 | US-08-758-417A-311 | Sequence 311, Appl |
| 35 | 38 | 74.5 | 150 | 3 | US-08-862-124-5 | Sequence 5, Appl1 |
| 36 | 38 | 74.5 | 226 | 4 | US-09-456-090A-38 | Sequence 38, Appl |
| 37 | 38 | 74.5 | 226 | 4 | US-09-456-090A-42 | Sequence 42, Appl |
| 38 | 38 | 74.5 | 226 | 4 | US-09-456-090A-50 | Sequence 50, Appl |
| 39 | 38 | 74.5 | 226 | 4 | US-09-456-090A-72 | Sequence 72, Appl |
| 40 | 38 | 74.5 | 226 | 4 | US-09-456-090A-74 | Sequence 74, Appl |
| 41 | 38 | 74.5 | 226 | 4 | US-09-456-090A-80 | Sequence 80, Appl |
| 42 | 38 | 74.5 | 226 | 4 | US-09-456-090A-86 | Sequence 86, Appl |
| 43 | 38 | 74.5 | 235 | 3 | US-08-812-586-16 | Sequence 16, Appl |
| 44 | 38 | 74.5 | 235 | 4 | US-09-535-832A-17 | Sequence 17, Appl |
| 45 | 38 | 74.5 | 239 | 3 | US-08-812-586-29 | Sequence 29, Appl |

ALIGNMENTS

RESULT 1
US-08-094-948A-29
; Sequence 29, Application US/08094948A
; Patent No. 5621075
; GENERAL INFORMATION:
; APPLICANT: Kahn, C. Ronald
; APPLICANT: White, Morris F.
; TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahnive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/094,948A
; FILING DATE: 21-JULY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,982
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis (PLM)
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: JDP-013DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-094-948A-29

Query Match 76.5%; Score 39; DB 1; Length 1155;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 2 QYGSSPC 8
Db 385 EYGSSPC 391

RESULT 2
PCT-US96-09319-29
; Sequence 29, Application PC/TUS9609319
; GENERAL INFORMATION:
; APPLICANT: Kahn, C. Ronald
; APPLICANT: White, Morris F.
; APPLICANT: Rothenberg, Paul Louis
; TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09319
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/094,948
; FILING DATE: 21-JULY-1993
; APPLICATION NUMBER: US 07/643,982
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis (PLM)
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: JDP-013DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-09319-29

Query Match 76.5%; Score 39; DB 5; Length 1155;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 QYGSPP 8
:|||||
Db 385 EYGSPP 391

RESULT 3
US-08-317-310A-15
; Sequence 15, Application US/08317310A
; Patent No. 5858701
; GENERAL INFORMATION:
; APPLICANT: WHITE, Morris F.
; APPLICANT: SUN, Xiao Jian
; APPLICANT: PIERCE, Jacalyn H.
; TITLE OF INVENTION: THE IRS FAMILY OF GENES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/317,310A
; FILING DATE: 03-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Louis Myers
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: JDP-022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-317-310A-15

Query Match 76.5%; Score 39; DB 2; Length 1234;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 QYGSPP 8
:|||||
Db 425 EYGSPP 431

RESULT 4
PCT-US95-13041-15
; Sequence 15, Application PC/TUS9513041
; GENERAL INFORMATION:
; APPLICANT: WHITE, Morris F.
; APPLICANT: SUN, Xiao Jian
; APPLICANT: PIERCE, Jacalyn H.
; TITLE OF INVENTION: THE IRS FAMILY OF GENES
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13041
; FILING DATE: Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/317,310
; FILING DATE: 03-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Louis Myers
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: JDP-022PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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;
; FRAGMENT TYPE: internal
; PCT-US95-13041-15
;
; Query Match 76.5%; Score 39; DB 5; Length 1234;
; Best Local Similarity 85.7%; Pred. No. 86;
; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 QYGSPPC 8
; DB 425 EYGSPPC 431
;
;
; RESULT 5
; US-09-508-691-1
; Sequence 1, Application US/09508691
; Patent No. 6498139
; GENERAL INFORMATION:
; APPLICANT: YAZAKI, YOSHIO
; APPLICANT: ASANO, TOMOICHIRO
; APPLICANT: KUBO, HIDEO
; APPLICANT: KANDA, AKIRA
; TITLE OF INVENTION: REMEDIES FOR DISEASES CAUSED BY INSULIN RESISTANCE
; FILE REFERENCE: 4895-0019-0PCT
; CURRENT APPLICATION NUMBER: US/09/508,691
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PCT/JP98/04293
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: JP9-263719
; PRIOR FILING DATE: 1997-09-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-508-691-1
;
; Query Match 76.5%; Score 39; DB 4; Length 1242;
; Best Local Similarity 85.7%; Pred. No. 86;
; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 QYGSPPC 8
; DB 430 EYGSPPC 436
;
;
; RESULT 6
; US-08-557-139-2
; Sequence 2, Application US/08557139
; Patent No. 5827730
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Oluf
; APPLICANT: Bjorbak, Christian
; APPLICANT: Frederiksen, Kathrine A.
; TITLE OF INVENTION: MUTANT DNA ENCODING INSULIN RECEPTOR
; SUBSTRATE 1
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827730 of No. 5827730 disk of No. 5827730th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,139
; FILING DATE: 12-FEB-1996
; CLASSIFICATION: 800
;
; Query Match 76.5%; Score 39; DB 2; Length 1243;
; Best Local Similarity 85.7%; Pred. No. 86;
; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 QYGSPPC 8
; DB 431 EYGSPPC 437
;
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J., 728
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4041.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-139-2
;
; Query Match 76.5%; Score 39; DB 2; Length 1243;
; Best Local Similarity 85.7%; Pred. No. 86;
; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 QYGSPPC 8
; DB 431 EYGSPPC 437
;
;
; RESULT 7
; US-08-350-260A-503
; Sequence 503, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00893
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
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/ FILING DATE: 31-MAR-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/307,619
/ FILING DATE: 16-SEP-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clough, David W
/ REGISTRATION NUMBER: 36,107
/ REFERENCE/DOCKET NUMBER: 28111/32372
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ INFORMATION FOR SEQ ID NO: 503:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-350-260A-503

Query Match 74.5%; Score 38; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSSP 7
Db 1 QQYGSSP 7

RESULT 8
US-09-042-353-362
/ Sequence 362, Application US/09042353
/ Patent No. 6255458
/ GENERAL INFORMATION:
/ APPLICANT: Lonberg, Nils
/ APPLICANT: Kay, Robert M.
/ TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
/ TITLE OF INVENTION: Producing Heterologous Antibodies
/ NUMBER OF SEQUENCES: 421
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/042,353
/ FILING DATE: 13-MAR-1998
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/810,279
/ FILING DATE: 17-DEC-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/853,408
/ FILING DATE: 18-MAR-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/904,068
/ FILING DATE: 23-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/990,860
/ FILING DATE: 16-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/053,131
/ FILING DATE: 26-APR-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/096,762
/ FILING DATE: 22-JUL-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/155,301

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/ FILING DATE: 18-NOV-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/161,739
/ FILING DATE: 03-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/165,699
/ FILING DATE: 10-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/209,741
/ FILING DATE: 09-MAR-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/352,322
/ FILING DATE: 07-DEC-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/544,404
/ FILING DATE: 10-OCT-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/728,463
/ FILING DATE: 10-OCT-1996
/ APPLICATION NUMBER: WO PCT/US96/16433
/ FILING DATE: 10-OCT-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/758,417
/ FILING DATE: 02-DEC-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/21803
/ FILING DATE: 01-DEC-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 014643-009040US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 362:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
US-09-042-353-362

Query Match 74.5%; Score 38; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSSP 7
Db 1 QQYGSSP 7

RESULT 9
US-08-758-417A-210
/ Sequence 210, Application US/08758417A
/ Patent No. 6300129
/ GENERAL INFORMATION:
/ APPLICANT: Lonberg, Nils
/ APPLICANT: Kay, Robert M.
/ TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
/ TITLE OF INVENTION: Producing Heterologous Antibodies
/ NUMBER OF SEQUENCES: 417
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 210:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 210:
US-08-758-417A-210

Query Match 74.5%; Score 38; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 1 QQYGSSP 7
| | | | |
Db 1 QQYGSSP 7

RESULT 10
US-09-104-337A-503
Sequence 503, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific binding pairs
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago

STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 503:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 503:
US-09-104-337A-503

Query Match 74.5%; Score 38; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 1 QQYGSSP 7
| | | | |
Db 1 QQYGSSP 7

RESULT 11
US-09-472-087-87
Sequence 87, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 87
LENGTH: 96
TYPE: PRT

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; ORGANISM: Homo sapiens
; US-09-472-087-87

Query Match      74.5%; Score 38; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QQYGSSP 7
Db      90 QQYGSSP 96

RESULT 12
US-08-107-669D-14
; Sequence 14, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; NAME: Michele A. Cimbala
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-107-669D-14

Query Match      74.5%; Score 38; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QQYGSSP 7
Db      89 QQYGSSP 95

RESULT 13
US-08-472-788A-14
; Sequence 14, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains

Query Match      74.5%; Score 38; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QQYGSSP 7
Db      89 QQYGSSP 95

RESULT 14
US-08-477-531B-14
; Sequence 14, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; NAME: Cimbala, Michele A.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-472-788A-14

Query Match      74.5%; Score 38; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QQYGSSP 7
Db      89 QQYGSSP 95
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Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QOYGSSP 7
Db 89 QOYGSSP 95

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QOYGSSP 7
Db 88 QOYGSSP 94

Search completed: April 21, 2004, 17:40:06
Job time : 11.8261 secs

FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 13-DEC-1991
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-531B-14

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QOYGSSP 7
Db 89 QOYGSSP 95

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QOYGSSP 7
Db 88 QOYGSSP 94

Search completed: April 21, 2004, 17:40:06
Job time : 11.8261 secs

RESULT 15
US-08-652-558-49
Sequence 49, Application US/08652558
Patent No. 5861155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QOYGSSP 7
Db 89 QOYGSSP 95

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QOYGSSP 7
Db 88 QOYGSSP 94

Search completed: April 21, 2004, 17:40:06
Job time : 11.8261 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:27:33 ; Search time 8.21739 Seconds
(without alignments)
105.353 Million cell updates/sec

Title: SEQ6
Perfect score: 51
Sequence: 1 qoygsspcs 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|----------|--------------------|
| 1 | 45 | 88.2 | 109 | 2 F30601 | Ig kappa chain V-I |
| 2 | 39 | 76.5 | 109 | 1 K3HUGO | Ig kappa chain V-I |
| 3 | 39 | 76.5 | 1231 | 2 S30185 | insulin receptor s |
| 4 | 39 | 76.5 | 1235 | 1 S16948 | insulin receptor s |
| 5 | 39 | 76.5 | 1240 | 2 JCS209 | insulin receptor s |
| 6 | 39 | 76.5 | 1242 | 2 JS0670 | alpha-2-macroglob |
| 7 | 39 | 76.5 | 4543 | 1 A53102 | Ig kappa chain V r |
| 8 | 38 | 74.5 | 54 | 2 A25521 | Ig kappa chain V r |
| 9 | 38 | 74.5 | 91 | 2 S37520 | Ig kappa chain V r |
| 10 | 38 | 74.5 | 91 | 2 S67940 | Ig kappa chain V r |
| 11 | 38 | 74.5 | 92 | 2 S37524 | Ig kappa chain V r |
| 12 | 38 | 74.5 | 92 | 2 S37513 | Ig kappa chain V r |
| 13 | 38 | 74.5 | 92 | 2 S37519 | Ig kappa chain V r |
| 14 | 38 | 74.5 | 92 | 2 S37517 | Ig kappa chain V r |
| 15 | 38 | 74.5 | 92 | 2 S37510 | Ig kappa chain V r |
| 16 | 38 | 74.5 | 92 | 2 S37518 | Ig kappa chain V r |
| 17 | 38 | 74.5 | 93 | 2 S37526 | Ig kappa chain V r |
| 18 | 38 | 74.5 | 93 | 2 S37528 | Ig kappa chain V r |
| 19 | 38 | 74.5 | 93 | 2 S37501 | Ig kappa chain V r |
| 20 | 38 | 74.5 | 96 | 2 A30601 | Ig kappa chain V-I |
| 21 | 38 | 74.5 | 108 | 1 K3HUB6 | Ig kappa chain V-I |
| 22 | 38 | 74.5 | 108 | 2 C30608 | Ig kappa chain V-I |
| 23 | 38 | 74.5 | 108 | 2 B30608 | Ig kappa chain V r |
| 24 | 38 | 74.5 | 108 | 2 H44151 | Ig kappa chain V-I |
| 25 | 38 | 74.5 | 109 | 1 K3HUSI | Ig kappa chain V-I |
| 26 | 38 | 74.5 | 109 | 1 K3HUTI | Ig kappa chain V r |
| 27 | 38 | 74.5 | 109 | 2 PH0963 | Ig kappa chain V r |
| 28 | 38 | 74.5 | 109 | 2 G30601 | Ig kappa chain V-I |
| 29 | 38 | 74.5 | 109 | 2 B30601 | Ig kappa chain V-I |

ALIGNMENTS

RESULT 1

F30601
Ig kappa chain V-III region (Neu) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C:Accession: F30601
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solor
J. Immunol. 142, 3158-3163, 1989
A:Title: Structural and idiotypic characterization of the L chains of human IgM autoantib
C:Keywords: heterotetramer; immunoglobulin
P:16-91/Domain: immunoglobulin homology <IMM>
Query Match 88.2%; Score 45; DB 2; Length 109;
Best Local Similarity 77.8%; Pred.No. 0.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

K3HUGO
Ig kappa chain V-III region (Gol) - human
N:Alternate names: rheumatoid factor
C:Species: Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
C:Accession: A01893
R:Newkirk, M.; Chen, P.P.; Carson, D.; Posnett, D.; Capra, J.D.
Mol. Immunol. 23, 239-244, 1986
A:Title: Amino acid sequence of a light chain variable region of a human rheumatoid fact
A:Reference number: A01893; MUID:86230578; PMID:3086710
A:Accession: A01893
A:Molecule type: protein
A:Residues: 1-109 <NEW>
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into lar
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:16-91/Domain: immunoglobulin homology <IMM>
P:23-89/Disulfide bonds: #status predicted

Ig kappa chain V-I
Ig kappa chain V-I
Ig kappa chain V-I
Ig kappa chain V-I
Ig kappa chain V-I
Ig kappa chain V r
Ig kappa chain - h
Ig kappa chain V-J
Ig kappa chain V-J
Ig kappa chain pre
Ig kappa chain pre
Ig kappa chain - h
Ig kappa chain pre
anti-Sm antibody V
Ig light chain var
Ig kappa chain - h

```

Query Match      76.5%; Score 39; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYGSPPCS 9
Db 90 QYGSPPCS 98

RESULT 3
S30185
insulin receptor substrate 1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S30185; S43514
R:Keller, S.R.; Aebersold, R.; Garner, C.W.; Lienhard, G.E.
Biochim. Biophys. Acta 1172, 323-326, 1993
A:Title: The insulin-elicited 160 kDa phosphotyrosine protein in mouse adipocytes is an
A:Reference number: S30185; MUID:93192326; PMID:8448209
A:Accession: S30185
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1231 <KEL>
A:Cross-references: EMBL:X59732; NID:9297913; PIDN:CAA49378.1; PID:9297914
R:Araki, E.; Haag III, B.L.; Kahn, C.R.
Biochim. Biophys. Acta 1221, 353-356, 1994
A:Title: Cloning of the mouse insulin receptor substrate-1 (IRS-1) gene and complete seq
A:Reference number: S43514; MUID:94220494; PMID:8167159
A:Accession: S43514
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1037, 'AS', 1038-1179, 'H', 1181-1231 <ARA>
A:Cross-references: EMBL:L24563; NID:9407993; PIDN:AAA39335.1; PID:9407994
C:Superfamily: Insulin receptor substrate IRS-1; pleckstrin repeat homology
F:11-113/Domain: pleckstrin repeat homology <PLK>

Query Match      76.5%; Score 39; DB 2; Length 1231;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
Db 425 EYGSPPC 431

RESULT 4
S16948
insulin receptor substrate IRS-1 - rat
N:Alternate names: insulin receptor substrate pp185
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C:Accession: S16948; A39811
R:Sun, X.J.; Rothenberg, P.; Kahn, C.R.; Backer, J.M.; Araki, E.; Wilden, P.A.; Cahill,
Nature 352, 73-77, 1991
A:Title: Structure of the insulin receptor substrate IRS-1 defines a unique signal trans
A:Reference number: S16948; MUID:91287824; PMID:1648180
A:Accession: S16948
A:Molecule type: mRNA
A:Residues: 1-1235 <SUN>
A:Cross-references: EMBL:X59375; NID:956503; PIDN:CAA41264.1; PID:956504
R:Rothenberg, P.L.; Lane, W.S.; Karasik, A.; Backer, J.; White, M.; Kahn, C.R.
J. Biol. Chem. 266, 8302-8311, 1991
A:Title: Purification and partial sequence analysis of pp185, the major cellular substra
A:Reference number: A39811; MUID:91217066; PMID:2022647
A:Accession: A39811
A:Molecule type: protein
A:Residues: 44-51; 173-178; 223-243; 489-506; 635-646; 871-882, 'I', 884, 'X', 886-888; 932-936, 'X'
A>Note: The phosphotyrosine residue was not identified
C:Comment: This protein and the beta chain of the insulin receptor itself are the major
C:Comment: Phosphorylation of this protein in response to insulin is maximal at 30 second
insulin.
C:Superfamily: insulin receptor substrate IRS-1; pleckstrin repeat homology
C:Keywords: Phosphoprotein; signal transduction

```

```

F:11-113/Domain: pleckstrin repeat homology <PLK>
F:872-891/Region: glutamine-rich

```

```

Query Match      76.5%; Score 39; DB 1; Length 1235;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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QY 2 QYGSPPC 8
Db 425 EYGSPPC 431

```

```

RESULT 5
JC5209
insulin receptor substrate 1 - chicken
C:Species: Gallus gallus (chicken)
C>Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 16-Jul-1999
C:Accession: JC5209; PC4305
R:Raouis, M.; Taylor, S.I.; Reitman, M.
Gene 178, 51-55, 1996
A:Title: Cloning of the chicken insulin receptor substrate 1 gene.
A:Reference number: JC5209; MUID:97080546; PMID:8921891
A:Accession: JC5209
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-1240 <TAO>
A:Cross-references: GB:U43502; NID:91685084; PIDN:AAC60050.1; PID:91685085
A:Accession: PC4305
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <TA2>
C:Comment: This protein acts as a docking protein and mediates multiple interactions amo
C:Genetics:
A:Gene: isr-1
C:Superfamily: insulin receptor substrate IRS-1; pleckstrin repeat homology
C:Keywords: phosphoprotein
F:11-112/Domain: pleckstrin repeat homology <PLK>
F:463,549,610,630,660,730,940,987,1010/Binding site: phosphate (Tyr) (covalent) #status :

```

```

Query Match      76.5%; Score 39; DB 2; Length 1240;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 2 QYGSPPC 8
Db 428 EYGSPPC 434

```

```

RESULT 6
JS0670
insulin receptor substrate-1 - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 23-Aug-1996 #text_change 16-Jul-1999
C:Accession: JS0670; JS0670; FN0678
R:Araki, E.; Sun, X.J.; Haag, B.L.; Chuang, L.; Zhang, Y.; Yang-Feng, T.L.; White, M.; K
Diabetes 42, 1041-1054, 1993
A:Title: Human skeletal muscle insulin receptor substrate-1. Characterization of the CDN
A:Reference number: JS0670; MUID:93292738; PMID:8513971
A:Accession: JS0670
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1242 <RS>
A:Cross-references: GB:S62539; NID:9386256; PIDN:AAB27175.1; PID:9386257
R:Nishiyama, M.; Wands, J.R.
Biochem. Biophys. Res. Commun. 183, 280-285, 1992
A:Title: Cloning and increased expression of an insulin receptor substrate-1-like gene i
A:Reference number: JS0670; MUID:92181456; PMID:1311924
A:Accession: JS0670
A:Molecule type: mRNA
A:Residues: 1-134, 'G', 135-361, 'R', 363-383, 'R', 385-1242 <NIS>
A:Cross-references: GB:S85963; NID:9246465; PIDN:AA521608.1; PID:9246466
A:Experimental source: hepatocellular carcinoma cell line FOCUS
R:Smith, L.K.; Bradshaw, M.; Croall, D.E.; Garner, C.W.

```

Biochem. Biophys. Res. Commun. 196, 767-772, 1993
 A>Title: The insulin receptor substrate (IRS-1) is a PEST protein that is susceptible to
 A:Reference number: PN0678; PMID:8240352
 A:Accession: PN0678
 A:Molecule type: protein
 A:Residues: 1-14,338-353;411-439;538-545,'V',547-567;656-697;724-758;932-943;1028-1056;1
 C:Comment: This protein appears to be the major substrate for insulin-stimulated tyrosin
 o dock various proteins containing the phosphotyrosine-binding Src-homology domain 2 (SH
 C:Comment: This protein contains at least 11 PEST regions, which suggests rapid turnover
 C:Genetics:
 A:Gene: GDB:IRSI
 A:Cross-references: GDB:133974; OMIM:147545
 A:Map position: 2q36-2q36
 A:Introns: #status absent
 C:Superfamily: insulin receptor substrate IRS-1; pleckstrin repeat homology
 C:Keywords: ATP; pleckstrin repeat homology <PLK>
 F:11-113/Domain: pleckstrin repeat homology <PLK>
 F:46,465,551,612,662,732,941,989,1012/Binding site: phosphate (Tyr) (covalent) #statu
 F:78,527,1100,1223/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #
 F:161/Binding site: ATP (Lys) #status predicted
 F:189,323,441,624,636,795,920,984,1084,1218/Binding site: phosphate (Ser) (covalent) (by
 F:300,351,774/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pre

Query Match 76.5%; Score 39; DB 2; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QVGSPP 8
 Db 430 EYGSPP 436

RESULT 7
 A53102
 Alpha-2-macroglobulin receptor precursor - chicken
 N:Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein recepto
 C:Species: Gallus gallus (chicken)
 C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 22-Jun-1999
 R:Accession: A53102
 R:Nimf, J.; Stifani, S.; Bilous, P.T.; Schneider, W.J.
 J. Biol. Chem. 269, 212-219, 1994
 A>Title: The somatic cell-specific low density lipoprotein receptor-related protein of b
 A:Reference number: A53102; PMID:94103212; PMID:7506255
 A:Accession: A53102
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-4543 <NIM>
 A:Cross-references: GB:X74904; NID:9438006; PIDN:CAAS2870.1; PID:9438007
 C:Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associat
 d protein.
 C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-3942,3943-4543/Product: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>
 F:29-66/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:117-150/Domain: EGF homology <EG1>
 F:156-190/Domain: EGF homology <EG2>
 F:200-241/Domain: LDL receptor WTD-containing repeat homology <YW01>
 F:242-283/Domain: LDL receptor WTD-containing repeat homology <YW02>
 F:294-336/Domain: LDL receptor WTD-containing repeat homology <YW03>
 F:337-380/Domain: LDL receptor WTD-containing repeat homology <YW04>
 F:381-422/Domain: LDL receptor WTD-containing repeat homology <YW05>
 F:423-470/Domain: LDL receptor WTD-containing repeat homology <YW06>
 F:480-521/Domain: LDL receptor WTD-containing repeat homology <EG3>
 F:573-615/Domain: LDL receptor WTD-containing repeat homology <YW07>
 F:616-661/Domain: LDL receptor WTD-containing repeat homology <YW08>
 F:662-712/Domain: LDL receptor WTD-containing repeat homology <YW09>
 F:713-754/Domain: LDL receptor WTD-containing repeat homology <YW10>
 F:755-797/Domain: LDL receptor WTD-containing repeat homology <YW11>
 F:805-840/Domain: EGF homology <EG4>
 F:852-888/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F:893-929/Domain: LDL receptor ligand-binding repeat homology <LDL4>
 F:934-969/Domain: LDL receptor ligand-binding repeat homology <LDL5>
 F:974-1009/Domain: LDL receptor ligand-binding repeat homology <LDL6>
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 F:1060-1095/Domain: LDL receptor ligand-binding repeat homology <LDL8>
 F:1102-1138/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:1143-1180/Domain: LDL receptor ligand-binding repeat homology <LDL10>
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 F:1846-1882/Domain: EGF homology <EG8>
 F:1930-1972/Domain: LDL receptor WTD-containing repeat homology <YW24>
 F:1973-2015/Domain: LDL receptor WTD-containing repeat homology <YW25>
 F:2016-2059/Domain: LDL receptor WTD-containing repeat homology <YW26>
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 F:2476-2511/Domain: EGF homology <EG10>
 F:2518-2555/Domain: LDL receptor ligand-binding repeat homology <LDL8>
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 F:2941-2977/Domain: EGF homology <EG11>
 F:2983-3018/Domain: EGF homology <EG12>
 F:3026-3065/Domain: LDL receptor WTD-containing repeat homology <YW34>
 F:3086-3110/Domain: LDL receptor WTD-containing repeat homology <YW35>
 F:3111-3153/Domain: LDL receptor WTD-containing repeat homology <YW36>
 F:3154-3197/Domain: LDL receptor WTD-containing repeat homology <YW37>
 F:3198-3238/Domain: LDL receptor WTD-containing repeat homology <YW38>
 F:3239-3281/Domain: LDL receptor WTD-containing repeat homology <YW39>
 F:3291-3327/Domain: EGF homology <EG13>
 F:3331-3366/Domain: LDL receptor ligand-binding repeat homology <LDL16>
 F:3371-3405/Domain: LDL receptor ligand-binding repeat homology <LDL17>
 F:3410-3445/Domain: LDL receptor ligand-binding repeat homology <LDL18>
 F:3450-3486/Domain: LDL receptor ligand-binding repeat homology <LDL19>
 F:3491-3528/Domain: LDL receptor ligand-binding repeat homology <LDL20>
 F:3533-3567/Domain: LDL receptor ligand-binding repeat homology <LDL21>
 F:3572-3606/Domain: LDL receptor ligand-binding repeat homology <LDL22>
 F:3610-3644/Domain: LDL receptor ligand-binding repeat homology <LDL23>
 F:3651-3687/Domain: LDL receptor ligand-binding repeat homology <LDL24>
 F:3692-3728/Domain: LDL receptor ligand-binding repeat homology <LDL25>
 F:3738-3774/Domain: LDL receptor ligand-binding repeat homology <LDL26>
 F:3783-3820/Domain: EGF homology <EG14>
 F:3826-3859/Domain: EGF homology <EG15>
 F:3866-3909/Domain: LDL receptor WTD-containing repeat homology <YW40>
 F:3910-3968/Domain: LDL receptor WTD-containing repeat homology <YW41>
 F:3943-4543/Domain: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>
 F:755-797/Domain: 85K chain extracellular #status predicted <EXT>
 F:3969-4011/Domain: LDL receptor WTD-containing repeat homology <YW42>
 F:4012-4055/Domain: LDL receptor WTD-containing repeat homology <YW43>

F:4056-4098/Domain: LDL receptor YWTD-containing repeat homology <YW44>
F:4099-4141/Domain: LDL receptor YWTD-containing repeat homology <YW45>
F:4150-4181/Domain: EGF homology <EG16>
F:4199-4230/Domain: EGF homology <EG17>
F:4235-4266/Domain: EGF homology <EG18>
F:4271-4302/Domain: EGF homology <EG19>
F:4307-4338/Domain: EGF homology <EG20>
F:4343-4373/Domain: EGF homology <EG21>
F:4376-4408/Domain: EGF homology <EG22>
F:4421-4443/Domain: transmembrane #status predicted <TM>
F:4444-4543/Domain: intracellular #status predicted <INT>
F:116,138,187,276,359,448,731,926,1048,1152,1193,1216,1305,1509,1556,1573,1614,1643
3485,3659,3786,3837,3952,4074,4124,4178,4278/binding site: carbohydrate (Asn) (covalent)
F:168,2995/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:2955/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

Query Match 76.5%; Score 39; DB 1; Length 4543;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQYGSSPCS 9
Db 1839 QQAGSNPCS 1847

RESULT 8

Ig kappa chain V region (321) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-May-1988 #sequence_revision 21-May-1990 #text_change 09-May-1997
C:Accession: A25521
R:Chen, P.P.; Albrandt, K.; Orida, N.K.; Radoux, V.; Chen, B.Y.; Schrantz, R.; Liu, F.T.
Proc. Natl. Acad. Sci. U.S.A. 83, 8318-8322, 1986
A:Title: Genetic basis for the cross-reactive idiotypes on the light chains of human IgM
A:Reference number: A94135; MUID:87041448; PMID:3095834
A:Accession: A25521
A:Molecule type: DNA
A:Residues: 1-54 <CHE>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSSP 7
Db 48 QQYGSSP 54

RESULT 9

Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37520
R:Klein, U.; Kueppers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37520
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <KLE>
A:Cross-references: EMBL:Z26612; NID:G405682; PIDN:CAA81365.1; PID:G405683
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSSP 7

Db 73 QQYGSSP 79

RESULT 10

Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
S67940
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C:Accession: S67940
R:Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992

A:Title: Cloning of a human autoimmune response: preparation and sequencing of a human a
A:Reference number: S67940; MUID:92314301; PMID:1617110
A:Accession: S67940
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <HEX>
A:Cross-references: EMBL:X73852
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 74.5%; Score 38; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSSP 7
Db 71 QQYGSSP 77

RESULT 11

Ig kappa chain V region (V-kappa 3) - human (fragment)
S37524
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37524
R:Klein, U.; Kueppers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37524
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26620; NID:G405690; PIDN:CAA81373.1; PID:G405691
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSSP 7
Db 73 QQYGSSP 79

RESULT 12

Ig kappa chain V region (V-kappa 3) - human (fragment)
S37513
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37513
R:Klein, U.; Kueppers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37513
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26598; NID:G405668; PIDN:CAA81352.1; PID:G405669
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGGSSP 7
| | | | |
Db 73 QOYGGSSP 79

RESULT 13

IG kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37519
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26613; NID:G405680; PIDN:CAA81366.1; PID:G405681
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGGSSP 7
| | | | |
Db 73 QOYGGSSP 79

RESULT 14

IG kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37517
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37517
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26615; NID:G405676; PIDN:CAA81368.1; PID:G405677
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGGSSP 7
| | | | |
Db 73 QOYGGSSP 79

RESULT 15

IG kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37510
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993

A;Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37510
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26601; NID:G405662; PIDN:CAA81355.1; PID:G405663
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGGSSP 7
| | | | |
Db 73 QOYGGSSP 79

Search completed: April 21, 2004, 17:38:30
Job time : 8.21739 secs